

# Saskia D Hiltemann

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9001868/publications.pdf>

Version: 2024-02-01

23  
papers

3,624  
citations

759233

12  
h-index

642732

23  
g-index

26  
all docs

26  
docs citations

26  
times ranked

7718  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W537-W544.	14.5	3,003
2	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018, 6, 752-758.e1.	6.2	141
3	CGtag: complete genomics toolkit and annotation in a cloud-based Galaxy. <i>GigaScience</i> , 2014, 3, 1.	6.4	97
4	Discriminating somatic and germline mutations in tumor DNA samples without matching normals. <i>Genome Research</i> , 2015, 25, 1382-1390.	5.5	66
5	Comparison of Illumina versus Nanopore 16S rRNA Gene Sequencing of the Human Nasal Microbiota. <i>Genes</i> , 2020, 11, 1105.	2.4	49
6	Galactic Circos: User-friendly Circos plots within the Galaxy platform. <i>GigaScience</i> , 2020, 9, .	6.4	32
7	Gene fusions by chromothripsis of chromosome 5q in the VCaP prostate cancer cell line. <i>Human Genetics</i> , 2013, 132, 709-713.	3.8	31
8	ImmunoGlobulin galaxy (IGGalaxy) for simple determination and quantitation of immunoglobulin heavy chain rearrangements from NGS. <i>BMC Immunology</i> , 2014, 15, 59.	2.2	30
9	ASaiM: a Galaxy-based framework to analyze microbiota data. <i>GigaScience</i> , 2018, 7, .	6.4	25
10	NanoGalaxy: Nanopore long-read sequencing data analysis in Galaxy. <i>GigaScience</i> , 2020, 9, .	6.4	23
11	Huvariome: a web server resource of whole genome next-generation sequencing allelic frequencies to aid in pathological candidate gene selection. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 19.	1.2	20
12	Galaxy mothur Toolset (GmT): a user-friendly application for 16S rRNA gene sequencing analysis using mothur. <i>GigaScience</i> , 2019, 8, .	6.4	17
13	Fostering accessible online education using Galaxy as an e-learning platform. <i>PLoS Computational Biology</i> , 2021, 17, e1008923.	3.2	15
14	Development and evaluation of a culture-free microbiota profiling platform (MYcrobiota) for clinical diagnostics. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1081-1089.	2.9	13
15	iFUSE: integrated fusion gene explorer. <i>Bioinformatics</i> , 2013, 29, 1700-1701.	4.1	9
16	Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data. <i>F1000Research</i> , 2017, 6, 1488.	1.6	8
17	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	8
18	FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. <i>Scientific Data</i> , 2022, 9, 169.	5.3	8

#	ARTICLE	IF	CITATIONS
19	Integration of EGA secure data access into Galaxy. F1000Research, 2016, 5, 2841.	1.6	7
20	iReport: a generalised Galaxy solution for integrated experimental reporting. GigaScience, 2014, 3, 19.	6.4	5
21	FuMa: reporting overlap in RNA-seq detected fusion genes. Bioinformatics, 2016, 32, 1226-1228.	4.1	4
22	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	1
23	The diagnostic value of nasal microbiota and clinical parameters in a multi-parametric prediction model to differentiate bacterial versus viral infections in lower respiratory tract infections. PLoS ONE, 2022, 17, e0267140.	2.5	1