

# Sven Nahnsen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4490384/publications.pdf>

Version: 2024-02-01

42  
papers

3,558  
citations

304602

22  
h-index

289141

40  
g-index

51  
all docs

51  
docs citations

51  
times ranked

6305  
citing authors

#	ARTICLE	IF	CITATIONS
1	nf-core/mag: a best-practice pipeline for metagenome hybrid assembly and binning. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac007.	1.5	24
2	A data management infrastructure for the integration of imaging and omics data in life sciences. <i>BMC Bioinformatics</i> , 2022, 23, 61.	1.2	18
3	ODGI: understanding pangenome graphs. <i>Bioinformatics</i> , 2022, 38, 3319-3326.	1.8	44
4	Genetic evolution of <i>in situ</i> follicular neoplasia to aggressive B-cell lymphoma of germinal center subtype. <i>Haematologica</i> , 2021, 106, 2673-2681.	1.7	21
5	Transcriptome Profiling Identifies TIGIT as a Marker of T Cell Exhaustion in Liver Cancer. <i>Hepatology</i> , 2021, 73, 1399-1418.	3.6	61
6	Sustainable data analysis with Snakemake. <i>F1000Research</i> , 2021, 10, 33.	0.8	188
7	Swarm Learning for decentralized and confidential clinical machine learning. <i>Nature</i> , 2021, 594, 265-270.	13.7	375
8	Absence of Non-Canonical, Inhibitory MYD88 Splice Variants in B Cell Lymphomas Correlates With Sustained NF- $\kappa$ B Signaling. <i>Frontiers in Immunology</i> , 2021, 12, 616451.	2.2	8
9	Downregulation of TGR5 (GPBAR1) in biliary epithelial cells contributes to the pathogenesis of sclerosing cholangitis. <i>Journal of Hepatology</i> , 2021, 75, 634-646.	1.8	51
10	Experimental glioma with high bHLH expression harbor increased replicative stress and are sensitive toward ATR inhibition. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa115.	0.4	2
11	Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. <i>Frontiers in Microbiology</i> , 2020, 11, 550420.	1.5	113
12	Specific Induction of Double Negative B Cells During Protective and Pathogenic Immune Responses. <i>Frontiers in Immunology</i> , 2020, 11, 606338.	2.2	42
13	Clinical and Genetic Tumor Characteristics of Responding and Non-Responding Patients to PD-1 Inhibition in Hepatocellular Carcinoma. <i>Cancers</i> , 2020, 12, 3830.	1.7	47
14	Ten simple rules for providing effective bioinformatics research support. <i>PLoS Computational Biology</i> , 2020, 16, e1007531.	1.5	15
15	The nf-core framework for community-curated bioinformatics pipelines. <i>Nature Biotechnology</i> , 2020, 38, 276-278.	9.4	963
16	Contribution of mTOR and PTEN to Radioresistance in Sporadic and NF2-Associated Vestibular Schwannomas: A Microarray and Pathway Analysis. <i>Cancers</i> , 2020, 12, 177.	1.7	13
17	Challenges of big data integration in the life sciences. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 6791-6800.	1.9	22
18	Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. <i>Genome Medicine</i> , 2019, 11, 28.	3.6	107

#	ARTICLE	IF	CITATIONS
19	Ring1b-dependent epigenetic remodelling is an essential prerequisite for pancreatic carcinogenesis. <i>Gut</i> , 2019, 68, 2007-2018.	6.1	27
20	Measles Virus-Based Treatments Trigger a Pro-inflammatory Cascade and a Distinctive Immunopeptidome in Glioblastoma. <i>Molecular Therapy - Oncolytics</i> , 2019, 12, 147-161.	2.0	38
21	CSIG-15. INHIBITION OF THE bHLH TRANSCRIPTIONAL NETWORKS BY A MUTATED E47 PROTEIN LEADS TO A STRONG ANTI-GLIOMA ACTIVITY IN VITRO AND IN VIVO. <i>Neuro-Oncology</i> , 2019, 21, vi47-vi47.	0.6	0
22	Potent Antitumor Activity of Liposomal Irinotecan in an Organoid- and CRISPR-Cas9-Based Murine Model of Gallbladder Cancer. <i>Cancers</i> , 2019, 11, 1904.	1.7	11
23	The Draft Whole-Genome Sequence of the Antibiotic Producer <i>Empedobacter haloabium</i> ATCC 31962 Provides Indications for Its Taxonomic Reclassification. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
24	Interactive Visualization for Large-Scale Multi-factorial Research Designs. <i>Lecture Notes in Computer Science</i> , 2019, , 75-84.	1.0	1
25	Proteome and phosphoproteome analysis of commensally induced dendritic cell maturation states. <i>Journal of Proteomics</i> , 2018, 180, 11-24.	1.2	6
26	The impact of winter feed type on intestinal microbiota and parasites in honey bees. <i>Apidologie</i> , 2018, 49, 252-264.	0.9	25
27	qPortal: A platform for data-driven biomedical research. <i>PLoS ONE</i> , 2018, 13, e0191603.	1.1	18
28	Personalized peptide vaccine-induced immune response associated with long-term survival of a metastatic cholangiocarcinoma patient. <i>Journal of Hepatology</i> , 2016, 65, 849-855.	1.8	75
29	Platforms and Pipelines for Proteomics Data Analysis and Management. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 203-215.	0.8	14
30	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	9.0	537
31	Mass-Spectrometry-Based Proteomics Reveals Organ-Specific Expression Patterns To Be Used as Forensic Evidence. <i>Journal of Proteome Research</i> , 2016, 15, 182-192.	1.8	19
32	Interdisciplinary management of central nervous system metastasis and neoplastic meningitis: recent developments and future perspectives. <i>Journal of Cancer Metastasis and Treatment</i> , 2016, 2, 163.	0.5	0
33	Intuitive Web-Based Experimental Design for High-Throughput Biomedical Data. <i>BioMed Research International</i> , 2015, 2015, 1-8.	0.9	3
34	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
35	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644.	1.8	146
36	Tools for Label-free Peptide Quantification. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 549-556.	2.5	198

#	ARTICLE	IF	CITATIONS
37	PTMeta: Increasing identification rates of modified peptides using modification prescanning and meta-analysis. <i>Proteomics</i> , 2013, 13, 1042-1051.	1.3	5
38	In silico design of targeted SRM-based experiments. <i>BMC Bioinformatics</i> , 2012, 13, S8.	1.2	9
39	Probabilistic Consensus Scoring Improves Tandem Mass Spectrometry Peptide Identification. <i>Journal of Proteome Research</i> , 2011, 10, 3332-3343.	1.8	45
40	Mass spectrometry at the interface of proteomics and genomics. <i>Molecular BioSystems</i> , 2011, 7, 284-291.	2.9	36
41	Suppression of Casein Kinase 1 $\beta$ in Melanoma Cells Induces a Switch in $\beta$ -Catenin Signaling to Promote Metastasis. <i>Cancer Research</i> , 2010, 70, 6999-7009.	0.4	77
42	Optimal de novo Design of MRM Experiments for Rapid Assay Development in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 2696-2704.	1.8	40