

Julia A Segre

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/890193/publications.pdf>

Version: 2024-02-01

87
papers

21,919
citations

38742

50
h-index

54911

84
g-index

88
all docs

88
docs citations

88
times ranked

21236
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifts in the Skin Bacterial and Fungal Communities of Healthy Children Transitioning through Puberty. <i>Journal of Investigative Dermatology</i> , 2022, 142, 212-219.	0.7	29
2	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant Enterobacteriaceae. <i>Microbiome</i> , 2022, 10, 43.	11.1	8
3	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. <i>Nature Microbiology</i> , 2022, 7, 169-179.	13.3	58
4	Long-term antibiotic exposure promotes mortality after systemic fungal infection by driving lymphocyte dysfunction and systemic escape of commensal bacteria. <i>Cell Host and Microbe</i> , 2022, 30, 1020-1033.e6.	11.0	37
5	Cutaneous T-Cell Lymphoma Skin Microbiome Is Characterized by Shifts in Certain Commensal Bacteria but not Viruses when Compared with Healthy Controls. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1604-1608.	0.7	21
6	Murine model of colonization with fungal pathogen <i>Candida auris</i> to explore skin tropism, host risk factors and therapeutic strategies. <i>Cell Host and Microbe</i> , 2021, 29, 210-221.e6.	11.0	52
7	Infection trains the host for microbiota-enhanced resistance to pathogens. <i>Cell</i> , 2021, 184, 615-627.e17.	28.9	148
8	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. <i>Nature Protocols</i> , 2021, 16, 2520-2541.	12.0	25
9	Integrated genomic, epidemiologic investigation of <i>Candida auris</i> skin colonization in a skilled nursing facility. <i>Nature Medicine</i> , 2021, 27, 1401-1409.	30.7	73
10	Skin Metagenomic Sequence Analysis of Early <i>Candida auris</i> Outbreaks in U.S. Nursing Homes. <i>MSphere</i> , 2021, 6, e0028721.	2.9	20
11	Treatment of Relapsing HPV Diseases by Restored Function of Natural Killer Cells. <i>New England Journal of Medicine</i> , 2021, 385, 921-929.	27.0	22
12	Disruption of the endopeptidase ADAM10-Notch signaling axis leads to skin dysbiosis and innate lymphoid cell-mediated hair follicle destruction. <i>Immunity</i> , 2021, 54, 2321-2337.e10.	14.3	35
13	Alterations of human skin microbiome and expansion of antimicrobial resistance after systemic antibiotics. <i>Science Translational Medicine</i> , 2021, 13, eabd8077.	12.4	38
14	A <i>Cutibacterium acnes</i> antibiotic modulates human skin microbiota composition in hair follicles. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	83
15	Cultivating fungal research. <i>Science</i> , 2020, 368, 365-366.	12.6	23
16	Preventing dysbiosis of the neonatal mouse intestinal microbiome protects against late-onset sepsis. <i>Nature Medicine</i> , 2019, 25, 1772-1782.	30.7	91
17	Plasmid Dissemination and Selection of a Multidrug-Resistant <i>Klebsiella pneumoniae</i> Strain during Transplant-Associated Antibiotic Therapy. <i>MBio</i> , 2019, 10, .	4.1	14
18	Responsible stewardship for communicating microbiome research to the press and public. <i>Nature Medicine</i> , 2019, 25, 872-874.	30.7	14

#	ARTICLE	IF	CITATIONS
19	Resistin-like Molecule $\hat{\pm}$ Provides Vitamin-A-Dependent Antimicrobial Protection in the Skin. <i>Cell Host and Microbe</i> , 2019, 25, 777-788.e8.	11.0	60
20	Editorial overview: Frontiers in microbiome studies: viewing vast vistas with roadmap in hand. <i>Current Opinion in Microbiology</i> , 2019, 50, iii-iv.	5.1	0
21	Injury, dysbiosis, and filaggrin deficiency drive skin inflammation through keratinocyte IL-1 $\hat{\pm}$ release. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1426-1443.e6.	2.9	56
22	Genomic Analysis of Hospital Plumbing Reveals Diverse Reservoir of Bacterial Plasmids Conferring Carbapenem Resistance. <i>MBio</i> , 2018, 9, .	4.1	155
23	The human skin microbiome. <i>Nature Reviews Microbiology</i> , 2018, 16, 143-155.	28.6	1,576
24	Expanded skin virome in DOCK8-deficient patients. <i>Nature Medicine</i> , 2018, 24, 1815-1821.	30.7	104
25	Investigation of a Cluster of <i>Sphingomonas koreensis</i> Infections. <i>New England Journal of Medicine</i> , 2018, 379, 2529-2539.	27.0	42
26	Emollient use alters skin barrier and microbes in infants at risk for developing atopic dermatitis. <i>PLoS ONE</i> , 2018, 13, e0192443.	2.5	95
27	Human defects in STAT3 promote oral mucosal fungal and bacterial dysbiosis. <i>JCI Insight</i> , 2018, 3, .	5.0	50
28	Performing Skin Microbiome Research: A Method to the Madness. <i>Journal of Investigative Dermatology</i> , 2017, 137, 561-568.	0.7	164
29	Building a Translational Microbiome Toolbox. <i>Cell</i> , 2017, 169, 378-380.	28.9	16
30	The Molecular Revolution in Cutaneous Biology: Investigating the Skin's Microbiome. <i>Journal of Investigative Dermatology</i> , 2017, 137, e119-e122.	0.7	39
31	Ectopic colonization of oral bacteria in the intestine drives T _H 1 cell induction and inflammation. <i>Science</i> , 2017, 358, 359-365.	12.6	612
32	<i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> strain diversity underlying pediatric atopic dermatitis. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	406
33	Whole-Genome Sequencing Overrules a Suspected Case of Carbapenem-Resistant <i>Enterobacter cloacae</i> Transmission. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2868-2870.	3.9	5
34	Skin microbiome before development of atopic dermatitis: Early colonization with commensal staphylococci at 2 months is associated with a lower risk of atopic dermatitis at 1 year. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 166-172.	2.9	276
35	Temporal Stability of the Human Skin Microbiome. <i>Cell</i> , 2016, 165, 854-866.	28.9	721
36	Diverse Human Skin Fungal Communities in Children Converge in Adulthood. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2356-2363.	0.7	107

#	ARTICLE	IF	CITATIONS
37	Complete Genome Sequence of a <i>Klebsiella pneumoniae</i> Strain Carrying <i>bla</i> _{NDM-1} on a Multidrug Resistance Plasmid. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
38	Hominid superorganisms. <i>Science</i> , 2016, 353, 350-351.	12.6	7
39	Adapting Koch's postulates. <i>Science</i> , 2016, 351, 224-226.	12.6	151
40	Resolving the Complexity of Human Skin Metagenomes Using Single-Molecule Sequencing. <i>MBio</i> , 2016, 7, e01948-15.	4.1	78
41	Detection and Whole-Genome Sequencing of Carbapenemase-Producing <i>Aeromonas hydrophila</i> Isolates from Routine Perirectal Surveillance Culture. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1167-1170.	3.9	30
42	Draft Genome Sequence of a <i>Klebsiella pneumoniae</i> Carbapenemase-Positive Sequence Type 111 <i>Pseudomonas aeruginosa</i> Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
43	Signaling in Host-Associated Microbial Communities. <i>Cell</i> , 2016, 164, 1288-1300.	28.9	130
44	Plasmid Dynamics in KPC-Positive <i>Klebsiella pneumoniae</i> during Long-Term Patient Colonization. <i>MBio</i> , 2016, 7, .	4.1	126
45	Elucidating microbial codes to distinguish individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6778-6779.	7.1	6
46	Commensal dendritic-cell interaction specifies a unique protective skin immune signature. <i>Nature</i> , 2015, 520, 104-108.	27.8	610
47	Integrating host gene expression and the microbiome to explore disease pathogenesis. <i>Genome Biology</i> , 2015, 16, 70.	8.8	6
48	Bringing Up Baby to Tolerate Germs. <i>Immunity</i> , 2015, 43, 842-844.	14.3	5
49	Complete Genome Sequence of a <i>Klebsiella pneumoniae</i> Isolate with Chromosomally Encoded Carbapenem Resistance and Colibactin Synthesis Loci. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
50	Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae. <i>Science Translational Medicine</i> , 2014, 6, 254ra126.	12.4	307
51	Dialogue between skin microbiota and immunity. <i>Science</i> , 2014, 346, 954-959.	12.6	500
52	Biogeography and individuality shape function in the human skin metagenome. <i>Nature</i> , 2014, 514, 59-64.	27.8	869
53	Meeting report for the 1st skin microbiota workshop, boulder, CO October 15-16 2012. <i>Standards in Genomic Sciences</i> , 2014, 9, .	1.5	0
54	The altered landscape of the human skin microbiome in patients with primary immunodeficiencies. <i>Genome Research</i> , 2013, 23, 2103-2114.	5.5	236

#	ARTICLE	IF	CITATIONS
55	The Neuropathic Diabetic Foot Ulcer Microbiome Is Associated With Clinical Factors. <i>Diabetes</i> , 2013, 62, 923-930.	0.6	249
56	Topographic diversity of fungal and bacterial communities in human skin. <i>Nature</i> , 2013, 498, 367-370.	27.8	950
57	What Does It Take to Satisfy Koch's Postulates Two Centuries Later?: Microbial Genomics and <i>Propionibacteria acnes</i> . <i>Journal of Investigative Dermatology</i> , 2013, 133, 2141-2142.	0.7	39
58	Pan-PCR, a Computational Method for Designing Bacterium-Typing Assays Based on Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2013, 51, 752-758.	3.9	23
59	<i>Staphylococcus epidermidis</i> pan-genome sequence analysis reveals diversity of skin commensal and hospital infection-associated isolates. <i>Genome Biology</i> , 2012, 13, R64.	9.6	206
60	Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 148ra116.	12.4	781
61	Temporal shifts in the skin microbiome associated with disease flares and treatment in children with atopic dermatitis. <i>Genome Research</i> , 2012, 22, 850-859.	5.5	1,401
62	Species-Level Analysis of DNA Sequence Data from the NIH Human Microbiome Project. <i>PLoS ONE</i> , 2012, 7, e47075.	2.5	151
63	Shifts in human skin and nares microbiota of healthy children and adults. <i>Genome Medicine</i> , 2012, 4, 77.	8.2	304
64	Compartmentalized Control of Skin Immunity by Resident Commensals. <i>Science</i> , 2012, 337, 1115-1119.	12.6	895
65	The Human Microbiome: Our Second Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 151-170.	6.2	498
66	Skin Microbiome: Looking Back to Move Forward. <i>Journal of Investigative Dermatology</i> , 2012, 132, 933-939.	0.7	274
67	Interaction of the Microbiome with the Innate Immune Response in Chronic Wounds. <i>Advances in Experimental Medicine and Biology</i> , 2012, 946, 55-68.	1.6	101
68	The skin microbiome. <i>Nature Reviews Microbiology</i> , 2011, 9, 244-253.	28.6	2,404
69	Bridging the Translational Research Gap: A Successful Partnership Involving a Physician and a Basic Scientist. <i>Journal of Investigative Dermatology</i> , 2010, 130, 1478-1480.	0.7	11
70	A milieu of regulatory elements in the epidermal differentiation complex syntenic block: implications for atopic dermatitis and psoriasis. <i>Human Molecular Genetics</i> , 2010, 19, 1453-1460.	2.9	92
71	Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14799-14804.	7.1	189
72	Matriptase-Deficient Mice Exhibit Ichthyotic Skin with a Selective Shift in Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2009, 129, 2435-2442.	0.7	60

#	ARTICLE	IF	CITATIONS
73	Topographical and Temporal Diversity of the Human Skin Microbiome. <i>Science</i> , 2009, 324, 1190-1192.	12.6	2,280
74	A diversity profile of the human skin microbiota. <i>Genome Research</i> , 2008, 18, 1043-1050.	5.5	818
75	Autosomal Ichthyosis with Hypotrichosis Syndrome Displays Low Matriptase Proteolytic Activity and Is Phenocopied in ST14 Hypomorphic Mice. <i>Journal of Biological Chemistry</i> , 2007, 282, 36714-36723.	3.4	92
76	Strain-dependent perinatal lethality of <i>Ovol1</i> -deficient mice and identification of <i>Ovol2</i> as a downstream target of <i>Ovol1</i> in skin epidermis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2007, 1772, 89-95.	3.8	57
77	Epidermal Differentiation Complex Yields a Secret: Mutations in the Cornification Protein Filaggrin Underlie Ichthyosis Vulgaris. <i>Journal of Investigative Dermatology</i> , 2006, 126, 1202-1204.	0.7	26
78	Lipid defect underlies selective skin barrier impairment of an epidermal-specific deletion of <i>Gata-3</i> . <i>Journal of Cell Biology</i> , 2006, 175, 661-670.	5.2	80
79	<i>Klf4</i> and corticosteroids activate an overlapping set of transcriptional targets to accelerate in utero epidermal barrier acquisition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18668-18673.	7.1	66
80	<i>Connexin 26</i> regulates epidermal barrier and wound remodeling and promotes psoriasiform response. <i>Journal of Clinical Investigation</i> , 2006, 116, 1243-1253.	8.2	109
81	Epidermal barrier formation and recovery in skin disorders. <i>Journal of Clinical Investigation</i> , 2006, 116, 1150-1158.	8.2	406
82	Long-range comparison of human and mouse <i>Sprr</i> loci to identify conserved noncoding sequences involved in coordinate regulation. <i>Genome Research</i> , 2004, 14, 2430-2438.	5.5	32
83	Transcriptional control of epidermal specification and differentiation. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 485-491.	3.3	83
84	Mouse <i>Sprr</i> locus: a tandem array of coordinately regulated genes. <i>Mammalian Genome</i> , 2003, 14, 140-148.	2.2	62
85	Ectopic expression of Kruppel like factor 4 (<i>Klf4</i>) accelerates formation of the epidermal permeability barrier. <i>Development (Cambridge)</i> , 2003, 130, 2767-2777.	2.5	101
86	Constructing Contigs from Large-Insert Clones. , 2001, Chapter 5, Unit 5.10.		0
87	<i>Klf4</i> is a transcription factor required for establishing the barrier function of the skin. <i>Nature Genetics</i> , 1999, 22, 356-360.	21.4	722