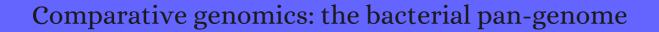
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791	The Core and Pan-Genome of the Vibrionaceae. <b>2009</b> ,		1
790	Ecological genomics of marine picocyanobacteria. <b>2009</b> , 73, 249-99		499
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586	Comparative Genomics of the Extreme Acidophile Acidithiobacillus thiooxidans Reveals Intraspecific Divergence and Niche Adaptation. <b>2016</b> , 17,		22
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583	Comparative Genome Analysis Provides Insights into the Pathogenicity of Flavobacterium psychrophilum. <b>2016</b> , 11, e0152515		26
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511	Pan-Genome Storage and Analysis Techniques. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1704, 29-53	1.4	14	
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495 494	Ecology and evolution of metabolic cross-feeding interactions in bacteria. 2018, 35, 455-488  Novel haloarchaeon Natrinema thermophila having the highest growth temperature among haloarchaea with a large genome size. 2018, 8, 7777		158 9
	Novel haloarchaeon Natrinema thermophila having the highest growth temperature among	7.2	
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494 493	Novel haloarchaeon Natrinema thermophila having the highest growth temperature among haloarchaea with a large genome size. <b>2018</b> , 8, 7777  A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the Escherichia coli strains. <i>Bioinformatics</i> , <b>2018</b> , 34, i89-i95	7.2	9
494 493 492	Novel haloarchaeon Natrinema thermophila having the highest growth temperature among haloarchaea with a large genome size. <b>2018</b> , 8, 7777  A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the Escherichia coli strains. <i>Bioinformatics</i> , <b>2018</b> , 34, i89-i95  Pathogenic: Advances in understanding the molecular pathogenesis and virulence. <b>2018</b> , 8, 13-24	7.2 5·7	9 45 2
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479	Pangenome analyses of the wheat pathogen Zymoseptoria tritici reveal the structural basis of a highly plastic eukaryotic genome. <b>2018</b> , 16, 5		84	
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476	Modules of co-occurrence in the cyanobacterial pan-genome reveal functional associations between groups of ortholog genes. <b>2018</b> , 14, e1007239		9	
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474	Durum Wheat Stress Tolerance Induced by Endophyte with Genes Contributing to Plant Functions and Secondary Metabolite Arsenal. <b>2019</b> , 20,		30	
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472	Deciphering the Ecology of Cystic Fibrosis Bacterial Communities: Towards Systems-Level Integration. <b>2019</b> , 25, 1110-1122		27	
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466	Comparative Genome Analysis of Uropathogenic Strains. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2019</b> , 9, 167	5.9	14
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464	Plant Pangenome: Impacts on Phenotypes and Evolution. 2019, 453-478		15
463	Assessing Spatial Accessibility to Medical Resources at the Community Level in Shenzhen, China. <b>2019</b> , 16,		23
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453	Whole Genome Sequencing-Based Comparison of Food Isolates of. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1464	5.7	15
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451	Worldwide phylogeography and history of wheat genetic diversity. <b>2019</b> , 5, eaav0536		64

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449	Phylogeny, Divergent Evolution, and Speciation of Sulfur-Oxidizing Acidithiobacillus Populations. <b>2019</b> , 20, 438	12
448	Large-Scale Genomics Reveals the Genetic Characteristics of Seven Species and Importance of Phylogenetic Distance for Estimating Pan-Genome Size. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 834	16
447	Pool-seq driven proteogenomic database for Group G Streptococcus. <b>2019</b> , 201, 84-92	2
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445	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <b>2019</b> , 51, 1044-1051	218
444	Analyses of Livestock-Associated Pan-Genomes Suggest Virulence Is Not Primary Interest in Evolution of Its Genome. <b>2019</b> , 23, 224-236	4
443	Diversification of Colonization Factors in a Multidrug-Resistant Escherichia coli Lineage Evolving under Negative Frequency-Dependent Selection. <b>2019</b> , 10,	55
442	Evolutionary and Genomic Insights into Sequence Type 11: a Diverse Zoonotic and Antimicrobial-Resistant Lineage of Global One Health Importance. <b>2019</b> , 10,	42
441	Comparative genome-scale modelling of the pathogenic Flavobacteriaceae species Riemerella anatipestifer in China. <b>2019</b> , 21, 2836-2851	5
440	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of Klebsiella pneumoniae. <b>2019</b> , 15, e1008114	115
439	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <b>2019</b> , 10,	44
438	Genomic analysis of Leptospira interrogans serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection. <b>2019</b> , 20, 168	3
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435	Multiple Recombination Events Drive the Current Genetic Structure of in Florida. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 448	21
434	Comparative genomic analysis of Bacillus paralicheniformis MDJK30 with its closely related species reveals an evolutionary relationship between B. paralicheniformis and B. licheniformis. <b>2019</b> , 20, 283	12
433	Comparative genomics of human Lactobacillus crispatus isolates reveals genes for glycosylation and glycogen degradation: implications for in vivo dominance of the vaginal microbiota. <b>2019</b> , 7, 49	47

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429	Whole-genome-based phylogeny of Bacillus cytotoxicus reveals different clades within the species and provides clues on ecology and evolution. <b>2019</b> , 9, 1984		18
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427	Comparative Genomic Analysis of : An Insight into Genomic Diversity and Genome Evolution. <b>2019</b> , 2019, 8987436		2
426	Pan-genome diversification and recombination in Cronobacter sakazakii, an opportunistic pathogen in neonates, and insights to its xerotolerant lifestyle. <b>2019</b> , 19, 306		6
425	An Escherichia coli ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates. <b>2019</b> , 9, 17394		39
424	Development and Application of a Software Tool/Package for Pan-Genomic Analysis. 2019,		
423	Comparative Genomic Analysis of and Key Genes Essential for the Pathogenicity of. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2774	5.7	6
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421	Genomic and metabolic features of the Bacillus amyloliquefaciens group- B. amyloliquefaciens, B. velezensis, and B. siamensis- revealed by pan-genome analysis. <b>2019</b> , 77, 146-157		26
420	Iron-associated protein interaction networks reveal the key functional modules related to survival and virulence of Pasteurella multocida. <b>2019</b> , 127, 257-266		2
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418	Evolution of the Large Nucleocytoplasmic DNA Viruses of Eukaryotes and Convergent Origins of		0
	Viral Gigantism. <b>2019</b> , 103, 167-202		80
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412	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1063-1070	4	80
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410	The subgingival microbiome associated with periodontitis in type 2 diabetes mellitus. <b>2020</b> , 14, 519-530		27
409	Pan-genome analysis of Riemerella anatipestifer reveals its genomic diversity and acquired antibiotic resistance associated with genomic islands. <b>2020</b> , 20, 307-320		1
408	The pan-genome of Treponema pallidum reveals differences in genome plasticity between subspecies related to venereal and non-venereal syphilis. <b>2020</b> , 21, 33		6
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406	Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. <b>2020</b> , 5, 343-353		48
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404	Investigation of genomic characteristics and carbohydrates' metabolic activity of Lactococcus lactis subsp. lactis during ripening of a Swiss-type cheese. <b>2020</b> , 87, 103392		5
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400	First Steps in the Analysis of Prokaryotic Pan-Genomes. 2020, 14, 1177932220938064		11
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398	Building genomes to understand biology. <b>2020</b> , 11, 6177		14
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389	Comparative Genomic Analysis Reveals Genetic Mechanisms of the Variety of Pathogenicity, Antibiotic Resistance, and Environmental Adaptation of Genus. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 5720	64 <sup>527</sup>	5
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387	Pangenomics in Crop Plants. <b>2020,</b> 1		1
387 386	Pangenomics in Crop Plants. 2020, 1  Comparative Analysis of Proteomes of a Number of Nosocomial Pathogens by KEGG Modules and KEGG Pathways. 2020, 21,		6
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386	Comparative Analysis of Proteomes of a Number of Nosocomial Pathogens by KEGG Modules and KEGG Pathways. <b>2020</b> , 21,  Comparative genomic analysis of Vibrios yields insights into genes associated with virulence	5.7	6
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386 385 384	Comparative Analysis of Proteomes of a Number of Nosocomial Pathogens by KEGG Modules and KEGG Pathways. 2020, 21,  Comparative genomic analysis of Vibrios yields insights into genes associated with virulence towards C. gigas larvae. 2020, 21, 599  Exploring the Diversity Within the Genus - An Integrated Pan-Genome and Genome-Mining Approach. Frontiers in Microbiology, 2020, 11, 1928  Horizontal Gene Transfer Clarifies Taxonomic Confusion and Promotes the Genetic Diversity and	5.7	<ul><li>6</li><li>3</li><li>5</li></ul>
386 385 384 383	Comparative Analysis of Proteomes of a Number of Nosocomial Pathogens by KEGG Modules and KEGG Pathways. 2020, 21,  Comparative genomic analysis of Vibrios yields insights into genes associated with virulence towards C. gigas larvae. 2020, 21, 599  Exploring the Diversity Within the Genus - An Integrated Pan-Genome and Genome-Mining Approach. Frontiers in Microbiology, 2020, 11, 1928  Horizontal Gene Transfer Clarifies Taxonomic Confusion and Promotes the Genetic Diversity and Pathogenicity of Plesiomonas shigelloides. 2020, 5,  Pan-genome analysis of Paenibacillus polymyxa strains reveals the mechanism of plant growth	5.7	<ul><li>6</li><li>3</li><li>5</li><li>7</li></ul>
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368	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. <b>2020</b> , 16, e1007732	35
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368 367 366	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. 2020, 16, e1007732  A megaplasmid family driving dissemination of multidrug resistance in Pseudomonas. 2020, 11, 1370  Comparative genomics and pangenome-oriented studies reveal high homogeneity of the agronomically relevant enterobacterial plant pathogen Dickeya solani. 2020, 21, 449  Population genomics of Vibrionaceae isolated from an endangered oasis reveals local adaptation	35 42 7
368 367 366 365	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. 2020, 16, e1007732  A megaplasmid family driving dissemination of multidrug resistance in Pseudomonas. 2020, 11, 1370  Comparative genomics and pangenome-oriented studies reveal high homogeneity of the agronomically relevant enterobacterial plant pathogen Dickeya solani. 2020, 21, 449  Population genomics of Vibrionaceae isolated from an endangered oasis reveals local adaptation after an environmental perturbation. 2020, 21, 418  Genomic epidemiology and carbon metabolism of Escherichia coli serogroup O145 reflect	35 42 7 5
368 367 366 365 364	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. 2020, 16, e1007732  A megaplasmid family driving dissemination of multidrug resistance in Pseudomonas. 2020, 11, 1370  Comparative genomics and pangenome-oriented studies reveal high homogeneity of the agronomically relevant enterobacterial plant pathogen Dickeya solani. 2020, 21, 449  Population genomics of Vibrionaceae isolated from an endangered oasis reveals local adaptation after an environmental perturbation. 2020, 21, 418  Genomic epidemiology and carbon metabolism of Escherichia coli serogroup O145 reflect contrasting phylogenies. 2020, 15, e0235066  Comparative genomic analyses of Lactobacillus rhamnosus isolated from Chinese subjects. 2020,	35 42 7 5

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354	Evolutionary pan-genomics and applications. <b>2020</b> , 65-80		
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344	Comparative Genomic Analyses Reveal Functional Insights Into Key Determinants of the Pathogenesis of in Kiwifruit. <b>2021</b> , 111, 789-798		O
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341	Active phase prebiotic feeding alters gut microbiota, induces weight-independent alleviation of hepatic steatosis and serum cholesterol in high-fat diet-fed mice. <b>2021</b> , 19, 448-458		3
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333	Phenotype and multi-omics comparison of Staphylococcus and Streptococcus uncovers pathogenic traits and predicts zoonotic potential. <b>2021</b> , 22, 102		1
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330	Genome-based reclassification of as a later heterotypic synonym of. <b>2021</b> , 71,		2
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328	Phylogenomic Framework for Taxonomic Delineation of spp. and Exploration of Core-Pan Genome. <b>2021</b> , 61, 180-194		0
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326	Toward quantifying the adaptive role of bacterial pangenomes during environmental perturbations.		0
325	Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era. <b>2021</b> , 12, 1523		12

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323	Identification of Novel Sensitive and Reliable Serovar-Specific Targets for PCR Detection of Serovars Hadar and Albany by Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 605984	5.7	4
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321	Mining and evaluating novel serovar-specific Salmonella C1 serogroup genes by polymerase chain reaction analysis. <b>2021</b> , 141, 110821		3
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319	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <b>2021</b> , 134, 1677-1690		10
318	Insights on the Evolutionary Genomics of the Genus: Potential New Species and Genetic Content Among Lineages. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 660920	5.7	3
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310	Comparative genomics analysis of Pediococcus acidilactici species. <b>2021</b> , 59, 573-583		1
309	Group Comparative Genomics: Toward Pangenome Features, Diversity, and Marine Environmental Adaptation. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 571212	5.7	1
308	Salmonella Genomics in Public Health and Food Safety. <b>2021</b> , eESP00082020		2
307	Comparative genomics of and prediction of new vaccines and drug targets. <b>2021</b> , 1-17		O

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302	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 639995	5.7	O
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299	Nationwide genomic atlas of soil-dwelling Listeria reveals effects of selection and population ecology on pangenome evolution. <b>2021</b> , 6, 1021-1030		14
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293	Comparative genomic analysis reveals the evolution and environmental adaptation of Acinetobacter johnsonii. <b>2022</b> , 808, 145985		2
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285	Mapping contigs using CONTIGuator. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1231, 163-76	5
284	Defining orthologs and pangenome size metrics. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1231, 191-202 1.4	5
283	The Pangenome: A Data-Driven Discovery in Biology. <b>2020</b> , 3-20	2
282	Eukaryotic Pangenomes. <b>2020</b> , 253-291	2
281	A Review of Pangenome Tools and Recent Studies. <b>2020</b> , 89-112	8
280	Plasmids of the Rhizobiaceae and Their Role in Interbacterial and Transkingdom Interactions. <b>2011</b> , 295-337	9
279	The Phylum Thermotogae. <b>2014</b> , 989-1015	10
278	Genomic and Functional Diversity of the Sinorhizobial Model Group. 2013, 69-85	2
277	Genomics of Xanthomonas citri and Related Species. <b>2014</b> , 151-176	1
276	PCR Methodology. <b>2010</b> , 11-47	2
275	Genomic profile of Brazilian methicillin-resistant Staphylococcus aureus resembles clones dispersed worldwide. <b>2019</b> , 68, 693-702	4
274	Phylogenomics and comparative genomics of , a mammalian gut commensal. <i>Microbial Genomics</i> , 4:4	30
273	panX: pan-genome analysis and exploration.	8
272	Strain-resolved microbiome sequencing reveals mobile elements that drive bacterial competition on a clinical timescale.	8
271	Disentangling the effects of selection and loss bias on gene dynamics.	1

270	Phylogenetic background and habitat drive the genetic diversification of Escherichia coli.	4
269	Unlocking the genomic taxonomy of the Prochlorococcus collective.	4
268	A proteogenomics workflow to uncover the world of small proteins in Staphylococcus aureus.	1
267	Phenotypic and molecular characterization of extended spectrum flactamase producing Escherichia coli and Klebsiella pneumoniae isolates from various samples of animal origin from Assam, India.	1
266	Comparison of two African rice species through a new pan-genomic approach on massive data.	1
265	Autometa: Automated extraction of microbial genomes from individual shotgun metagenomes.	3
264	Predicting evolution using frequency-dependent selection in bacterial populations.	5
263	Virus genomes from deep sea sediments expand the ocean megavirome and support independent origins of viral gigantism.	2
262	Tracking microbial evolution in the human gut using Hi-C.	2
261	An Escherichia coli ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates.	O
260	Massive gene presence/absence variation in the mussel genome as an adaptive strategy: first evidence of a pan-genome in Metazoa.	11
259	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen Zymoseptoria tritici.	4
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257	The Evolutionary Success of the Marine Bacterium SAR11 Analyzed through a Metagenomic Perspective. <b>2020</b> , 5,	11
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237	Whole Genome Sequencing Analysis of Serovar Typhi: History and Current Approaches.  **Microorganisms**, <b>2021</b> , 9,  4-9	1
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