

# Guilhem Faure

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2172990/publications.pdf>

Version: 2024-02-01

33  
papers

2,479  
citations

257450

24  
h-index

395702

33  
g-index

37  
all docs

37  
docs citations

37  
times ranked

4100  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape. <i>MBio</i> , 2022, 13, e0013522.	4.1	35
2	Human pathogenic RNA viruses establish noncompeting lineages by occupying independent niches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	9
3	Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021, 34, 108873.	6.4	76
4	Dual modes of CRISPR-associated transposon homing. <i>Cell</i> , 2021, 184, 2441-2453.e18.	28.9	86
5	Ongoing global and regional adaptive evolution of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	196
6	Cargo Genes of Tn <i>7</i> -Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. <i>MBio</i> , 2021, 12, e0293821.	4.1	34
7	Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing. <i>New England Journal of Medicine</i> , 2020, 383, 1492-1494.	27.0	506
8	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15193-15199.	7.1	196
9	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. <i>Frontiers in Microbiology</i> , 2020, 11, 381.	3.5	6
10	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	3.1	45
11	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019, 10, 4006.	12.8	45
12	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019, 14, 3013-3031.	12.0	21
13	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019, 17, 513-525.	28.6	205
14	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. <i>Source Code for Biology and Medicine</i> , 2019, 14, 5.	1.7	14
15	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019, 431, 3-20.	4.2	73
16	Discovery and Evolution of New Domains in Yeast Heterochromatin Factor Sir4 and Its Partner Esc1. <i>Genome Biology and Evolution</i> , 2019, 11, 572-585.	2.5	7
17	Adaptation of mRNA structure to control protein folding. <i>RNA Biology</i> , 2017, 14, 1649-1654.	3.1	23
18	Role of mRNA structure in the control of protein folding. <i>Nucleic Acids Research</i> , 2016, 44, 10898-10911.	14.5	99

#	ARTICLE	IF	CITATIONS
19	Protein flexibility in the light of structural alphabets. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 20.	3.5	71
20	Universal distribution of mutational effects on protein stability, uncoupling of protein robustness from sequence evolution and distinct evolutionary modes of prokaryotic and eukaryotic proteins. <i>Physical Biology</i> , 2015, 12, 035001.	1.8	27
21	Sumoylation of Human Argonaute 2 at Lysine-402 Regulates Its Stability. <i>PLoS ONE</i> , 2014, 9, e102957.	2.5	31
22	The C-terminal extension of human RTEL1, mutated in Hoyerall-Hreidarsson syndrome, contains Harmonin-like domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 897-903.	2.6	31
23	Expanding the SRI domain family: A common scaffold for binding the phosphorylated C-terminal domain of RNA polymerase II. <i>FEBS Letters</i> , 2014, 588, 4431-4437.	2.8	19
24	Identification of hidden relationships from the coupling of Hydrophobic Cluster Analysis and Domain Architecture information. <i>Bioinformatics</i> , 2013, 29, 1726-1733.	4.1	29
25	Comprehensive Repertoire of Foldable Regions within Whole Genomes. <i>PLoS Computational Biology</i> , 2013, 9, e1003280.	3.2	38
26	InterEvScore: a novel coarse-grained interface scoring function using a multi-body statistical potential coupled to evolution. <i>Bioinformatics</i> , 2013, 29, 1742-1749.	4.1	79
27	InterEvol database: exploring the structure and evolution of protein complex interfaces. <i>Nucleic Acids Research</i> , 2012, 40, D847-D856.	14.5	47
28	Versatility and Invariance in the Evolution of Homologous Heteromeric Interfaces. <i>PLoS Computational Biology</i> , 2012, 8, e1002677.	3.2	42
29	Structural characterization of filaments formed by human Xrcc4-Cernunnos/XLF complex involved in nonhomologous DNA end-joining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12663-12668.	7.1	126
30	Detection of novel recombinases in bacteriophage genomes unveils Rad52, Rad51 and Gp2.5 remote homologs. <i>Nucleic Acids Research</i> , 2010, 38, 3952-3962.	14.5	117
31	Delineation of the Xrcc4-interacting Region in the Globular Head Domain of Cernunnos/XLF. <i>Journal of Biological Chemistry</i> , 2010, 285, 26475-26483.	3.4	44
32	Analysis of protein contacts into Protein Units. <i>Biochimie</i> , 2009, 91, 876-887.	2.6	15
33	Protein contacts, inter-residue interactions and side-chain modelling. <i>Biochimie</i> , 2008, 90, 626-639.	2.6	55