

# 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  | modLAMP: Python for antimicrobial peptides. <i>Bioinformatics</i> , 2017, 33, 2753-2755.  | 1.8 | 106       |
| 2  | Membranolytic anticancer peptides. <i>MedChemComm</i> , 2016, 7, 2232-2245.   | 3.5 | 68        |
| 3  | Designing Anticancer Peptides by Constructive Machine Learning. <i>ChemMedChem</i> , 2018, 13, 1300-1302.   | 1.6 | 67        |
| 4  | 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        |
| 5  | 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        |
| 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  | In silico design and optimization of selective membranolytic anticancer peptides. <i>Scientific Reports</i> , 2019, 9, 11282.   | 1.6 | 40        |
| 8  | Hybrid Network Model for "Deep Learning" of Chemical Data: Application to Antimicrobial Peptides. <i>Molecular Informatics</i> , 2017, 36, 1600011.   | 1.4 | 39        |
| 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 | De Novo Fragment Design for Drug Discovery and Chemical Biology. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15079-15083.  | 7.2 | 30        |
| 11 | 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        |
| 12 | Characterisation of anticancer peptides at the single-cell level. <i>Lab on A Chip</i> , 2017, 17, 2933-2940.   | 3.1 | 26        |
| 13 | 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        |
| 14 | Simulated Molecular Evolution for Anticancer Peptide Design. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 1674-1678.  | 7.2 | 20        |
| 15 | 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        |
| 16 | Sparse Neural Network Models of Antimicrobial Peptide-Activity Relationships. <i>Molecular Informatics</i> , 2016, 35, 606-614.   | 1.4 | 15        |
| 17 | Morphing of Amphipathic Helices to Explore the Activity and Selectivity of Membranolytic Antimicrobial Peptides. <i>Biochemistry</i> , 2020, 59, 3772-3781.   | 1.2 | 4         |
| 18 | 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         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Simulated Molecular Evolution for Anticancer Peptide Design. <i>Angewandte Chemie</i> , 2019, 131, 1688-1692. | 1.6 | 0         |