

# Gisela Gabernet

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/980996/publications.pdf>

Version: 2024-02-01

19  
papers

676  
citations

623574

14  
h-index

839398

18  
g-index

23  
all docs

23  
docs citations

23  
times ranked

935  
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	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
4	Next Generation Sequencing of Cerebrospinal Fluid B Cell Repertoires in Multiple Sclerosis and Other Neuro-Inflammatory Diseases—A Comprehensive Review. <i>Diagnostics</i> , 2021, 11, 1871.	1.3	2
5	Morphing of Amphipathic Helices to Explore the Activity and Selectivity of Membranolytic Antimicrobial Peptides. <i>Biochemistry</i> , 2020, 59, 3772-3781.	1.2	4
6	Specific Induction of Double Negative B Cells During Protective and Pathogenic Immune Responses. <i>Frontiers in Immunology</i> , 2020, 11, 606338.	2.2	42
7	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
8	In silico design and optimization of selective membranolytic anticancer peptides. <i>Scientific Reports</i> , 2019, 9, 11282.	1.6	40
9	De novo design of anticancer peptides by ensemble artificial neural networks. <i>Journal of Molecular Modeling</i> , 2019, 25, 112.	0.8	36
10	Simulated Molecular Evolution for Anticancer Peptide Design. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 1674-1678.	7.2	20
11	Simulated Molecular Evolution for Anticancer Peptide Design. <i>Angewandte Chemie</i> , 2019, 131, 1688-1692.	1.6	0
12	Designing Anticancer Peptides by Constructive Machine Learning. <i>ChemMedChem</i> , 2018, 13, 1300-1302.	1.6	67
13	Hybrid Network Model for “Deep Learning” of Chemical Data: Application to Antimicrobial Peptides. <i>Molecular Informatics</i> , 2017, 36, 1600011.	1.4	39
14	modLAMP: Python for antimicrobial peptides. <i>Bioinformatics</i> , 2017, 33, 2753-2755.	1.8	106
15	Characterisation of anticancer peptides at the single-cell level. <i>Lab on A Chip</i> , 2017, 17, 2933-2940.	3.1	26
16	Sparse Neural Network Models of Antimicrobial Peptide–Activity Relationships. <i>Molecular Informatics</i> , 2016, 35, 606-614.	1.4	15
17	Membranolytic anticancer peptides. <i>MedChemComm</i> , 2016, 7, 2232-2245.	3.5	68
18	De Novo Fragment Design for Drug Discovery and Chemical Biology. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15079-15083.	7.2	30

#	ARTICLE	IF	CITATIONS
19	Apoptotic DNA Degradation into Oligonucleosomal Fragments, but Not Apoptotic Nuclear Morphology, Relies on a Cytosolic Pool of DFF40/CAD Endonuclease. <i>Journal of Biological Chemistry</i> , 2012, 287, 7766-7779.	1.6	28