

Clelia Peano

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

8,371
citations

117453

34
h-index

56606

83
g-index

98
all docs

98
docs citations

98
times ranked

14929
citing authors

#	ARTICLE	IF	CITATIONS
1	A "Multiomic" Approach of Saliva Metabolomics, Microbiota, and Serum Biomarkers to Assess the Need of Hospitalization in Coronavirus Disease 2019. , 2022, 1, 194-209.		11
2	Lipid-loaded tumor-associated macrophages sustain tumor growth and invasiveness in prostate cancer. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	53
3	Side-by-side comparison of next-generation sequencing, cytology, and histology in diagnosing locally advanced pancreatic adenocarcinoma. <i>Gastrointestinal Endoscopy</i> , 2021, 93, 597-604.e5.	0.5	22
4	Macrophage expression and prognostic significance of the long pentraxin PTX3 in COVID-19. <i>Nature Immunology</i> , 2021, 22, 19-24.	7.0	101
5	Gut Microbiota Functional Dysbiosis Relates to Individual Diet in Subclinical Carotid Atherosclerosis. <i>Nutrients</i> , 2021, 13, 304.	1.7	16
6	Complement activation promoted by the lectin pathway mediates C3aR-dependent sarcoma progression and immunosuppression. <i>Nature Cancer</i> , 2021, 2, 218-232.	5.7	34
7	Mutated clones driving leukemic transformation are already detectable at the single-cell level in CD34-positive cells in the chronic phase of primary myelofibrosis. <i>Npj Precision Oncology</i> , 2021, 5, 4.	2.3	10
8	Single-keratinocyte transcriptomic analyses identify different clonal types and proliferative potential mediated by FOXM1 in human epidermal stem cells. <i>Nature Communications</i> , 2021, 12, 2505.	5.8	31
9	Mitochondrial oxidative metabolism contributes to a cancer stem cell phenotype in cholangiocarcinoma. <i>Journal of Hepatology</i> , 2021, 74, 1373-1385.	1.8	60
10	Single-cell profiling identifies impaired adaptive NK cells expanded after HCMV reactivation in haploidentical HSCT. <i>JCI Insight</i> , 2021, 6, .	2.3	19
11	Clinical relevance of clonal hematopoiesis in persons aged ≥80 years. <i>Blood</i> , 2021, 138, 2093-2105.	0.6	37
12	Interplay between Non-Coding RNA Transcription, Stringent/Relaxed Phenotype and Antibiotic Production in <i>Streptomyces ambofaciens</i> . <i>Antibiotics</i> , 2021, 10, 947.	1.5	4
13	The <i>Helicobacter pylori</i> CagY Protein Drives Gastric Th1 and Th17 Inflammation and B Cell Proliferation in Gastric MALT Lymphoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9459.	1.8	14
14	Single-cell profiling defines the prognostic benefit of CD39 ^{high} tissue resident memory CD8 ⁺ T cells in luminal-like breast cancer. <i>Communications Biology</i> , 2021, 4, 1117.	2.0	11
15	PBX1-directed stem cell transcriptional program drives tumor progression in myeloproliferative neoplasm. <i>Stem Cell Reports</i> , 2021, 16, 2607-2616.	2.3	8
16	Prenatal interleukin 6 elevation increases glutamatergic synapse density and disrupts hippocampal connectivity in offspring. <i>Immunity</i> , 2021, 54, 2611-2631.e8.	6.6	63
17	Two subsets of stem-like CD8 ⁺ memory T cell progenitors with distinct fate commitments in humans. <i>Nature Immunology</i> , 2020, 21, 1552-1562.	7.0	167
18	GATA Factor-Mediated Gene Regulation in Human Erythropoiesis. <i>IScience</i> , 2020, 23, 101018.	1.9	11

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19	Defining the <i>Helicobacter pylori</i> Disease-Specific Antigenic Repertoire. <i>Frontiers in Microbiology</i> , 2020, 11, 1551.	1.5	6
20	InteractomeSeq: a web server for the identification and profiling of domains and epitopes from phage display and next generation sequencing data. <i>Nucleic Acids Research</i> , 2020, 48, W200-W207.	6.5	7
21	Behçet's Disease Under Microbiotic Surveillance? A Combined Analysis of Two Cohorts of Behçet's Disease Patients. <i>Frontiers in Immunology</i> , 2020, 11, 1192.	2.2	28
22	Global characterization of tumor infiltrate of Intrahepatic Cholangiocarcinoma by single cell sequencing. <i>Digestive and Liver Disease</i> , 2020, 52, e48-e49.	0.4	0
23	Mitochondrial oxidative metabolism contributes to maintain a cancer stem cell phenotype in cholangiocarcinoma. <i>Digestive and Liver Disease</i> , 2020, 52, e47.	0.4	0
24	Macrophage morphology correlates with single-cell diversity and prognosis in colorectal liver metastasis. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	99
25	IRF4 instructs effector Treg differentiation and immune suppression in human cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 3137-3150.	3.9	103
26	High-dimensional single cell-based immune profiling of the tumor immune microenvironment in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2020, 38, 376-376.	0.8	0
27	3073 " PBX1 GENETIC ABLATION INHIBITS TUMOR GROWTH IN A MOUSE MODEL OF MYELOPROLIFERATIVE NEOPLASM. <i>Experimental Hematology</i> , 2020, 88, S60-S61.	0.2	0
28	Neutrophils Driving Unconventional T Cells Mediate Resistance against Murine Sarcomas and Selected Human Tumors. <i>Cell</i> , 2019, 178, 346-360.e24.	13.5	176
29	Single-Cell Sequencing of Mouse Heart Immune Infiltrate in Pressure Overload-Driven Heart Failure Reveals Extent of Immune Activation. <i>Circulation</i> , 2019, 140, 2089-2107.	1.6	212
30	<i>Helicobacter pylori</i> Stress-Response: Definition of the HrcA Regulon. <i>Microorganisms</i> , 2019, 7, 436.	1.6	11
31	Transcriptome Analysis of Reticulated Platelets Reveals a Prothrombotic Profile. <i>Thrombosis and Haemostasis</i> , 2019, 119, 1795-1806.	1.8	54
32	The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. <i>FASEB Journal</i> , 2019, 33, 13572-13589.	0.2	20
33	RhoTermPredict: an algorithm for predicting Rho-dependent transcription terminators based on <i>Escherichia coli</i> , <i>Bacillus subtilis</i> and <i>Salmonella enterica</i> databases. <i>BMC Bioinformatics</i> , 2019, 20, 117.	1.2	32
34	CXCR3 Identifies Human Naive CD8+ T Cells with Enhanced Effector Differentiation Potential. <i>Journal of Immunology</i> , 2019, 203, 3179-3189.	0.4	34
35	RNA Sequencing and Analysis in Microorganisms for Metabolic Network Reconstruction. <i>Methods in Molecular Biology</i> , 2018, 1716, 239-265.	0.4	5
36	Mutation and Suppressor Analysis of the Essential Lipopolysaccharide Transport Protein LptA Reveals Strategies To Overcome Severe Outer Membrane Permeability Defects in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	36

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37	<i>Pseudomonas aeruginosa</i> mutants defective in glucose uptake have pleiotropic phenotype and altered virulence in non-mammal infection models. <i>Scientific Reports</i> , 2018, 8, 16912.	1.6	23
38	Interactome-Seq: A Protocol for Domainome Library Construction, Validation and Selection by Phage Display and Next Generation Sequencing. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	5
39	The <i>Helicobacter pylori</i> Heat-Shock Repressor HspR: Definition of Its Direct Regulon and Characterization of the Cooperative DNA-Binding Mechanism on Its Own Promoter. <i>Frontiers in Microbiology</i> , 2018, 9, 1887.	1.5	9
40	Pirin: A novel redox-sensitive modulator of primary and secondary metabolism in <i>Streptomyces</i> . <i>Metabolic Engineering</i> , 2018, 48, 254-268.	3.6	29
41	G4PromFinder: an algorithm for predicting transcription promoters in GC-rich bacterial genomes based on AT-rich elements and G-quadruplex motifs. <i>BMC Bioinformatics</i> , 2018, 19, 36.	1.2	30
42	Clinical Relevance of Clonal Hematopoiesis in the Oldest-Old Population: Analysis of the "Health and Anemia" Study. <i>Blood</i> , 2018, 132, 750-750.	0.6	2
43	Colonization with <i>Helicobacter</i> is concomitant with modified gut microbiota and drastic failure of the immune control of <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , 2017, 10, 1178-1189.	2.7	46
44	Comprehensive mapping of the <i>Helicobacter pylori</i> NikR regulon provides new insights in bacterial nickel responses. <i>Scientific Reports</i> , 2017, 7, 45458.	1.6	35
45	WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes. <i>Nucleic Acids Research</i> , 2017, 45, W109-W115.	6.5	16
46	Temporal dynamics of the gut microbiota in people sharing a confined environment, a 520-day ground-based space simulation, MARS500. <i>Microbiome</i> , 2017, 5, 39.	4.9	89
47	Insight into the essential role of the <i>Helicobacter pylori</i> HP1043 orphan response regulator: genome-wide identification and characterization of the DNA-binding sites. <i>Scientific Reports</i> , 2017, 7, 41063.	1.6	34
48	Retroviral Scanning: Mapping MLV Integration Sites to Define Cell-specific Regulatory Regions. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	0
49	Time-Resolved Transcriptomics and Constraint-Based Modeling Identify System-Level Metabolic Features and Overexpression Targets to Increase Spiramycin Production in <i>Streptomyces ambofaciens</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 835.	1.5	14
50	Enterocyte-Associated Microbiome of the Hadza Hunter-Gatherers. <i>Frontiers in Microbiology</i> , 2016, 7, 865.	1.5	17
51	The Lack of the Essential LptC Protein in the Trans-Envelope Lipopolysaccharide Transport Machine Is Circumvented by Suppressor Mutations in LptF, an Inner Membrane Component of the <i>Escherichia coli</i> Transporter. <i>PLoS ONE</i> , 2016, 11, e0161354.	1.1	26
52	Modulation of gut microbiota dysbioses in type 2 diabetic patients by macrobiotic Ma-Pi 2 diet. <i>British Journal of Nutrition</i> , 2016, 116, 80-93.	1.2	181
53	Dynamic Transcriptional and Epigenetic Regulation of Human Epidermal Keratinocyte Differentiation. <i>Stem Cell Reports</i> , 2016, 6, 618-632.	2.3	55
54	Glucose availability enhances lipopolysaccharide production and immunogenicity in the opportunistic pathogen <i>Acinetobacter baumannii</i> . <i>Future Microbiology</i> , 2016, 11, 335-349.	1.0	14

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55	Transcriptional, epigenetic and retroviral signatures identify regulatory regions involved in hematopoietic lineage commitment. <i>Scientific Reports</i> , 2016, 6, 24724.	1.6	18
56	The bottlenose dolphin (<i>Tursiops truncatus</i>) faecal microbiota. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw055.	1.3	38
57	The Typhoid Toxin Promotes Host Survival and the Establishment of a Persistent Asymptomatic Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005528.	2.1	60
58	Selecting soluble/foldable protein domains through single-gene or genomic ORF filtering: structure of the head domain of <i>Burkholderia pseudomallei</i> antigen BPSL2063. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2227-2235.	2.5	15
59	Characterization of the <i>Escherichia coli</i> λ S core regulon by Chromatin Immunoprecipitation-sequencing (ChIP-seq) analysis. <i>Scientific Reports</i> , 2015, 5, 10469.	1.6	52
60	Behçet's syndrome patients exhibit specific microbiome signature. <i>Autoimmunity Reviews</i> , 2015, 14, 269-276.	2.5	195
61	Gut microbiota trajectory in pediatric patients undergoing hematopoietic SCT. <i>Bone Marrow Transplantation</i> , 2015, 50, 992-998.	1.3	111
62	Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota. <i>Current Biology</i> , 2015, 25, 1682-1693.	1.8	342
63	The <i>Dlx5</i> and <i>Foxg1</i> transcription factors, linked via miRNA-9 and -200, are required for the development of the olfactory and GnRH system. <i>Molecular and Cellular Neurosciences</i> , 2015, 68, 103-119.	1.0	51
64	Identification of novel proteins binding the AU-rich element of β -prothymosin mRNA through the selection of open reading frames (RIDome). <i>RNA Biology</i> , 2015, 12, 1289-1300.	1.5	5
65	Genome-Wide Definition of Promoter and Enhancer Usage during Neural Induction of Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2015, 10, e0126590.	1.1	4
66	A Genomic, Transcriptomic and Proteomic Look at the GE2270 Producer <i>Planobispora rosea</i> , an Uncommon Actinomycete. <i>PLoS ONE</i> , 2015, 10, e0133705.	1.1	14
67	Gene and Protein Expression in Response to Different Growth Temperatures and Oxygen Availability in <i>Burkholderia thailandensis</i> . <i>PLoS ONE</i> , 2014, 9, e93009.	1.1	31
68	Gut Microbiome in Down Syndrome. <i>PLoS ONE</i> , 2014, 9, e112023.	1.1	51
69	Gut microbiome of the Hadza hunter-gatherers. <i>Nature Communications</i> , 2014, 5, 3654.	5.8	1,067
70	Tet-Trap, a genetic approach to the identification of bacterial RNA thermometers: application to <i>Pseudomonas aeruginosa</i> . <i>Rna</i> , 2014, 20, 1963-1976.	1.6	32
71	Comparative genomics revealed key molecular targets to rapidly convert a reference rifamycin-producing bacterial strain into an overproducer by genetic engineering. <i>Metabolic Engineering</i> , 2014, 26, 1-16.	3.6	29
72	An efficient rRNA removal method for RNA sequencing in GC-rich bacteria. <i>Microbial Informatics and Experimentation</i> , 2013, 3, 1.	7.6	44

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73	Profiling, Bioinformatic, and Functional Data on the Developing Olfactory/GnRH System Reveal Cellular and Molecular Pathways Essential for This Process and Potentially Relevant for the Kallmann Syndrome. <i>Frontiers in Endocrinology</i> , 2013, 4, 203.	1.5	9
74	The Enterocyte-Associated Intestinal Microbiota of Breast-Fed Infants and Adults Responds Differently to a TNF- α -Mediated Pro-Inflammatory Stimulus. <i>PLoS ONE</i> , 2013, 8, e81762.	1.1	19
75	Array Platform for Food Safety and Quality. , 2012, , 13-56.		1
76	Comparative genomics and transcriptional profiles of <i>Saccharopolyspora erythraea</i> NRRL 2338 and a classically improved erythromycin over-producing strain. <i>Microbial Cell Factories</i> , 2012, 11, 32.	1.9	36
77	Diversity of Bifidobacteria within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	1.1	512
78	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
79	In vitro transcription profiling of the σ^S subunit of bacterial RNA polymerase: re-definition of the σ^S regulon and identification of σ^S -specific promoter sequence elements. <i>Nucleic Acids Research</i> , 2011, 39, 5338-5355.	6.5	80
80	A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets $\hat{=}$. <i>Nucleic Acids Research</i> , 2009, 37, 5057-5070.	6.5	27
81	Phenotypes and gene expression profiles of <i>Saccharopolyspora erythraea</i> rifampicin-resistant (rif) mutants affected in erythromycin production. <i>Microbial Cell Factories</i> , 2009, 8, 18.	1.9	45
82	Methods for detection of GMOs in food and feed. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 392, 369-384.	1.9	138
83	Genome-wide screening of copy number alterations and LOH events in renal cell carcinomas and integration with gene expression profile. <i>Molecular Cancer</i> , 2008, 7, 6.	7.9	67
84	Complete gene expression profiling of <i>Saccharopolyspora erythraea</i> using GeneChip DNA microarrays. <i>Microbial Cell Factories</i> , 2007, 6, 37.	1.9	25
85	Strategies for comparing gene expression profiles from different microarray platforms: Application to a case $\hat{=}$ control experiment. <i>Analytical Biochemistry</i> , 2006, 353, 43-56.	1.1	40
86	Transcriptome amplification methods in gene expression profiling. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 465-480.	1.5	23
87	Development of a peptide nucleic acid polymerase chain reaction clamping assay for semiquantitative evaluation of genetically modified organism content in food. <i>Analytical Biochemistry</i> , 2005, 344, 174-182.	1.1	23
88	Multiplex polymerase chain reaction and ligation detection reaction/universal array technology for the traceability of genetically modified organisms in foods. <i>Analytical Biochemistry</i> , 2005, 346, 90-100.	1.1	52
89	Qualitative and Quantitative Evaluation of the Genomic DNA Extracted from GMO and Non-GMO Foodstuffs with Four Different Extraction Methods. <i>Journal of Agricultural and Food Chemistry</i> , 2004, 52, 6962-6968.	2.4	114
90	Advanced PCR techniques in identifying food components. , 2003, , 3-33.		15

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91	Clinical Relevance of Clonal Hematopoiesis in the Oldest-Old Population. SSRN Electronic Journal, 0, , .	0.4	0