# Francesco Strozzi

List of Publications by Year
in descending order

| 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 | De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. Nature Protocols, 2013, 8, 1494-1512. | 12.0 | 7,054 |
| 2 | A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114. | 17.5 | 628 |
| 3 | The ruminal microbiome associated with methane emissions from ruminant livestock. Journal of Animal Science and Biotechnology, 2017, 8, 7. | 5.3 | 246 |
| 4 | A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances, 2019, 5, eaav8391. | 10.3 | 218 |
| 5 | Second asymptomatic carotid surgery trial (ACST-2): a randomised comparison of carotid artery stenting versus carotid endarterectomy. Lancet, The, 2021, 398, 1065-1073. | 13.7 | 133 |
| 6 | A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. PLoS ONE, 2014, 9, e90574. | 2.5 | 86 |
| 7 | Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. Oncotarget, 2016, 7, 14814-14830. | 1.8 | 79 |
| 8 | Genetic Loci Involved in Antibody Response to Mycobacterium avium ssp. paratuberculosis in Cattle. PLoS ONE, 2010, 5, e11117. | 2.5 | 54 |
| 9 | Exome sequences and multi‐environment field trials elucidate the genetic basis of adaptation in barley. Plant Journal, 2019, 99, 1172-1191. | 5.7 | 50 |
| 10 | Meta-Analysis of Two Genome-Wide Association Studies of Bovine Paratuberculosis. PLoS ONE, 2012, 7, e32578. | 2.5 | 49 |
| 11 | Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7. | 2.6 | 42 |
| 12 | Scalable Workflows and Reproducible Data Analysis for Genomics. Methods in Molecular Biology, 2019, 1910, 723-745. | 0.9 | 25 |
| 13 | A new primer set for DNA metabarcoding of soil Metazoa. European Journal of Soil Biology, 2016, 77, 53-59. | 3.2 | 24 |
| 14 | Johne's disease in cattle: an in vitro model to study early response to infection of Mycobacterium avium subsp. paratuberculosis using RNA-seq.. Molecular Immunology, 2017, 91, 259-271. | 2.2 | 23 |
| 15 | Antimicrobial Resistance Profiles of Adherent Invasive Escherichia coli Show Increased Resistance to β-Lactams. Antibiotics, 2020, 9, 251. | 3.7 | 9 |
| 16 | Transcript profiling of common bean nodules subjected to oxidative stress. Physiologia Plantarum, 2013, 149, 389-407. | 5.2 | 8 |
| 17 | Sprints, Hackathons and Codefests as community gluons in computational biology. EMBnet Journal, 2013, 19, 40. | 0.6 | 5 |
| 18 | GeneMark-HM: improving gene prediction in DNA sequences of human microbiome. NAR Genomics and Bioinformatics, 2021, 3, lqab047. | 3.2 | 4 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 19 | Pipengine: an ultra light YAML-based pipeline execution engine. Journal of Open Source Software, 2017, 2, 341. | 4.6 | 1 |
| 20 | Abstract 1475: Microbiome derived peptides stimulate strong immune response against tumor associated antigens and trigger in vivo tumor regression after vaccination. , 2019, , . | | 0 |
| 21 | BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677. | 1.6 | 0 |