

Sarah K Highlander

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

10,304
citations

29
h-index

72
g-index

72
ext. papers

13,160
ext. citations

7.3
avg, IF

5.99
L-index

#	Paper	IF	Citations
61	Nivolumab plus ipilimumab with or without live bacterial supplementation in metastatic renal cell carcinoma: a randomized phase 1 trial.. <i>Nature Medicine</i> , 2022 ,	50.5	24
60	A Randomized Open Label Pilot Study of Clostridium Butyricum Miyairi 588 (CBM588) in Recipients of Allogeneic Hematopoietic Cell Transplantation. <i>Blood</i> , 2021 , 138, 334-334	2.2	
59	Analysis of Gut Microbiome Using Explainable Machine Learning Predicts Risk of Diarrhea Associated With Tyrosine Kinase Inhibitor Neratinib: A Pilot Study. <i>Frontiers in Oncology</i> , 2021 , 11, 604584	5.3	3
58	Randomized trial assessing impact of probiotic supplementation on gut microbiome and clinical outcome from targeted therapy in metastatic renal cell carcinoma. <i>Cancer Medicine</i> , 2021 , 10, 79-86	4.8	9
57	A Phase II Clinical Trial of Pembrolizumab and Enobosarm in Patients with Androgen Receptor-Positive Metastatic Triple-Negative Breast Cancer. <i>Oncologist</i> , 2021 , 26, 99-e217	5.7	12
56	Stool Microbiome Profiling of Patients with Metastatic Renal Cell Carcinoma Receiving Anti-PD-1 Immune Checkpoint Inhibitors. <i>European Urology</i> , 2020 , 78, 498-502	10.2	32
55	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018 , 6, 201	16.6	10
54	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. <i>MBio</i> , 2018 , 9,	7.8	42
53	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. <i>Cell Metabolism</i> , 2017 , 25, 1054-1062.e5	24.6	457
52	Host Genetic Control of the Oral Microbiome in Health and Disease. <i>Cell Host and Microbe</i> , 2017 , 22, 269-278.e10	27.8	104
51	Gastrointestinal microbial populations can distinguish pediatric and adolescent Acute Lymphoblastic Leukemia (ALL) at the time of disease diagnosis. <i>BMC Genomics</i> , 2016 , 17, 635	4.5	67
50	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. <i>Scientific Reports</i> , 2016 , 6, 31731	4.9	41
49	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. <i>PeerJ</i> , 2016 , 4, e1869	3.1	153
48	Library preparation methodology can influence genomic and functional predictions in human microbiome research. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14024-9	11.5	126
47	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. <i>Genome Announcements</i> , 2015 , 3,		23
46	Acylation Enhances, but Is Not Required for, the Cytotoxic Activity of <i>Mannheimia haemolytica</i> Leukotoxin in Bighorn Sheep. <i>Infection and Immunity</i> , 2015 , 83, 3982-8	3.7	3
45	Characterization of the human gut microbiome during travelers' diarrhea. <i>Gut Microbes</i> , 2015 , 6, 110-9	8.8	85

44	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system 2015 ,		9
43	Molecular and evolutionary analysis of NEAr-iron Transporter (NEAT) domains. <i>PLoS ONE</i> , 2014 , 9, e104794	3.7	25
42	Development and accuracy of quantitative real-time polymerase chain reaction assays for detection and quantification of enterotoxigenic Escherichia coli (ETEC) heat labile and heat stable toxin genes in travelers' diarrhea samples. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014 , 90, 124-32	3.2	20
41	Phylogenomics and the dynamic genome evolution of the genus Streptococcus. <i>Genome Biology and Evolution</i> , 2014 , 6, 741-53	3.9	91
40	From prediction to function using evolutionary genomics: human-specific ecotypes of <i>Lactobacillus reuteri</i> have diverse probiotic functions. <i>Genome Biology and Evolution</i> , 2014 , 6, 1772-89	3.9	62
39	Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5112-20	4.8	3924
38	Adenosine-5' triphosphate release by <i>Mannheimia haemolytica</i> , lipopolysaccharide, and interleukin-1 stimulated bovine pulmonary epithelial cells. <i>Veterinary Immunology and Immunopathology</i> , 2012 , 149, 58-65	2	1
37	High throughput sequencing methods for microbiome profiling: application to food animal systems. <i>Animal Health Research Reviews</i> , 2012 , 13, 40-53	2.1	19
36	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011 , 21, 494-504	9.7	2174
35	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
34	Microbial reference genomes for human metagenomics 2011 , 12, 17		78
33	A snap-shot of <i>Mannheimia hemolytica</i> A1 gene expression during infection in the bovine host. <i>FEMS Microbiology Letters</i> , 2011 , 325, 148-54	2.9	9
32	Selection and Sequencing of Strains as References for Human Microbiome Studies 2011 , 79-90		
31	Transmission of <i>Mannheimia haemolytica</i> from domestic sheep (<i>Ovis aries</i>) to bighorn sheep (<i>Ovis canadensis</i>): unequivocal demonstration with green fluorescent protein-tagged organisms. <i>Journal of Wildlife Diseases</i> , 2010 , 46, 706-17	1.3	28
30	A catalog of reference genomes from the human microbiome. <i>Science</i> , 2010 , 328, 994-9	33.3	508
29	Comparative genomics of <i>Gardnerella vaginalis</i> strains reveals substantial differences in metabolic and virulence potential. <i>PLoS ONE</i> , 2010 , 5, e12411	3.7	98
28	Metagenomic pyrosequencing and microbial identification. <i>Clinical Chemistry</i> , 2009 , 55, 856-66	5.5	394
27	Subtle genetic changes enhance virulence of methicillin resistant and sensitive <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2007 , 7, 99	4.5	186

26	Identification and characterization of transcriptional regulation of the Mannheimia haemolytica ferric uptake regulator. <i>Veterinary Microbiology</i> , 2007 , 124, 298-309	3.3	3
25	Genome sequence of Fusobacterium nucleatum subspecies polymorphum - a genetically tractable fusobacterium. <i>PLoS ONE</i> , 2007 , 2, e659	3.7	47
24	Paradoxical DNA repair and peroxide resistance gene conservation in Bacillus pumilus SAFR-032. <i>PLoS ONE</i> , 2007 , 2, e928	3.7	100
23	Complete nucleotide sequence of a P2 family lysogenic bacteriophage, varphiMhaA1-PHL101, from Mannheimia haemolytica serotype A1. <i>Virology</i> , 2006 , 350, 79-89	3.6	17
22	Chromosome rearrangement and diversification of Francisella tularensis revealed by the type B (OSU18) genome sequence. <i>Journal of Bacteriology</i> , 2006 , 188, 6977-85	3.5	81
21	The genome sequence of Mannheimia haemolytica A1: insights into virulence, natural competence, and Pasteurellaceae phylogeny. <i>Journal of Bacteriology</i> , 2006 , 188, 7257-66	3.5	73
20	Complete genome sequence of Rickettsia typhi and comparison with sequences of other rickettsiae. <i>Journal of Bacteriology</i> , 2004 , 186, 5842-55	3.5	192
19	Use of operon fusions in Mannheimia haemolytica to identify environmental and cis-acting regulators of leukotoxin transcription. <i>Infection and Immunity</i> , 2001 , 69, 6231-9	3.7	15
18	Molecular genetic analysis of virulence in Mannheimia (pasteurella) haemolytica. <i>Frontiers in Bioscience - Landmark</i> , 2001 , 6, D1128-50	2.8	48
17	Molecular genetic analysis of virulence in Mannheimia pasteurella haemolytica. <i>Frontiers in Bioscience - Landmark</i> , 2001 , 6, d1128-1150	2.8	6
16	Ultrastructural characterization of apoptosis in bovine lymphocytes exposed to Pasteurella haemolytica leukotoxin. <i>American Journal of Veterinary Research</i> , 2000 , 61, 51-6	1.1	19
15	Inactivation of Pasteurella (Mannheimia) haemolytica leukotoxin causes partial attenuation of virulence in a calf challenge model. <i>Infection and Immunity</i> , 2000 , 68, 3916-22	3.7	70
14	Pasteurella haemolytica leukotoxin induced apoptosis of bovine lymphocytes involves DNA fragmentation. <i>Veterinary Microbiology</i> , 1999 , 65, 153-66	3.3	110
13	Plasmids for heterologous expression in Pasteurella haemolytica. <i>Gene</i> , 1997 , 186, 207-11	3.8	19
12	Isolation and characterization of the integration host factor genes of Pasteurella haemolytica. <i>FEMS Microbiology Letters</i> , 1997 , 146, 181-8	2.9	3
11	The restriction-modification system of Pasteurella haemolytica is a member of a new family of type I enzymes. <i>Gene</i> , 1996 , 178, 89-96	3.8	24
10	Static DNA bending and protein interactions within the Pasteurella haemolytica leukotoxin promoter region: development of an activation model for leukotoxin transcriptional control. <i>DNA and Cell Biology</i> , 1994 , 13, 171-81	3.6	13
9	Transcriptional elements in Pasteurella haemolytica leukotoxin expression. <i>Developments in Plant Pathology</i> , 1994 , 447-462		

8	Bacterial Virulence Factors as Targets for Chemotherapy 1992 , 323-346		1
7	Mutational and physiological analyses of plasmid pT181 functions expressing incompatibility. <i>Plasmid</i> , 1990 , 23, 1-15	3.3	20
6	DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster. <i>DNA and Cell Biology</i> , 1989 , 8, 15-28		82
5	Plasmid repopulation kinetics in Staphylococcus aureus. <i>Plasmid</i> , 1987 , 17, 210-21	3.3	25
4	Replication control for pT181, an indirectly regulated plasmid. <i>Basic Life Sciences</i> , 1985 , 30, 299-320		22
3	Partial characterization of a small, multiple-copy plasmid from Streptomyces spinosus and the derivation of a high copy-number deletion mutant. <i>Gene</i> , 1982 , 18, 13-20	3.8	8
2	Supragingival plaque microbiome ecology and functional potential in the context of health and disease		2
1	The Human Microbiome226-237		1