

Francesco Strozzi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5671990/publications.pdf>

Version: 2024-02-01

21
papers

8,758
citations

623734

14
h-index

794594

19
g-index

23
all docs

23
docs citations

23
times ranked

16270
citing authors

#	ARTICLE	IF	CITATIONS
1	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	17.5	628
2	GeneMark-HM: improving gene prediction in DNA sequences of human microbiome. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab047.	3.2	4
3	Second asymptomatic carotid surgery trial (ACST-2): a randomised comparison of carotid artery stenting versus carotid endarterectomy. <i>Lancet, The</i> , 2021, 398, 1065-1073.	13.7	133
4	Antimicrobial Resistance Profiles of Adherent Invasive <i>Escherichia coli</i> Show Increased Resistance to β -Lactams. <i>Antibiotics</i> , 2020, 9, 251.	3.7	9
5	Scalable Workflows and Reproducible Data Analysis for Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 723-745.	0.9	25
6	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	10.3	218
7	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	5.7	50
8	Abstract 1475: Microbiome derived peptides stimulate strong immune response against tumor associated antigens and trigger in vivo tumor regression after vaccination. , 2019, , .		0
9	The ruminal microbiome associated with methane emissions from ruminant livestock. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 7.	5.3	246
10	Johne's disease in cattle: an in vitro model to study early response to infection of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> using RNA-seq. <i>Molecular Immunology</i> , 2017, 91, 259-271.	2.2	23
11	Pipengine: an ultra light YAML-based pipeline execution engine. <i>Journal of Open Source Software</i> , 2017, 2, 341.	4.6	1
12	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. <i>Oncotarget</i> , 2016, 7, 14814-14830.	1.8	79
13	A new primer set for DNA metabarcoding of soil Metazoa. <i>European Journal of Soil Biology</i> , 2016, 77, 53-59.	3.2	24
14	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	42
15	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. <i>PLoS ONE</i> , 2014, 9, e90574.	2.5	86
16	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
17	Transcript profiling of common bean nodules subjected to oxidative stress. <i>Physiologia Plantarum</i> , 2013, 149, 389-407.	5.2	8
18	Sprints, Hackathons and Codefests as community gluons in computational biology. <i>EMBnet Journal</i> , 2013, 19, 40.	0.6	5

#	ARTICLE	IF	CITATIONS
19	Meta-Analysis of Two Genome-Wide Association Studies of Bovine Paratuberculosis. PLoS ONE, 2012, 7, e32578.	2.5	49
20	Genetic Loci Involved in Antibody Response to Mycobacterium avium ssp. paratuberculosis in Cattle. PLoS ONE, 2010, 5, e11117.	2.5	54
21	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0