

Sushim K Gupta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/727581/publications.pdf>

Version: 2024-02-01

44
papers

2,102
citations

516710

16
h-index

315739

38
g-index

46
all docs

46
docs citations

46
times ranked

3624
citing authors

#	ARTICLE	IF	CITATIONS
1	Resistance Genes, Plasmids, Multilocus Sequence Typing (MLST), and Phenotypic Resistance of Non-Typhoidal Salmonella (NTS) Isolated from Slaughtered Chickens in Burkina Faso. <i>Antibiotics</i> , 2022, 11, 782.	3.7	5
2	Serotyping of sub-Saharan Africa Salmonella strains isolated from poultry feces using multiplex PCR and whole genome sequencing. <i>BMC Microbiology</i> , 2021, 21, 29.	3.3	7
3	Genome Analysis of Multidrug-Resistant <i>Escherichia coli</i> Isolated from Poultry in Nigeria. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 1-7.	1.8	12
4	Genomic Analysis of Multidrug-Resistant <i>Escherichia coli</i> from Surface Water in Northeast Georgia, United States: Presence of an ST131 Epidemic Strain Containing <i>bla</i> _{CTX-M-15} on a Phage-Like Plasmid. <i>Microbial Drug Resistance</i> , 2020, 26, 447-455.	2.0	4
5	Circulation of emerging NDM-producing <i>Escherichia coli</i> among humans and dogs in Egypt. <i>Zoonoses and Public Health</i> , 2020, 67, 324-329.	2.2	26
6	Comparison of Antimicrobial Resistance and Pan-Genome of Clinical and Non-Clinical Enterococcus cecorum from Poultry Using Whole-Genome Sequencing. <i>Foods</i> , 2020, 9, 686.	4.3	13
7	Genomic comparison of diverse Salmonella serovars isolated from swine. <i>PLoS ONE</i> , 2019, 14, e0224518.	2.5	25
8	Draft genome sequence of a human-associated streptogramin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 72-73.	2.2	2
9	Antimicrobial Resistance Genes, Cassettes, and Plasmids Present in <i>Salmonella enterica</i> Associated With United States Food Animals. <i>Frontiers in Microbiology</i> , 2019, 10, 832.	3.5	95
10	Genomic comparison of diverse Salmonella serovars isolated from swine. , 2019, 14, e0224518.		0
11	Genomic comparison of diverse Salmonella serovars isolated from swine. , 2019, 14, e0224518.		0
12	Genomic comparison of diverse Salmonella serovars isolated from swine. , 2019, 14, e0224518.		0
13	Genomic comparison of diverse Salmonella serovars isolated from swine. , 2019, 14, e0224518.		0
14	An assay for determining the susceptibility of Salmonella isolates to commercial and household biocides. <i>PLoS ONE</i> , 2018, 13, e0209072.	2.5	31
15	Draft genome sequences of two ciprofloxacin-resistant <i>Salmonella enterica</i> subsp. <i>enterica</i> serotype Kentucky ST198 isolated from retail chicken carcasses in Egypt. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 14, 101-103.	2.2	13
16	Multidrug resistant <i>Mannheimia haemolytica</i> isolated from high-risk beef stocker cattle after antimicrobial metaphylaxis and treatment for bovine respiratory disease. <i>Veterinary Microbiology</i> , 2018, 221, 143-152.	1.9	45
17	Draft Genome Sequences of Eight Streptogramin-Resistant Enterococcus Species Isolated from Animal and Environmental Sources in the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
18	Draft Genome Sequence Analysis of Multidrug-Resistant <i>Escherichia coli</i> Strains Isolated in 2013 from Humans and Chickens in Nigeria. <i>Genome Announcements</i> , 2017, 5, .	0.8	5

#	ARTICLE	IF	CITATIONS
19	In Silico Prediction of Antibiotic Resistance in Mycobacterium ulcerans Agy99 through Whole Genome Sequence Analysis. American Journal of Tropical Medicine and Hygiene, 2017, 97, 810-814.	1.4	8
20	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Orion Strain CRJJGF_00093 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	6
21	Draft Genome Sequence of Salmonella enterica subsp. <i>diarizonae</i> Serovar 61:k:1,5,(7) Strain CRJJGF_00165 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
22	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Bardo Strain CRJJGF_00099 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	7
23	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Putten Strain CRJJGF_00159 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
24	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Blockley Strain CRJJGF_00147 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
25	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Kiambu Strain CRJJGF_00061 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
26	Draft Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Lille Strain CRJJGF_000101 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
27	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Widemarsh Strain CRJJGF_00058 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	4
28	MUS-2, a novel variant of the chromosome-encoded β -lactamase MUS-1, from Myroides odoratimimus. New Microbes and New Infections, 2015, 7, 67-71.	1.6	15
29	Whole-Genome Sequence of Chryseobacterium oranimense, a Colistin-Resistant Bacterium Isolated from a Cystic Fibrosis Patient in France. Antimicrobial Agents and Chemotherapy, 2015, 59, 1696-1706.	3.2	29
30	Abiotic stress induces change in Cinnamoyl CoA Reductase (CCR) protein abundance and lignin deposition in developing seedlings of Leucaena leucocephala. Physiology and Molecular Biology of Plants, 2015, 21, 197-205.	3.1	79
31	Whole-genome assembly of Akkermansia muciniphila sequenced directly from human stool. Biology Direct, 2015, 10, 5.	4.6	32
32	Loss of LPS is involved in the virulence and resistance to colistin of colistin-resistant <i>Acinetobacter nosocomialis</i> mutants selected <i>in vitro</i> . Journal of Antimicrobial Chemotherapy, 2015, 70, 2981-2986.	3.0	24
33	Whole genome sequencing of bacteria in cystic fibrosis as a model for bacterial genome adaptation and evolution. Expert Review of Anti-Infective Therapy, 2014, 12, 343-355.	4.4	11
34	Worldwide emergence of colistin resistance in Klebsiella pneumoniae from healthy humans and patients in Lao PDR, Thailand, Israel, Nigeria and France owing to inactivation of the PhoP/PhoQ regulator mgrB: an epidemiological and molecular study. International Journal of Antimicrobial Agents, 2014, 44, 500-507.	2.5	246
35	ARG-ANNOT, a New Bioinformatic Tool To Discover Antibiotic Resistance Genes in Bacterial Genomes. Antimicrobial Agents and Chemotherapy, 2014, 58, 212-220.	3.2	1,158
36	Genome analysis of NDM-1 producing <i>Morganella morganii</i> clinical isolate. Expert Review of Anti-Infective Therapy, 2014, 12, 1297-1305.	4.4	34

#	ARTICLE	IF	CITATIONS
37	NDM-5 Carbapenemase-Encoding Gene in Multidrug-Resistant Clinical Isolates of <i>Escherichia coli</i> from Algeria. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 5606-5608.	3.2	55
38	Emergence of VIM-2 and IMP-15 Carbapenemases and Inactivation of <i>oprD</i> Gene in Carbapenem-Resistant <i>Pseudomonas aeruginosa</i> Clinical Isolates from Lebanon. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4966-4970.	3.2	34
39	Reply to "Comparison of the Web Tools ARG-ANNOT and ResFinder for Detection of Resistance Genes in Bacteria". <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4987-4987.	3.2	6
40	86 Real time genome sequencing to decipher the molecular mechanism of resistance of <i>Chryseobacterium oranimense</i> , a new multidrug resistant species isolated from a cystic fibrosis patient. <i>Journal of Cystic Fibrosis</i> , 2013, 12, S70.	0.7	0
41	In Vitro Propagation and Approaches for Metabolites Production in Medicinal Plants. <i>Advances in Botanical Research</i> , 2012, 62, 35-55.	1.1	4
42	Development of pollen mediated activation tagging system for <i>Phalaenopsis</i> and <i>Doritaenopsis</i> . <i>Electronic Journal of Biotechnology</i> , 2012, 15, .	2.2	3
43	Molecular and Morphological Characterization of a Taxol-Producing Endophytic Fungus, <i>Gliocladium</i> sp., from <i>Taxus baccata</i> . <i>Mycobiology</i> , 2011, 39, 151-157.	1.7	25
44	Improved method of in vitro regeneration in <i>Leucaena leucocephala</i> "a leguminous pulpwood tree species. <i>Physiology and Molecular Biology of Plants</i> , 2009, 15, 311-318.	3.1	19