

Shiraz A Shah

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

7,280
citations

136950

32
h-index

214800

47
g-index

63
all docs

63
docs citations

63
times ranked

5938
citing authors

#	ARTICLE	IF	CITATIONS
1	Vaginal dysbiosis in pregnancy associates with risk of emergency caesarean section: a prospective cohort study. <i>Clinical Microbiology and Infection</i> , 2022, 28, 588-595.	6.0	4
2	CRISPR-Cas systems are widespread accessory elements across bacterial and archaeal plasmids. <i>Nucleic Acids Research</i> , 2022, 50, 4315-4328.	14.5	44
3	Genome binning of viral entities from bulk metagenomics data. <i>Nature Communications</i> , 2022, 13, 965.	12.8	41
4	A short prokaryotic Argonaute activates membrane effector to confer antiviral defense. <i>Cell Host and Microbe</i> , 2022, 30, 930-943.e6.	11.0	38
5	UG/Abi: a highly diverse family of prokaryotic reverse transcriptases associated with defense functions. <i>Nucleic Acids Research</i> , 2022, 50, 6084-6101.	14.5	11
6	The developing airway and gut microbiota in early life is influenced by age of older siblings. <i>Microbiome</i> , 2022, 10, .	11.1	21
7	Urbanized microbiota in infants, immune constitution, and later risk of atopic diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 234-243.	2.9	54
8	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
9	Streamlining CRISPR spacer-based bacterial host predictions to decipher the viral dark matter. <i>Nucleic Acids Research</i> , 2021, 49, 3127-3138.	14.5	72
10	The Airway Microbiota Modulates Effect of Azithromycin Treatment for Episodes of Recurrent Asthma-like Symptoms in Preschool Children: A Randomized Clinical Trial. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 204, 149-158.	5.6	27
11	<tt>CRISPRloci:</tt>Âcomprehensive and accurate annotation of CRISPRâ€Cas systems. <i>Nucleic Acids Research</i> , 2021, 49, W125-W130.	14.5	16
12	The infant gut resistome associates withÂE. coli, environmental exposures, gut microbiome maturity, and asthma-associated bacterial composition. <i>Cell Host and Microbe</i> , 2021, 29, 975-987.e4.	11.0	64
13	Casboundary: automated definition of integral Cas cassettes. <i>Bioinformatics</i> , 2021, 37, 1352-1359.	4.1	8
14	Type IV CRISPRâ€Cas systems are highly diverse and involved in competition between plasmids. <i>Nucleic Acids Research</i> , 2020, 48, 2000-2012.	14.5	128
15	Evolutionary classification of CRISPRâ€Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
16	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	92
17	CRISPRCasTyper: Automated Identification, Annotation, and Classification of CRISPR-Cas Loci. <i>CRISPR Journal</i> , 2020, 3, 462-469.	2.9	128
18	Ecological succession in the vaginal microbiota during pregnancy and birth. <i>ISME Journal</i> , 2020, 14, 2325-2335.	9.8	45

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19	CRISPRcasIdentifier: Machine learning for accurate identification and classification of CRISPR-Cas systems. <i>GigaScience</i> , 2020, 9, .	6.4	31
20	Prenatal dietary supplements influence the infant airway microbiota in a randomized factorial clinical trial. <i>Nature Communications</i> , 2020, 11, 426.	12.8	25
21	Virulent coliphages in 1-year-old children fecal samples are fewer, but more infectious than temperate coliphages. <i>Nature Communications</i> , 2020, 11, 378.	12.8	59
22	Archaeal Viruses and Their Interactions with CRISPR-Cas Systems. , 2020, , 199-220.		0
23	Comprehensive search for accessory proteins encoded with archaeal and bacterial type III CRISPR- <i>cas</i> gene cassettes reveals 39 new <i>cas</i> gene families. <i>RNA Biology</i> , 2019, 16, 530-542.	3.1	97
24	A Protocol for Extraction of Infective Viromes Suitable for Metagenomics Sequencing from Low Volume Fecal Samples. <i>Viruses</i> , 2019, 11, 667.	3.3	32
25	Predicted highly derived class 1 CRISPR-Cas system in Haloarchaea containing diverged Cas5 and Cas7 homologs but no CRISPR array. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	10
26	CRISPRStudio: A User-Friendly Software for Rapid CRISPR Array Visualization. <i>Viruses</i> , 2018, 10, 602.	3.3	45
27	Toxin inhibition in <i>C. crescentus</i> VapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. <i>Nucleic Acids Research</i> , 2016, 45, gkw1266.	14.5	13
28	Characterizing leader sequences of CRISPR loci. <i>Bioinformatics</i> , 2016, 32, i576-i585.	4.1	81
29	CRISPR-Cas Adaptive Immune Systems of the Sulfolobales: Unravelling Their Complexity and Diversity. <i>Life</i> , 2015, 5, 783-817.	2.4	39
30	Archaeal Extrachromosomal Genetic Elements. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 117-152.	6.6	64
31	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	28.6	2,081
32	CRISPR adaptive immune systems of Archaea. <i>RNA Biology</i> , 2014, 11, 156-167.	3.1	129
33	CRISPRstrand: predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci. <i>Bioinformatics</i> , 2014, 30, i489-i496.	4.1	57
34	A novel single-tailed fusiform Sulfolobus virus STSV2 infecting model Sulfolobus species. <i>Extremophiles</i> , 2014, 18, 51-60.	2.3	38
35	Archaeal Type II Toxin-Antitoxins. , 2013, , 225-238.		4
36	SMV1 virus-induced CRISPR spacer acquisition from the conjugative plasmid pMGB1 in <i>Sulfolobus solfataricus</i> P2. <i>Biochemical Society Transactions</i> , 2013, 41, 1449-1458.	3.4	22

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37	A novel interference mechanism by a type IIIB CRISPR-Cmr module in <i>Sulfolobus</i> . <i>Molecular Microbiology</i> , 2013, 87, 1088-1099.	2.5	224
38	Protospacer recognition motifs. <i>RNA Biology</i> , 2013, 10, 891-899.	3.1	309
39	CRISPR/Cas and CRISPR/Cmr Immune Systems of Archaea. , 2012, , 163-181.		2
40	Archaeal CRISPR-based immune systems: exchangeable functional modules. <i>Trends in Microbiology</i> , 2011, 19, 549-556.	7.7	96
41	CRISPR/Cas and Cmr modules, mobility and evolution of adaptive immune systems. <i>Research in Microbiology</i> , 2011, 162, 27-38.	2.1	92
42	CRISPR-based immune systems of the Sulfolobales: complexity and diversity. <i>Biochemical Society Transactions</i> , 2011, 39, 51-57.	3.4	64
43	Genomic analysis of <i>Acidianus hospitalis</i> W1 a host for studying crenarchaeal virus and plasmid life cycles. <i>Extremophiles</i> , 2011, 15, 487-497.	2.3	35
44	Genome Analyses of Icelandic Strains of <i>Sulfolobus islandicus</i> , Model Organisms for Genetic and Virus-Host Interaction Studies. <i>Journal of Bacteriology</i> , 2011, 193, 1672-1680.	2.2	139
45	Metagenomic analyses of novel viruses and plasmids from a cultured environmental sample of hyperthermophilic neutrophiles. <i>Environmental Microbiology</i> , 2010, 12, 2918-2930.	3.8	39
46	CRISPR families of the crenarchaeal genus <i>Sulfolobus</i> : bidirectional transcription and dynamic properties. <i>Molecular Microbiology</i> , 2009, 72, 259-272.	2.5	214
47	Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible interviral recombination mechanism. <i>Environmental Microbiology</i> , 2009, 11, 2849-2862.	3.8	85
48	Distribution of CRISPR spacer matches in viruses and plasmids of crenarchaeal acidothermophiles and implications for their inhibitory mechanism. <i>Biochemical Society Transactions</i> , 2009, 37, 23-28.	3.4	93
49	Stygiolobus Rod-Shaped Virus and the Interplay of Crenarchaeal Rudiviruses with the CRISPR Antiviral System. <i>Journal of Bacteriology</i> , 2008, 190, 6837-6845.	2.2	58
50	Identification of putative noncoding RNA genes in the <i>Burkholderia cenocepacia</i> J2315 genome. <i>FEMS Microbiology Letters</i> , 2007, 276, 83-92.	1.8	35