

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

304743
22
h-index

289244
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. NAR Genomics and Bioinformatics, 2022, 4, lqac007. | 3.2 | 24 |
| 2 | A data management infrastructure for the integration of imaging and omics data in life sciences. BMC Bioinformatics, 2022, 23, 61. | 2.6 | 18 |
| 3 | ODGI: understanding pangenome graphs. Bioinformatics, 2022, 38, 3319-3326. | 4.1 | 44 |
| 4 | Genetic evolution of <i>in situ</i> follicular neoplasia to aggressive B-cell lymphoma of germinal center subtype. Haematologica, 2021, 106, 2673-2681. | 3.5 | 21 |
| 5 | Transcriptome Profiling Identifies TIGIT as a Marker of T Cell Exhaustion in Liver Cancer. Hepatology, 2021, 73, 1399-1418. | 7.3 | 61 |
| 6 | Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33. | 1.6 | 188 |
| 7 | Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270. | 27.8 | 375 |
| 8 | Absence of Non-Canonical, Inhibitory MYD88 Splice Variants in B Cell Lymphomas Correlates With Sustained NF- κ B Signaling. Frontiers in Immunology, 2021, 12, 616451. | 4.8 | 8 |
| 9 | Downregulation of TGR5 (GPBAR1) in biliary epithelial cells contributes to the pathogenesis of sclerosing cholangitis. Journal of Hepatology, 2021, 75, 634-646. | 3.7 | 51 |
| 10 | Experimental glioma with high bHLH expression harbor increased replicative stress and are sensitive toward ATR inhibition. Neuro-Oncology Advances, 2020, 2, vdaa115. | 0.7 | 2 |
| 11 | Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. Frontiers in Microbiology, 2020, 11, 550420. | 3.5 | 113 |
| 12 | Specific Induction of Double Negative B Cells During Protective and Pathogenic Immune Responses. Frontiers in Immunology, 2020, 11, 606338. | 4.8 | 42 |
| 13 | Clinical and Genetic Tumor Characteristics of Responding and Non-Responding Patients to PD-1 Inhibition in Hepatocellular Carcinoma. Cancers, 2020, 12, 3830. | 3.7 | 47 |
| 14 | Ten simple rules for providing effective bioinformatics research support. PLoS Computational Biology, 2020, 16, e1007531. | 3.2 | 15 |
| 15 | The nf-core framework for community-curated bioinformatics pipelines. Nature Biotechnology, 2020, 38, 276-278. | 17.5 | 963 |
| 16 | Contribution of mTOR and PTEN to Radioresistance in Sporadic and NF2-Associated Vestibular Schwannomas: A Microarray and Pathway Analysis. Cancers, 2020, 12, 177. | 3.7 | 13 |
| 17 | Challenges of big data integration in the life sciences. Analytical and Bioanalytical Chemistry, 2019, 411, 6791-6800. | 3.7 | 22 |
| 18 | Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. Genome Medicine, 2019, 11, 28. | 8.2 | 107 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Ring1b-dependent epigenetic remodelling is an essential prerequisite for pancreatic carcinogenesis. Gut, 2019, 68, 2007-2018. | 12.1 | 27 |
| 20 | Measles Virus-Based Treatments Trigger a Pro-inflammatory Cascade and a Distinctive Immunopeptidome in Glioblastoma. Molecular Therapy - Oncolytics, 2019, 12, 147-161. | 4.4 | 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. Neuro-Oncology, 2019, 21, vi47-vi47. | 1.2 | 0 |
| 22 | Potent Antitumor Activity of Liposomal Irinotecan in an Organoid- and CRISPR-Cas9-Based Murine Model of Gallbladder Cancer. Cancers, 2019, 11, 1904. | 3.7 | 11 |
| 23 | The Draft Whole-Genome Sequence of the Antibiotic Producer Empedobacter haloabium ATCC 31962 Provides Indications for Its Taxonomic Reclassification. Microbiology Resource Announcements, 2019, 8, . | 0.6 | 4 |
| 24 | Interactive Visualization for Large-Scale Multi-factorial Research Designs. Lecture Notes in Computer Science, 2019, , 75-84. | 1.3 | 1 |
| 25 | Proteome and phosphoproteome analysis of commensally induced dendritic cell maturation states. Journal of Proteomics, 2018, 180, 11-24. | 2.4 | 6 |
| 26 | The impact of winter feed type on intestinal microbiota and parasites in honey bees. Apidologie, 2018, 49, 252-264. | 2.0 | 25 |
| 27 | qPortal: A platform for data-driven biomedical research. PLoS ONE, 2018, 13, e0191603. | 2.5 | 18 |
| 28 | Personalized peptide vaccine-induced immune response associated with long-term survival of a metastatic cholangiocarcinoma patient. Journal of Hepatology, 2016, 65, 849-855. | 3.7 | 75 |
| 29 | Platforms and Pipelines for Proteomics Data Analysis and Management. Advances in Experimental Medicine and Biology, 2016, 919, 203-215. | 1.6 | 14 |
| 30 | OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748. | 19.0 | 537 |
| 31 | Mass-Spectrometry-Based Proteomics Reveals Organ-Specific Expression Patterns To Be Used as Forensic Evidence. Journal of Proteome Research, 2016, 15, 182-192. | 3.7 | 19 |
| 32 | Interdisciplinary management of central nervous system metastasis and neoplastic meningitis: recent developments and future perspectives. Journal of Cancer Metastasis and Treatment, 2016, 2, 163. | 0.8 | 0 |
| 33 | Intuitive Web-Based Experimental Design for High-Throughput Biomedical Data. BioMed Research International, 2015, 2015, 1-8. | 1.9 | 3 |
| 34 | qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913. | 3.8 | 42 |
| 35 | An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. Journal of Proteome Research, 2013, 12, 1628-1644. | 3.7 | 146 |
| 36 | Tools for Label-free Peptide Quantification. Molecular and Cellular Proteomics, 2013, 12, 549-556. | 3.8 | 198 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | PTMeta: Increasing identification rates of modified peptides using modification prescanning and meta-analysis. Proteomics, 2013, 13, 1042-1051. | 2.2 | 5 |
| 38 | In silico design of targeted SRM-based experiments. BMC Bioinformatics, 2012, 13, S8. | 2.6 | 9 |
| 39 | Probabilistic Consensus Scoring Improves Tandem Mass Spectrometry Peptide Identification. Journal of Proteome Research, 2011, 10, 3332-3343. | 3.7 | 45 |
| 40 | Mass spectrometry at the interface of proteomics and genomics. Molecular BioSystems, 2011, 7, 284-291. | 2.9 | 36 |
| 41 | Suppression of Casein Kinase 1 β in Melanoma Cells Induces a Switch in β -Catenin Signaling to Promote Metastasis. Cancer Research, 2010, 70, 6999-7009. | 0.9 | 77 |
| 42 | Optimal de novo Design of MRM Experiments for Rapid Assay Development in Targeted Proteomics. Journal of Proteome Research, 2010, 9, 2696-2704. | 3.7 | 40 |