## Sarah K Highlander

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Development of a Dual-Index Sequencing Strategy and Curation Pipeline for Analyzing Amplicon Sequence Data on the MiSeq Illumina Sequencing Platform. Applied and Environmental Microbiology, 2013, 79, 5112-5120.	3.1	5,923
2	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 2011, 21, 494-504.	5.5	3,015
3	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. Cell Metabolism, 2017, 25, 1054-1062.e5.	16.2	748
4	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	12.6	621
5	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
6	Metagenomic Pyrosequencing and Microbial Identification. Clinical Chemistry, 2009, 55, 856-866.	3.2	459
7	Subtle genetic changes enhance virulence of methicillin resistant and sensitive Staphylococcus aureus. BMC Microbiology, 2007, 7, 99.	3.3	227
8	Complete Genome Sequence of Rickettsia typhi and Comparison with Sequences of Other Rickettsiae. Journal of Bacteriology, 2004, 186, 5842-5855.	2.2	223
9	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. PeerJ, 2016, 4, e1869.	2.0	200
10	Nivolumab plus ipilimumab with or without live bacterial supplementation in metastatic renal cell carcinoma: a randomized phase 1 trial. Nature Medicine, 2022, 28, 704-712.	30.7	181
11	Library preparation methodology can influence genomic and functional predictions in human microbiome research. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14024-14029.	7.1	179
12	Host Genetic Control of the Oral Microbiome in Health and Disease. Cell Host and Microbe, 2017, 22, 269-278.e3.	11.0	165
13	Phylogenomics and the Dynamic Genome Evolution of the Genus Streptococcus. Genome Biology and Evolution, 2014, 6, 741-753.	2.5	149
14	Pasteurella haemolytica leukotoxin induced apoptosis of bovine lymphocytes involves DNA fragmentation1This report represents a portion of a dissertation submitted by the first author as partial fulfillment of the requirements for the Ph.D. degree.1. Veterinary Microbiology, 1999, 65, 153-166.	1.9	132
15	Comparative Genomics of Gardnerella vaginalis Strains Reveals Substantial Differences in Metabolic and Virulence Potential. PLoS ONE, 2010, 5, e12411.	2.5	124
16	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in Bacillus pumilus SAFR-032. PLoS ONE, 2007, 2, e928.	2.5	118
17	Characterization of the human gut microbiome during travelers' diarrhea. Gut Microbes, 2015, 6, 110-119.	9.8	111
18	Stool Microbiome Profiling of Patients with Metastatic Renal Cell Carcinoma Receiving Anti–PD-1 Immune Checkpoint Inhibitors. European Urology, 2020, 78, 498-502.	1.9	108

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19	DNA Sequence of thePasteurella haemolyticaLeukotoxin Gene Cluster. DNA and Cell Biology, 1989, 8, 15-28.	5.2	107
20	Gastrointestinal microbial populations can distinguish pediatric and adolescent Acute Lymphoblastic Leukemia (ALL) at the time of disease diagnosis. BMC Genomics, 2016, 17, 635.	2.8	103
21	The Genome Sequence of Mannheimia haemolytica A1: Insights into Virulence, Natural Competence, and Pasteurellaceae Phylogeny. Journal of Bacteriology, 2006, 188, 7257-7266.	2.2	94
22	Chromosome Rearrangement and Diversification of Francisella tularensis Revealed by the Type B (OSU18) Genome Sequence. Journal of Bacteriology, 2006, 188, 6977-6985.	2.2	91
23	From Prediction to Function Using Evolutionary Genomics: Human-Specific Ecotypes of Lactobacillus reuteri Have Diverse Probiotic Functions. Genome Biology and Evolution, 2014, 6, 1772-1789.	2.5	83
24	Inactivation of Pasteurella ( Mannheimia ) haemolytica Leukotoxin Causes Partial Attenuation of Virulence in a Calf Challenge Model. Infection and Immunity, 2000, 68, 3916-3922.	2.2	74
25	Molecular genetic analysis of virulence in Mannheimia (pasteurella) haemolytica. Frontiers in Bioscience - Landmark, 2001, 6, d1128.	3.0	67
26	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. Scientific Reports, 2016, 6, 31731.	3.3	59
27	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. MBio, 2018, 9, .	4.1	58
28	Genome Sequence of Fusobacterium nucleatum Subspecies Polymorphum — a Genetically Tractable Fusobacterium. PLoS ONE, 2007, 2, e659.	2.5	56
29	A Phase II Clinical Trial of Pembrolizumab and Enobosarm in Patients with Androgen Receptor-Positive Metastatic Triple-Negative Breast Cancer. Oncologist, 2021, 26, 99-e217.	3.7	49
30	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. PLoS ONE, 2014, 9, e104794.	2.5	43
31	TRANSMISSION OF MANNHEIMIA HAEMOLYTICA FROM DOMESTIC SHEEP (OVIS ARIES) TO BIGHORN SHEEP (OVIS CANADENSIS): UNEQUIVOCAL DEMONSTRATION WITH GREEN FLUORESCENT PROTEIN-TAGGED ORGANISMS. Journal of Wildlife Diseases, 2010, 46, 706-717.	0.8	36
32	Randomized trial assessing impact of probiotic supplementation on gut microbiome and clinical outcome from targeted therapy in metastatic renal cell carcinoma. Cancer Medicine, 2021, 10, 79-86.	2.8	36
33	Replication Control for PT181, an Indirectly Regulated Plasmid. , 1985, 30, 299-320.		32
34	Plasmid repopulation kinetics in Staphylococcus aureus. Plasmid, 1987, 17, 210-221.	1.4	28
35	The restriction-modification system of Pasteurella haemolytica is a member of a new family of type I enzymes. Gene, 1996, 178, 89-96.	2.2	27
36	High throughput sequencing methods for microbiome profiling: application to food animal systems. Animal Health Research Reviews, 2012, 13, 40-53.	3.1	27

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37	Mutational and physiological analyses of plasmid pT181 functions expressing incompatibility. Plasmid, 1990, 23, 1-15.	1.4	25
38	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. Genome Announcements, 2015, 3, .	0.8	25
39	Plasmids for heterologous expression in Pasteurella haemolytica. Gene, 1997, 186, 207-211.	2.2	24
40	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. American Journal of Tropical Medicine and Hygiene, 2014, 90, 124-132.	1.4	22
41	Ultrastructural characterization of apoptosis in bovine lymphocytes exposed toPasteurella haemolyticaleukotoxin. American Journal of Veterinary Research, 2000, 61, 51-56.	0.6	20
42	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. Microbiome, 2018, 6, 201.	11.1	20
43	Complete nucleotide sequence of a P2 family lysogenic bacteriophage, ϕMhaA1-PHL101, from Mannheimia haemolytica serotype A1. Virology, 2006, 350, 79-89.	2.4	18
44	Static DNA Bending and Protein Interactions Within thePasteurella haemolyticaLeukotoxin Promoter Region: Development of an Activation Model for Leukotoxin Transcriptional Control. DNA and Cell Biology, 1994, 13, 171-181.	1.9	16
45	Use of Operon Fusions in Mannheimia haemolytica To Identify Environmental and cis -Acting Regulators of Leukotoxin Transcription. Infection and Immunity, 2001, 69, 6231-6239.	2.2	16
46	Analysis of Gut Microbiome Using Explainable Machine Learning Predicts Risk of Diarrhea Associated With Tyrosine Kinase Inhibitor Neratinib: A Pilot Study. Frontiers in Oncology, 2021, 11, 604584.	2.8	16
47	A snap-shot of Mannheimia hemolyticaA1 gene expression during infection in the bovine host. FEMS Microbiology Letters, 2011, 325, 148-154.	1.8	10
48	Partial characterization of a small, multi-copy plasmid from Streptomyces espinosus and the derivation of a high copy-number deletion mutant. Gene, 1982, 18, 13-20.	2.2	9
49	Molecular genetic analysis of virulence in Mannheimia pasteurella haemolytica. Frontiers in Bioscience - Landmark, 2001, 6, d1128-1150.	3.0	7
50	Mock Community Analysis. , 2014, , 1-7.		5
51	Acylation Enhances, but Is Not Required for, the Cytotoxic Activity of Mannheimia haemolytica Leukotoxin in Bighorn Sheep. Infection and Immunity, 2015, 83, 3982-3988.	2.2	4
52	Isolation and characterization of the integration host factor genes of Pasteurella haemolytica. FEMS Microbiology Letters, 2006, 146, 181-188.	1.8	3
53	Identification and characterization of transcriptional regulation of the Mannheimia haemolytica ferric uptake regulator. Veterinary Microbiology, 2007, 124, 298-309.	1.9	3
54	Adenosine-5′-triphosphate release by Mannheimia haemolytica, lipopolysaccharide, and interleukin-1 stimulated bovine pulmonary epithelial cells. Veterinary Immunology and Immunopathology, 2012, 149, 58-65.	1.2	2

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55	Bacterial Virulence Factors as Targets for Chemotherapy. , 1992, , 323-346.		2
56	Microbial Disease Signatures Characterize the Gastrointestinal Microbiomes in Irritable Bowel Syndrome. Gastroenterology, 2011, 140, S-102.	1.3	1
57	Transcriptional elements in Pasteurella haemolytica leukotoxin expression. Developments in Plant Pathology, 1994, , 447-462.	0.1	1
58	Mock Community Analysis. , 2015, , 497-503.		1
59	The Human Microbiome. , 0, , 226-237.		1
60	A Randomized Open Label Pilot Study of <i>Clostridium Butyricum</i> Miyairi 588 (CBM588) in Recipients of Allogeneic Hematopoietic Cell Transplantation. Blood, 2021, 138, 334-334.	1.4	1
61	Microbial reference genomes for human metagenomics. Genome Biology, 2011, 12, .	9.6	0
62	Selection and Sequencing of Strains as References for Human Microbiome Studies. , 2011, , 79-90.		0
63	Culturing. , 2014, , 1-4.		0
64	Human Microbiome Project, Reference Genomes, Rationale, Selection, Acquisition, Sequencing, and Annotation. , 2014, , 1-4.		0
65	Human Microbiota and Pathogen-Associated Gastrointestinal Disease. , 2015, , 264-271.		0
66	Culturing. , 2015, , 114-117.		0
67	Human Microbiome Project, Reference Genomes, Rationale, Selection, Acquisition, Sequencing, and Annotation. , 2015, , 231-234.		0