

Sarah K Highlander

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	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
4	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.	1.3	16
5	A Randomized Open Label Pilot Study of <i>Clostridium Butyricum</i> Miyairi 588 (CBM588) in Recipients of Allogeneic Hematopoietic Cell Transplantation. <i>Blood</i> , 2021, 138, 334-334.	0.6	1
6	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
7	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	4.9	20
8	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. <i>MBio</i> , 2018, 9, .	1.8	58
9	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
10	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
11	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
12	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
13	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. <i>PeerJ</i> , 2016, 4, e1869.	0.9	200
14	Characterization of the human gut microbiome during travelers' diarrhea. <i>Gut Microbes</i> , 2015, 6, 110-119.	4.3	111
15	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
16	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, .	0.8	25
17	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, 3982-3988.	1.0	4
18	Human Microbiota and Pathogen-Associated Gastrointestinal Disease. , 2015, , 264-271.		0

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19	Culturing. , 2015, , 114-117.		0
20	Mock Community Analysis. , 2015, , 497-503.		1
21	Human Microbiome Project, Reference Genomes, Rationale, Selection, Acquisition, Sequencing, and Annotation. , 2015, , 231-234.		0
22	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. PLoS ONE, 2014, 9, e104794.	1.1	43
23	Development and Accuracy of Quantitative Real-Time Polymerase Chain Reaction Assays for Detection and Quantification of Enterotoxigenic Escherichia coli (EPEC) 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
24	Phylogenomics and the Dynamic Genome Evolution of the Genus Streptococcus. Genome Biology and Evolution, 2014, 6, 741-753.	1.1	149
25	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.	1.1	83
26	Mock Community Analysis. , 2014, , 1-7.		5
27	Culturing. , 2014, , 1-4.		0
28	Human Microbiome Project, Reference Genomes, Rationale, Selection, Acquisition, Sequencing, and Annotation. , 2014, , 1-4.		0
29	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.	1.4	5,923
30	Adenosine-5â€²-triphosphate release by Mannheimia haemolytica, lipopolysaccharide, and interleukin-1 stimulated bovine pulmonary epithelial cells. Veterinary Immunology and Immunopathology, 2012, 149, 58-65.	0.5	2
31	High throughput sequencing methods for microbiome profiling: application to food animal systems. Animal Health Research Reviews, 2012, 13, 40-53.	1.4	27
32	Microbial Disease Signatures Characterize the Gastrointestinal Microbiomes in Irritable Bowel Syndrome. Gastroenterology, 2011, 140, S-102.	0.6	1
33	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 2011, 21, 494-504.	2.4	3,015
34	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
35	Microbial reference genomes for human metagenomics. Genome Biology, 2011, 12, .	13.9	0
36	A snap-shot of Mannheimia hemolyticaA1 gene expression during infection in the bovine host. FEMS Microbiology Letters, 2011, 325, 148-154.	0.7	10

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37	Selection and Sequencing of Strains as References for Human Microbiome Studies. , 2011, , 79-90.		0
38	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.	0.3	36
39	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	6.0	621
40	Comparative Genomics of Gardnerella vaginalis Strains Reveals Substantial Differences in Metabolic and Virulence Potential. PLoS ONE, 2010, 5, e12411.	1.1	124
41	Metagenomic Pyrosequencing and Microbial Identification. Clinical Chemistry, 2009, 55, 856-866.	1.5	459
42	Subtle genetic changes enhance virulence of methicillin resistant and sensitive Staphylococcus aureus. BMC Microbiology, 2007, 7, 99.	1.3	227
43	Identification and characterization of transcriptional regulation of the Mannheimia haemolytica ferric uptake regulator. Veterinary Microbiology, 2007, 124, 298-309.	0.8	3
44	Genome Sequence of Fusobacterium nucleatum Subspecies Polymorphum " a Genetically Tractable Fusobacterium. PLoS ONE, 2007, 2, e659.	1.1	56
45	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in Bacillus pumilus SAFR-032. PLoS ONE, 2007, 2, e928.	1.1	118
46	Isolation and characterization of the integration host factor genes of Pasteurella haemolytica. FEMS Microbiology Letters, 2006, 146, 181-188.	0.7	3
47	Complete nucleotide sequence of a P2 family lysogenic bacteriophage, "MhaA1-PHL101, from Mannheimia haemolytica serotype A1. Virology, 2006, 350, 79-89.	1.1	18
48	Chromosome Rearrangement and Diversification of Francisella tularensis Revealed by the Type B (OSU18) Genome Sequence. Journal of Bacteriology, 2006, 188, 6977-6985.	1.0	91
49	The Genome Sequence of Mannheimia haemolytica A1: Insights into Virulence, Natural Competence, and Pasteurellaceae Phylogeny. Journal of Bacteriology, 2006, 188, 7257-7266.	1.0	94
50	Complete Genome Sequence of Rickettsia typhi and Comparison with Sequences of Other Rickettsiae. Journal of Bacteriology, 2004, 186, 5842-5855.	1.0	223
51	Molecular genetic analysis of virulence in Mannheimia (pasteurella) haemolytica. Frontiers in Bioscience - Landmark, 2001, 6, d1128.	3.0	67
52	Use of Operon Fusions in Mannheimia haemolytica To Identify Environmental and cis -Acting Regulators of Leukotoxin Transcription. Infection and Immunity, 2001, 69, 6231-6239.	1.0	16
53	Molecular genetic analysis of virulence in Mannheimia pasteurella haemolytica. Frontiers in Bioscience - Landmark, 2001, 6, d1128-1150.	3.0	7
54	Ultrastructural characterization of apoptosis in bovine lymphocytes exposed toPasteurella haemolytical leukotoxin. American Journal of Veterinary Research, 2000, 61, 51-56.	0.3	20

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55	Inactivation of <i>Pasteurella (Mannheimia) 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
56	<i>Pasteurella haemolytica</i> 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. <i>Veterinary Microbiology</i> , 1999, 65, 153-166.	0.8	132
57	Plasmids for heterologous expression in <i>Pasteurella haemolytica</i> . <i>Gene</i> , 1997, 186, 207-211.	1.0	24
58	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
59	Static DNA Bending and Protein Interactions Within the <i>Pasteurella haemolytica</i> Leukotoxin Promoter Region: Development of an Activation Model for Leukotoxin Transcriptional Control. <i>DNA and Cell Biology</i> , 1994, 13, 171-181.	0.9	16
60	Transcriptional elements in <i>Pasteurella haemolytica</i> leukotoxin expression. <i>Developments in Plant Pathology</i> , 1994, , 447-462.	0.1	1
61	Bacterial Virulence Factors as Targets for Chemotherapy. , 1992, , 323-346.		2
62	Mutational and physiological analyses of plasmid pT181 functions expressing incompatibility. <i>Plasmid</i> , 1990, 23, 1-15.	0.4	25
63	DNA Sequence of the <i>Pasteurella haemolytica</i> Leukotoxin Gene Cluster. <i>DNA and Cell Biology</i> , 1989, 8, 15-28.	5.1	107
64	Plasmid repopulation kinetics in <i>Staphylococcus aureus</i> . <i>Plasmid</i> , 1987, 17, 210-221.	0.4	28
65	Replication Control for PT181, an Indirectly Regulated Plasmid. , 1985, 30, 299-320.		32
66	Partial characterization of a small, multi-copy plasmid from <i>Streptomyces spinosus</i> and the derivation of a high copy-number deletion mutant. <i>Gene</i> , 1982, 18, 13-20.	1.0	9
67	The Human Microbiome. , 0, , 226-237.		1