

# Sarah K Highlander

## List of Publications by Year in descending order

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67  
papers

14,714  
citations

136740  
32  
h-index

155451  
55  
g-index

72  
all docs

72  
docs citations

72  
times ranked

22801  
citing authors

#	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. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5112-5120.	1.4	5,923
2	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011, 21, 494-504.	2.4	3,015
3	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.	7.2	748
4	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
5	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
6	Metagenomic Pyrosequencing and Microbial Identification. <i>Clinical Chemistry</i> , 2009, 55, 856-866.	1.5	459
7	Subtle genetic changes enhance virulence of methicillin resistant and sensitive <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2007, 7, 99.	1.3	227
8	Complete Genome Sequence of <i>Rickettsia typhi</i> and Comparison with Sequences of Other <i>Rickettsiae</i> . <i>Journal of Bacteriology</i> , 2004, 186, 5842-5855.	1.0	223
9	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. <i>PeerJ</i> , 2016, 4, e1869.	0.9	200
10	Nivolumab plus ipilimumab with or without live bacterial supplementation in metastatic renal cell carcinoma: a randomized phase 1 trial. <i>Nature Medicine</i> , 2022, 28, 704-712.	15.2	181
11	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, 14024-14029.	3.3	179
12	Host Genetic Control of the Oral Microbiome in Health and Disease. <i>Cell Host and Microbe</i> , 2017, 22, 269-278.e3.	5.1	165
13	Phylogenomics and the Dynamic Genome Evolution of the Genus <i>Streptococcus</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 741-753.	1.1	149
14	<i>Pasteurella haemolytica</i> leukotoxin induced apoptosis of bovine lymphocytes involves DNA fragmentation <sup>1</sup> This report represents a portion of a dissertation submitted by the first author as partial fulfillment of the requirements for the Ph.D. degree. <sup>1</sup> <i>Veterinary Microbiology</i> , 1999, 65, 153-166.	0.8	132
15	Comparative Genomics of <i>Gardnerella vaginalis</i> Strains Reveals Substantial Differences in Metabolic and Virulence Potential. <i>PLoS ONE</i> , 2010, 5, e12411.	1.1	124
16	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in <i>Bacillus pumilus</i> SAFR-032. <i>PLoS ONE</i> , 2007, 2, e928.	1.1	118
17	Characterization of the human gut microbiome during travelers' diarrhea. <i>Gut Microbes</i> , 2015, 6, 110-119.	4.3	111
18	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.	0.9	108

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19	DNA Sequence of the <i>Pasteurella haemolytica</i> Leukotoxin Gene Cluster. <i>DNA and Cell Biology</i> , 1989, 8, 15-28.	5.1	107
20	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.	1.2	103
21	The Genome Sequence of <i>Mannheimia haemolytica</i> A1: Insights into Virulence, Natural Competence, and Pasteurellaceae Phylogeny. <i>Journal of Bacteriology</i> , 2006, 188, 7257-7266.	1.0	94
22	Chromosome Rearrangement and Diversification of <i>Francisella tularensis</i> Revealed by the Type B (OSU18) Genome Sequence. <i>Journal of Bacteriology</i> , 2006, 188, 6977-6985.	1.0	91
23	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, 1772-1789.	1.1	83
24	Inactivation of <i>Pasteurella</i> ( <i>Mannheimia</i> ) <i>haemolytica</i> Leukotoxin Causes Partial Attenuation of Virulence in a Calf Challenge Model. <i>Infection and Immunity</i> , 2000, 68, 3916-3922.	1.0	74
25	Molecular genetic analysis of virulence in <i>Mannheimia</i> ( <i>pasteurella</i> ) <i>haemolytica</i> . <i>Frontiers in Bioscience - Landmark</i> , 2001, 6, d1128.	3.0	67
26	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. <i>Scientific Reports</i> , 2016, 6, 31731.	1.6	59
27	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. <i>MBio</i> , 2018, 9, .	1.8	58
28	Genome Sequence of <i>Fusobacterium nucleatum</i> Subspecies <i>Polymorphum</i> – a Genetically Tractable <i>Fusobacterium</i> . <i>PLoS ONE</i> , 2007, 2, e659.	1.1	56
29	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.	1.9	49
30	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. <i>PLoS ONE</i> , 2014, 9, e104794.	1.1	43
31	TRANSMISSION OF MANNHEIMIA HAEMOLYTICA FROM DOMESTIC SHEEP (OVIS ARIES) TO BIGHORN SHEEP (OVIS CANADENSIS): UNEQUIVOCAL DEMONSTRATION WITH GREEN FLUORESCENT PROTEIN-TAGGED ORGANISMS. <i>Journal of Wildlife Diseases</i> , 2010, 46, 706-717.	0.3	36
32	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.	1.3	36
33	Replication Control for PT181, an Indirectly Regulated Plasmid. , 1985, 30, 299-320.		32
34	Plasmid repopulation kinetics in <i>Staphylococcus aureus</i> . <i>Plasmid</i> , 1987, 17, 210-221.	0.4	28
35	The restriction-modification system of <i>Pasteurella haemolytica</i> is a member of a new family of type I enzymes. <i>Gene</i> , 1996, 178, 89-96.	1.0	27
36	High throughput sequencing methods for microbiome profiling: application to food animal systems. <i>Animal Health Research Reviews</i> , 2012, 13, 40-53.	1.4	27

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37	Mutational and physiological analyses of plasmid pT181 functions expressing incompatibility. Plasmid, 1990, 23, 1-15.	0.4	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 <i>Pasteurella haemolytica</i> . Gene, 1997, 186, 207-211.	1.0	24
40	Development and Accuracy of Quantitative Real-Time Polymerase Chain Reaction Assays for Detection and Quantification of Enterotoxigenic <i>Escherichia coli</i> (ETEC) Heat Labile and Heat Stable Toxin Genes in Travelers' Diarrhea Samples. American Journal of Tropical Medicine and Hygiene, 2014, 90, 124-132.	0.6	22
41	Ultrastructural characterization of apoptosis in bovine lymphocytes exposed to <i>Pasteurella haemolytica</i> leukotoxin. American Journal of Veterinary Research, 2000, 61, 51-56.	0.3	20
42	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. Microbiome, 2018, 6, 201.	4.9	20
43	Complete nucleotide sequence of a P2 family lysogenic bacteriophage, $\phi$ MhaA1-PHL101, from <i>Mannheimia haemolytica</i> serotype A1. Virology, 2006, 350, 79-89.	1.1	18
44	Static DNA Bending and Protein Interactions Within the <i>Pasteurella haemolytica</i> Leukotoxin Promoter Region: Development of an Activation Model for Leukotoxin Transcriptional Control. DNA and Cell Biology, 1994, 13, 171-181.	0.9	16
45	Use of Operon Fusions in <i>Mannheimia haemolytica</i> To Identify Environmental and cis-Acting Regulators of Leukotoxin Transcription. Infection and Immunity, 2001, 69, 6231-6239.	1.0	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.	1.3	16
47	A snap-shot of <i>Mannheimia haemolytica</i> A1 gene expression during infection in the bovine host. FEMS Microbiology Letters, 2011, 325, 148-154.	0.7	10
48	Partial characterization of a small, multi-copy plasmid from <i>Streptomyces spinosus</i> and the derivation of a high copy-number deletion mutant. Gene, 1982, 18, 13-20.	1.0	9
49	Molecular genetic analysis of virulence in <i>Mannheimia pasteurella haemolytica</i> . 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 <i>Mannheimia haemolytica</i> Leukotoxin in Bighorn Sheep. Infection and Immunity, 2015, 83, 3982-3988.	1.0	4
52	Isolation and characterization of the integration host factor genes of <i>Pasteurella haemolytica</i> . FEMS Microbiology Letters, 2006, 146, 181-188.	0.7	3
53	Identification and characterization of transcriptional regulation of the <i>Mannheimia haemolytica</i> ferric uptake regulator. Veterinary Microbiology, 2007, 124, 298-309.	0.8	3
54	Adenosine-5'-triphosphate release by <i>Mannheimia haemolytica</i> , lipopolysaccharide, and interleukin-1 stimulated bovine pulmonary epithelial cells. Veterinary Immunology and Immunopathology, 2012, 149, 58-65.	0.5	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.	0.6	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.	0.6	1
61	Microbial reference genomes for human metagenomics. Genome Biology, 2011, 12, .	13.9	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