

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	Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing. <i>New England Journal of Medicine</i> , 2020, 383, 1492-1494.	27.0	506
2	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019, 17, 513-525.	28.6	205
3	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
4	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
5	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
6	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
7	Role of mRNA structure in the control of protein folding. <i>Nucleic Acids Research</i> , 2016, 44, 10898-10911.	14.5	99
8	Dual modes of CRISPR-associated transposon homing. <i>Cell</i> , 2021, 184, 2441-2453.e18.	28.9	86
9	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
10	Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021, 34, 108873.	6.4	76
11	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019, 431, 3-20.	4.2	73
12	Protein flexibility in the light of structural alphabets. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 20.	3.5	71
13	Protein contacts, inter-residue interactions and side-chain modelling. <i>Biochimie</i> , 2008, 90, 626-639.	2.6	55
14	InterEvol database: exploring the structure and evolution of protein complex interfaces. <i>Nucleic Acids Research</i> , 2012, 40, D847-D856.	14.5	47
15	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
16	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019, 10, 4006.	12.8	45
17	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
18	Versatility and Invariance in the Evolution of Homologous Heteromeric Interfaces. <i>PLoS Computational Biology</i> , 2012, 8, e1002677.	3.2	42

#	ARTICLE	IF	CITATIONS
19	Comprehensive Repertoire of Foldable Regions within Whole Genomes. PLoS Computational Biology, 2013, 9, e1003280.	3.2	38
20	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape. MBio, 2022, 13, e0013522.	4.1	35
21	Cargo Genes of Tn <i>7</i> -Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. MBio, 2021, 12, e0293821.	4.1	34
22	Sumoylation of Human Argonaute 2 at Lysine-402 Regulates Its Stability. PLoS ONE, 2014, 9, e102957.	2.5	31
23	The C-terminal extension of human RTEL1, mutated in HoyeraaalâHreidarsson syndrome, contains HarmoninâNlike domains. Proteins: Structure, Function and Bioinformatics, 2014, 82, 897-903.	2.6	31
24	Identification of hidden relationships from the coupling of Hydrophobic Cluster Analysis and Domain Architecture information. Bioinformatics, 2013, 29, 1726-1733.	4.1	29
25	Universal distribution of mutational effects on protein stability, uncoupling of protein robustness from sequence evolution and distinct evolutionary modes of prokaryotic and eukaryotic proteins. Physical Biology, 2015, 12, 035001.	1.8	27
26	Adaptation of mRNA structure to control protein folding. RNA Biology, 2017, 14, 1649-1654.	3.1	23
27	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. Nature Protocols, 2019, 14, 3013-3031.	12.0	21
28	Expanding the SRI domain family: A common scaffold for binding the phosphorylated C-terminal domain of RNA polymerase II. FEBS Letters, 2014, 588, 4431-4437.	2.8	19
29	Analysis of protein contacts into Protein Units. Biochimie, 2009, 91, 876-887.	2.6	15
30	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. Source Code for Biology and Medicine, 2019, 14, 5.	1.7	14
31	Human pathogenic RNA viruses establish noncompeting lineages by occupying independent niches. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
32	Discovery and Evolution of New Domains in Yeast Heterochromatin Factor Sir4 and Its Partner Esc1. Genome Biology and Evolution, 2019, 11, 572-585.	2.5	7
33	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. Frontiers in Microbiology, 2020, 11, 381.	3.5	6