

CITATION REPORT

List of articles citing

eggNOG v4.0: nested orthology inference across 3686 organisms

DOI: 10.1093/nar/gkt1253

Nucleic Acids Research, 2014, 42, D231-9.

Source: <https://exaly.com/paper-pdf/58648909/citation-report.pdf>

Version: 2024-04-24

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
472	Fast and sensitive alignment of microbial whole genome sequencing reads to large sequence datasets on a desktop PC: application to metagenomic datasets and pathogen identification. 2014 , 9, e103441		8
471	Draft Genome Sequence of the Yeast <i>Pseudozyma antarctica</i> Type Strain JCM10317, a Producer of the Glycolipid Biosurfactants, Mannosylerythritol Lipids. 2014 , 2,		20
470	Big data and other challenges in the quest for orthologs. 2014 , 30, 2993-8		84
469	Information gateway for integrated pharmacogenomics data- IGIPD. 2014 ,		0
468	An introduction to the analysis of shotgun metagenomic data. 2014 , 5, 209		308
467	Determining microbial products and identifying molecular targets in the human microbiome. 2014 , 20, 731-741		68
466	T cell transcripts and T cell activities in the gills of the teleost fish sea bass (<i>Dicentrarchus labrax</i>). 2014 , 47, 309-18		50
465	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. 2014 , 549, 186-91		15
464	MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. 2014 , 2, 26		347
463	Integrative workflows for metagenomic analysis. 2014 , 2, 70		28
462	Orthology and paralogy constraints: satisfiability and consistency. 2014 , 15 Suppl 6, S12		32
461	<i>Escherichia coli</i> inner membrane protein YciB interacts with ZipA that is important for cell division. 2015 , 20, 956-65		3
460	<i>Bifidobacteria</i> exhibit social behavior through carbohydrate resource sharing in the gut. 2015 , 5, 15782		168
459	Transcriptomic variation of hepatopancreas reveals the energy metabolism and biological processes associated with molting in Chinese mitten crab, <i>Eriocheir sinensis</i> . 2015 , 5, 14015		56
458	Phosphoproteomic screening identifies Rab GTPases as novel downstream targets of PINK1. 2015 , 34, 2840-61		127
457	Prediction of microbial phenotypes based on comparative genomics. 2015 , 16 Suppl 14, S1		22
456	Optimizing and benchmarking de novo transcriptome sequencing: from library preparation to assembly evaluation. 2015 , 16, 977		56

455	Improved orthologous databases to ease protozoan targets inference. 2015 , 8, 494	1
454	Following the Footsteps of Chlamydial Gene Regulation. 2015 , 32, 3035-46	17
453	Comprehensive analysis of the endoplasmic reticulum stress response in the soybean genome: conserved and plant-specific features. 2015 , 16, 783	20
452	MycoBASE: expanding the functional annotation coverage of mycobacterial genomes. 2015 , 16, 1102	9
451	Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. 2015 , 13, 42	44
450	OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. 2015 , 16, 157	1591
449	Coiled-coil length: Size does matter. 2015 , 83, 2162-9	9
448	Dominant ectosymbiotic bacteria of cellulolytic protists in the termite gut also have the potential to digest lignocellulose. 2015 , 17, 4942-53	37
447	Functional interactions among filamentous Epsilonproteobacteria and Bacteroidetes in a deep-sea hydrothermal vent biofilm. 2015 , 17, 4063-77	36
446	Uncovering major genomic features of essential genes in Bacteria and a methanogenic Archaea. 2015 , 282, 3395-3411	23
445	Colonic metaproteomic signatures of active bacteria and the host in obesity. 2015 , 15, 3544-52	56
444	Functional Basis of Microorganism Classification. 2015 , 11, e1004472	18
443	Identification of Newly Synthesized Proteins by Echinococcus granulosus Protoscoleces upon Induction of Strobilation. 2015 , 9, e0004085	17
442	Identification of Putative Nuclear Receptors and Steroidogenic Enzymes in Murray-Darling Rainbowfish (<i>Melanotaenia fluviatilis</i>) Using RNA-Seq and De Novo Transcriptome Assembly. 2015 , 10, e0142636	2
441	Investigation of Yersinia pestis Laboratory Adaptation through a Combined Genomics and Proteomics Approach. 2015 , 10, e0142997	14
440	orthoFind Facilitates the Discovery of Homologous and Orthologous Proteins. 2015 , 10, e0143906	2
439	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. 2015 , 10, e0143959	9
438	Metagenomic Analysis of Chicken Gut Microbiota for Improving Metabolism and Health of Chickens - A Review. 2015 , 28, 1217-25	61

437	Metagenomics: tools and insights for analyzing next-generation sequencing data derived from biodiversity studies. 2015 , 9, 75-88		222
436	Evolution of an epigenetic gene ensemble within the genus Anopheles. 2015 , 7, 901-15		6
435	Enrichment of <i>Triticum aestivum</i> gene annotations using ortholog cliques and gene ontologies in other plants. 2015 , 16, 299		5
434	OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2015 , 43, W78-84	20.1	291
433	Revisiting bacterial cyclic nucleotide phosphodiesterases: cyclic AMP hydrolysis and beyond. 2015 , 362,		17
432	An event-driven approach for studying gene block evolution in bacteria. 2015 , 31, 2075-83		13
431	Comparative Genomics and Evolutionary Modularity of Prokaryotes. 2015 , 883, 77-96		1
430	Genomics of <i>Weissella cibaria</i> with an examination of its metabolic traits. 2015 , 161, 914-30		28
429	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cell-lines. 2015 , 15, 3163-8		283
428	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015 , 43, D261-9	20.1	818
427	Comparison of sister species identifies factors underpinning plastid compatibility in green sea slugs. 2015 , 282,		29
426	SMART: recent updates, new developments and status in 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D257-60	20.1	1137
425	Systematic characterization and prediction of post-translational modification cross-talk. 2015 , 14, 761-70		27
424	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015 , 43, D447-52	20.1	6276
423	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015 , 43, D974-81	20.1	248
422	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015 , 43, D494-502	20.1	67
421	Genomic Tools for the Study of <i>Azospirillum</i> and Other Plant Growth-Promoting Rhizobacteria. 2015 , 83-97		
420	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. 2015 , 81, 7078-87		150

419	Genenames.org: the HGNC resources in 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D1079-85	20.1	397
418	Rumen Microbiology: From Evolution to Revolution. 2015 ,		30
417	A Drosophila-centric view of protein tyrosine phosphatases. 2015 , 589, 951-66		11
416	MBGD update 2015: microbial genome database for flexible ortholog analysis utilizing a diverse set of genomic data. <i>Nucleic Acids Research</i> , 2015 , 43, D270-6	20.1	60
415	Average genome size estimation improves comparative metagenomics and sheds light on the functional ecology of the human microbiome. 2015 , 16, 51		126
414	The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. <i>Nucleic Acids Research</i> , 2015 , 43, D240-9	20.1	168
413	Cyclebase 3.0: a multi-organism database on cell-cycle regulation and phenotypes. <i>Nucleic Acids Research</i> , 2015 , 43, D1140-4	20.1	122
412	Characterization of 14-3-3 isoforms expressed in the Echinococcus granulosus pathogenic larval stage. 2015 , 14, 1700-15		18
411	TFClass: a classification of human transcription factors and their rodent orthologs. <i>Nucleic Acids Research</i> , 2015 , 43, D97-102	20.1	63
410	Complex archaea that bridge the gap between prokaryotes and eukaryotes. 2015 , 521, 173-179		726
409	B4-Dependent Response to Nitrogen Limitation and Virulence in Burkholderia cenocepacia Strain H111. 2015 , 81, 4077-89		27
408	Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. 2015 , 106, 1-6		21
407	Domain similarity based orthology detection. 2015 , 16, 154		9
406	Using the taxon-specific genes for the taxonomic classification of bacterial genomes. 2015 , 16, 396		12
405	PlantOrDB: a genome-wide ortholog database for land plants and green algae. 2015 , 15, 161		10
404	LCGserver: A Webserver for Exploring Evolutionary Trajectory of Gene Orders in a Large Number of Genomes. 2015 , 19, 574-7		
403	Endosymbiotic origin and differential loss of eukaryotic genes. 2015 , 524, 427-32		190
402	ProtPhylo: identification of protein-phenotype and protein-protein functional associations via phylogenetic profiling. <i>Nucleic Acids Research</i> , 2015 , 43, W160-8	20.1	22

401	Rumen Metagenomics. 2015 , 223-245		4
400	Phylogenetic Profiling for Probing the Modular Architecture of the Human Genome. 2015 , 1, 106-15		11
399	Genomic factors related to tissue tropism in Chlamydia pneumoniae infection. 2015 , 16, 268		6
398	Insights from genomes of representatives of the human gut commensal Bifidobacterium bifidum. 2015 , 17, 2515-31		61
397	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. <i>Nucleic Acids Research</i> , 2015 , 43, D250-6	20.1	217
396	Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 Anopheles mosquitoes. 2015 , 347, 1258522		372
395	XGSA: A statistical method for cross-species gene set analysis. 2016 , 32, i620-i628		12
394	Gene content dissimilarity for subclassification of highly similar microbial strains. 2016 , 17, 647		10
393	Transcriptome Sequencing of to Identify Genes and Enzymes Involved in Triterpenoid Biosynthesis. 2016 , 2016, 7840914		6
392	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , 2016 , 7, 822	5-7	31
391	Whole-Metagenome-Sequencing-Based Community Profiles of Vitis vinifera L. cv. Corvina Berries Withered in Two Post-harvest Conditions. <i>Frontiers in Microbiology</i> , 2016 , 7, 937	5-7	33
390	Genomic Analysis of Type Strain CBA1501 Isolated from Solfataric Soil. <i>Frontiers in Microbiology</i> , 2016 , 7, 1639	5-7	
389	The Verrucomicrobia LexA-Binding Motif: Insights into the Evolutionary Dynamics of the SOS Response. 2016 , 3, 33		8
388	Computational Identification of the Paralogs and Orthologs of Human Cytochrome P450 Superfamily and the Implication in Drug Discovery. 2016 , 17,		17
387	A tissue-specific protein purification approach in Caenorhabditis elegans identifies novel interaction partners of DLG-1/Discs large. 2016 , 14, 66		23
386	WORMHOLE: Novel Least Diverged Ortholog Prediction through Machine Learning. 2016 , 12, e1005182		9
385	Comparative Proteomics of Leaves from Phytase-Transgenic Maize and Its Non-transgenic Isogenic Variety. 2016 , 7, 1211		11
384	Insights into the biodiversity of the gut microbiota of broiler chickens. 2016 , 18, 4727-4738		89

- 383 A novel skew analysis reveals substitution asymmetries linked to genetic code GC-biases and PolIII a-subunit isoforms. **2016**, 23, 353-63 2
- 382 ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. **2016**, 32, 3327-3329 7
- 381 RNA-seq-based evaluation of bicolor tepal pigmentation in Asiatic hybrid lilies (*Lilium* spp.). **2016**, 17, 611 42
- 380 Evaluation of genetic diversity among strains of the human gut commensal *Bifidobacterium adolescentis*. **2016**, 6, 23971 70
- 379 Integrative Systems Biology. **2016**, 245-251
- 378 Genome Sequence of *Pseudomonas citronellolis* SJTE-3, an Estrogen- and Polycyclic Aromatic Hydrocarbon-Degrading Bacterium. **2016**, 4, 13
- 377 Gene expression profiling analysis reveals a crucial gene regulating metabolism in adventitious roots of neem (*Azadirachta indica*). **2016**, 6, 114889-114898 3
- 376 Improving the catalytic activity of isopentenyl phosphate kinase through protein coevolution analysis. **2016**, 6, 24117 20
- 375 Metagenomes provide valuable comparative information on soil microeukaryotes. **2016**, 167, 436-50 28
- 374 Standardized benchmarking in the quest for orthologs. **2016**, 13, 425-30 133
- 373 Identification of myogenic regulatory genes in the muscle transcriptome of beltfish (*Trichiurus lepturus*): A major commercial marine fish species with robust swimming ability. **2016**, 8, 81-4 7
- 372 Genomic and metagenomic analysis of microbes in a soil environment affected by the 2011 Great East Japan Earthquake tsunami. **2016**, 17, 53 18
- 371 Big Data, Evolution, and Metagenomes: Predicting Disease from Gut Microbiota Codon Usage Profiles. **2016**, 1415, 509-31 6
- 370 Proteomic profiling of Gram-negative bacterial outer membrane vesicles: Current perspectives. **2016**, 10, 897-909 59
- 369 The Conserved Tetratricopeptide Repeat-Containing C-Terminal Domain of *Pseudomonas aeruginosa* FimV Is Required for Its Cyclic AMP-Dependent and -Independent Functions. **2016**, 198, 2263-74 17
- 368 Systems biology of bacteria-host interactions. **2016**, 113-137 1
- 367 Incorporating tree-thinking and evolutionary time scale into developmental biology. **2016**, 58, 131-42 13
- 366 Reannotation of *Yersinia pestis* Strain 91001 Based on Omics Data. **2016**, 95, 562-70 6

365	Soil and leaf litter metaproteomics-a brief guideline from sampling to understanding. 2016 , 92,	28
364	Extensive complementarity between gene function prediction methods. 2016 , 32, 3645-3653	8
363	Gut microbiota composition and Clostridium difficile infection in hospitalized elderly individuals: a metagenomic study. 2016 , 6, 25945	132
362	- Next-Generation Sequencing and Metagenomics. 2016 , 344-364	
361	A Bayesian inference method for the analysis of transcriptional regulatory networks in metagenomic data. 2016 , 11, 19	7
360	Osmoadaptative Strategy and Its Molecular Signature in Obligately Halophilic Heterotrophic Protists. 2016 , 8, 2241-58	43
359	A reference gene catalogue of the pig gut microbiome. 2016 , 1, 16161	233
358	Analytic framework for peptidomics applied to large-scale neuropeptide identification. 2016 , 7, 11436	66
357	The Lungfish Transcriptome: A Glimpse into Molecular Evolution Events at the Transition from Water to Land. 2016 , 6, 21571	55
356	Tongue Coating and the Salivary Microbial Communities Vary in Children with Halitosis. 2016 , 6, 24481	39
355	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. 2016 , 7, 11362	130
354	A single gene of a commensal microbe affects host susceptibility to enteric infection. 2016 , 7, 11606	23
353	pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana. 2016 , 12, 1-7	8
352	Abasy Atlas: a comprehensive inventory of systems, global network properties and systems-level elements across bacteria. 2016 , 2016,	12
351	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. 2016 , 1,	22
350	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. 2016 ,	4
349	A Hitchhiker's Guide to Metatranscriptomics. 2016 , 313-342	4
348	Heterogeneous molecular processes among the causes of how sequence similarity scores can fail to recapitulate phylogeny. 2017 , 18, 451-457	14

347	Machine Learning for Microbial Phenotype Prediction. 2016 ,	1
346	Distinct metabolic changes between wheat embryo and endosperm during grain development revealed by 2D-DIGE-based integrative proteome analysis. 2016 , 16, 1515-36	29
345	PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. 2016 , 2016,	5
344	Genome Structural Diversity among 31 <i>Bordetella pertussis</i> Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. 2016 , 1,	35
343	RNA-seq analysis for secondary metabolite pathway gene discovery in <i>Polygonum minus</i> . 2016 , 7, 12-3	16
342	Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. 2016 , 88, 95-121	45
341	The Transporter Classification Database (TCDB): recent advances. <i>Nucleic Acids Research</i> , 2016 , 44, D3722-9.1	434
340	De novo analysis of transcriptome reveals genes associated with leaf abscission in sugarcane (<i>Saccharum officinarum</i> L.). 2016 , 17, 195	37
339	The Stress-Induced Soybean NAC Transcription Factor GmNAC81 Plays a Positive Role in Developmentally Programmed Leaf Senescence. 2016 , 57, 1098-114	30
338	Yeast Interspecies Comparative Proteomics Reveals Divergence in Expression Profiles and Provides Insights into Proteome Resource Allocation and Evolutionary Roles of Gene Duplication. 2016 , 15, 218-35	12
337	NCG 5.0: updates of a manually curated repository of cancer genes and associated properties from cancer mutational screenings. <i>Nucleic Acids Research</i> , 2016 , 44, D992-9	20.1 77
336	Transcriptome analyses of insect cells to facilitate baculovirus-insect expression. 2016 , 7, 373-82	10
335	Proteins with Highly Evolvable Domain Architectures Are Nonessential but Highly Retained. 2016 , 33, 1219-30	6
334	Peroxisomes in parasitic protists. 2016 , 209, 35-45	39
333	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. 2016 , 14, 1246-1257	30
332	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. 2016 , 531, 101-4	161
331	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. 2016 , 10, 735-46	23
330	Global biogeography of <i>Prochlorococcus</i> genome diversity in the surface ocean. 2016 , 10, 1856-65	50

329	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
328	RNA-seq analysis for plant carnivory gene discovery in <i>Nepenthes</i> <i>ventrata</i> . 2016 , 7, 18-9		16
327	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016 , 44, D1172-80	20.1	31
326	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
325	EffectiveDB--updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. <i>Nucleic Acids Research</i> , 2016 , 44, D669-74	20.1	74
324	LRRC31 is induced by IL-13 and regulates kallikrein expression and barrier function in the esophageal epithelium. 2016 , 9, 744-56		19
323	A Rickettsiales symbiont of amoebae with ancient features. 2016 , 18, 2326-42		41
322	Protein complex analysis: From raw protein lists to protein interaction networks. 2017 , 36, 600-614		15
321	Physiological adjustments and transcriptome reprogramming are involved in the acclimation to salinity gradients in diatoms. 2017 , 19, 909-925		15
320	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. 2017 , 7, 40248		27
319	Comparative genomic analysis of wide and narrow host range strains of <i>Xanthomonas citri</i> subsp. <i>citri</i> , showing differences in the genetic content of their pathogenicity and virulence factors. 2017 , 46, 49-61		4
318	MetaSort untangles metagenome assembly by reducing microbial community complexity. 2017 , 8, 14306		43
317	Age influences the olfactory profiles of the migratory oriental armyworm <i>mythimna separate</i> at the molecular level. 2017 , 18, 32		21
316	Comparative Analysis of Mitochondrial N-Termini from Mouse, Human, and Yeast. 2017 , 16, 512-523		48
315	Viruses comprise an extensive pool of mobile genetic elements in eukaryote cell cultures and human clinical samples. 2017 , 31, 1987-2000		29
314	The History of <i>Bordetella pertussis</i> Genome Evolution Includes Structural Rearrangement. 2017 , 199,		40
313	New natural products identified by combined genomics-metabolomics profiling of marine <i>Streptomyces</i> sp. MP131-18. 2017 , 7, 42382		49
312	An introduction to metagenomic data generation, analysis, visualization, and interpretation. 2017 , 94-126		2

311	Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to <i>Mycobacterium tuberculosis</i> . 2017 , 18, 201	11
310	Complete genome sequence of a versatile hydrocarbon degrader, <i>Pseudomonas aeruginosa</i> DN1 isolated from petroleum-contaminated soil. 2017 , 7, 123-126	11
309	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. 2017 , 18, 33	10
308	Draft Genome Sequence of sp. Strain IB2014011-1, Isolated from sp. Larvae of Lake Baikal. 2017 , 5,	1
307	Systems-level metabolism of the altered Schaedler flora, a complete gut microbiota. 2017 , 11, 426-438	37
306	Comparative genomics of the DNA damage-inducible network in the Patescibacteria. 2017 , 19, 3465-3474	26
305	De novo transcriptome sequencing and comparative analysis of midgut tissues of four non-model insects pertaining to Hemiptera, Coleoptera, Diptera and Lepidoptera. 2017 , 627, 85-93	7
304	Tracking the evolution of 3D gene organization demonstrates its connection to phenotypic divergence. <i>Nucleic Acids Research</i> , 2017 , 45, 4330-4343	20.1 6
303	Comparative study the expression of calcium cycling genes in Bombay duck () and beltfish () with different swimming activities. 2017 , 12, 58-61	7
302	Tandem Mass Spectrometry in Resolving Complex Gut Microbiota Functions. 2017 , 505-528	1
301	Genomic characterization of Nontuberculous Mycobacteria. 2017 , 7, 45258	106
300	Identification of Genes Involved in Flavonoid Biosynthesis in <i>Sophora japonica</i> Through Transcriptome Sequencing. 2017 , 14, e1700369	10
299	<i>Lactobacillus fermentum</i> FTDC 8312 combats hypercholesterolemia via alteration of gut microbiota. 2017 , 262, 75-83	33
298	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . 2017 , 19, 5010-5024	17
297	Alterations in the proteome of wheat primary roots after wortmannin application during seed germination. 2017 , 39, 1	2
296	The chromosomal organization of horizontal gene transfer in bacteria. 2017 , 8, 841	93
295	Cloning and expression analysis of , and cryopreservation research of trehalose from Antarctic strain sp. 2017 , 7, 343	2
294	Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. 2017 , 7, 7741	40

293	A clinician's guide to microbiome analysis. 2017 , 14, 585-595	85
292	The Plant Orthology Browser: An Orthology and Gene-Order Visualizer for Plant Comparative Genomics. 2017 , 10, plantgenome2016.08.0078	7
291	Complete Genome Sequence of ICMP 19535, a Highly Specific, Nitrogen-Fixing Symbiont of New Zealand Endemic spp. 2017 , 5,	0
290	Metagenomic analysis reveals wastewater treatment plants as hotspots of antibiotic resistance genes and mobile genetic elements. 2017 , 123, 468-478	381
289	Complete genome sequence of bacteriocin-producing <i>Lactobacillus plantarum</i> KLDS1.0391, a probiotic strain with gastrointestinal tract resistance and adhesion to the intestinal epithelial cells. 2017 , 109, 432-437	33
288	An Inducible Operon Is Involved in Inulin Utilization in <i>Lactobacillus plantarum</i> Strains, as Revealed by Comparative Proteogenomics and Metabolic Profiling. 2017 , 83,	28
287	Genome of ' <i>Ca. Desulfovibrio trichonymphae</i> ', an H-oxidizing bacterium in a tripartite symbiotic system within a protist cell in the termite gut. 2017 , 11, 766-776	20
286	Distinct gene expression profile of <i>Xanthomonas retroflexus</i> engaged in synergistic multispecies biofilm formation. 2017 , 11, 300-303	35
285	A scored human protein-protein interaction network to catalyze genomic interpretation. 2017 , 14, 61-64	307
284	Global transcriptomic response of <i>Anoxybacillus</i> sp. SK 3-4 to aluminum exposure. 2017 , 57, 151-161	5
283	Managing workflows on top of a cloud computing orchestrator for using heterogeneous environments on e-Science. 2017 , 13, 375	2
282	Comparative Analysis of Methylomes. 2017 , 8, 504	8
281	Proteomics and the human microbiome: where we are today and where we would like to be. 2017 , 1, 401-409	2
280	Development of Gene-Based SSR Markers in Winged Bean (<i>Psophocarpus tetragonolobus</i> (L.) DC.) for Diversity Assessment. <i>Genes</i> , 2017 , 8,	4.2 19
279	Metagenomic Analysis of Hot Springs in Central India Reveals Hydrocarbon Degrading Thermophiles and Pathways Essential for Survival in Extreme Environments. <i>Frontiers in Microbiology</i> , 2016 , 7, 2123	5.7 50
278	Adaptations to High Salt in a Halophilic Protist: Differential Expression and Gene Acquisitions through Duplications and Gene Transfers. <i>Frontiers in Microbiology</i> , 2017 , 8, 944	5.7 36
277	Draft Genome Sequence of a Rare Pigmented subsp. Type C Strain. 2017 , 5,	
276	Transcriptome Analysis of <i>Taxillusi chinensis</i> (DC.) Danser Seeds in Response to Water Loss. 2017 , 12, e0169177	22

275	NtrC-dependent control of exopolysaccharide synthesis and motility in Burkholderia cenocepacia H111. 2017 , 12, e0180362		11
274	Transcriptologs: A Transcriptome-Based Approach to Predict Orthology Relationships. 2017 , 11, 1177932217690136		136
273	Biochemical Properties of α -Amylase from Midgut of Alphitobius diaperinus (Panzer) (Coleoptera: Tenebrionidae) Larvae. 2018 , 47, 698-708		2
272	Function and functional redundancy in microbial systems. 2018 , 2, 936-943		423
271	Phylostratigraphic analysis of tumor and developmental transcriptomes reveals relationship between oncogenesis, phylogenesis and ontogenesis. 2018 , 4, 025002		12
270	Screening and Genomic Characterization of Filamentous Hemagglutinin-Deficient Bordetella pertussis. 2018 , 86,		15
269	The molecular basis of essential fatty acid limitation in Daphnia magna: A transcriptomic approach. <i>Molecular Ecology</i> , 2018 , 27, 871-885	5-7	18
268	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. 2018 , 20, 402-419		82
267	Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. 2018 , 20, 1041-1063		120
266	PANDA: Protein function prediction using domain architecture and affinity propagation. 2018 , 8, 3484		12
265	Whole community transcriptome of a sequencing batch reactor transforming 2,4-dinitroanisole (DNAN) and 3-nitro-1,2,4-triazol-5-one (NTO). 2018 , 29, 71-88		7
264	Complete Genome Sequence of the Endophytic Bacterium Chryseobacterium indologenes PgBE177, Isolated from Panax quinquefolius. 2018 , 7,		3
263	Laboratory strains of Bacillus anthracis exhibit pervasive alteration in expression of proteins related to sporulation under laboratory conditions relative to genetically related wild strains. 2018 , 13, e0209120		5
262	Abnormal Gut Microbiota Metabolism Specific for Liver Cirrhosis. <i>Frontiers in Microbiology</i> , 2018 , 9, 305157		9
261	Systematic characterization and prediction of post-translational modification cross-talk between proteins. 2019 , 35, 2626-2633		2
260	Complete Genome Sequence of the Endophytic Bacterium Bacillus cereus PgBE311, Isolated from. 2018 , 7,		2
259	Performance Evaluation of Normalization Approaches for Metagenomic Compositional Data on Differential Abundance Analysis. 2018 , 329-344		3
258	New Frontiers of Biostatistics and Bioinformatics. 2018 ,		2

257	Progress of analytical tools and techniques for human gut microbiome research. 2018 , 56, 693-705	36
256	Identification and genome analysis of SJTR1, a novel 17 β -estradiol degradation bacterium. 2018 , 8, 433	11
255	Efficient inference of homologs in large eukaryotic pan-proteomes. 2018 , 19, 340	2
254	Predicting Protein Function Using Homology-Based Methods. 2018 , 289-305	0
253	Comprehensive transcriptome analysis reveals genes in response to water deficit in the leaves of <i>Saccharum narenga</i> (Nees ex Steud.) Hack. 2018 , 18, 250	22
252	Comparison of Healthy and Dandruff Scalp Microbiome Reveals the Role of Commensals in Scalp Health. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 346	5.9 35
251	Floral pigmentation pattern in Oriental hybrid lily (<i>Lilium</i> spp.) cultivar 'Dizzy' is caused by transcriptional regulation of anthocyanin biosynthesis genes. 2018 , 228, 85-91	16
250	Using WormBase: A Genome Biology Resource for <i>Caenorhabditis elegans</i> and Related Nematodes. 2018 , 1757, 399-470	21
249	DNA sequencing and metagenomics of cultivated and uncultivated chernozems in Russia. 2018 , 14, e00180	6
248	Landscape of the genome and host cell response of <i>Mycobacterium shigaense</i> reveals pathogenic features. 2018 , 7, 112	2
247	Eukaryotic Genomic Databases. 2018 ,	1
246	The evolutionary signal in metagenome phyletic profiles predicts many gene functions. 2018 , 6, 129	2
245	Induced Salt Tolerance of Perennial Ryegrass by a Novel Bacterium Strain from the Rhizosphere of a Desert Shrub <i>Haloxylon ammodendron</i> . 2018 , 19,	36
244	Integrated physiology and proteome analysis of embryo and endosperm highlights complex metabolic networks involved in seed germination in wheat (<i>Triticum aestivum</i> L.). 2018 , 229, 63-76	17
243	Comparative Metagenomic Analysis of Rhizosphere Microbial Community Composition and Functional Potentials under Consecutive Monoculture. 2018 , 19,	20
242	Homology Inference Based on a Reconciliation Approach for the Comparative Genomics of Protozoa. 2018 , 14, 1176934318785138	
241	Metagenomic Analysis and its Applications. 2019 , 184-193	14
240	Comparative transcriptome analyses of adzuki bean weevil (<i>Callosobruchus chinensis</i>) response to hypoxia and hypoxia/hypercapnia. 2019 , 109, 266-277	3

239	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. 2019 , 175-223	2
238	Transcriptomic analysis of Pacific white shrimp (<i>Litopenaeus vannamei</i> , Boone 1931) in response to acute hepatopancreatic necrosis disease caused by <i>Vibrio parahaemolyticus</i> . 2019 , 14, e0220993	17
237	Patient-specific cancer genes contribute to recurrently perturbed pathways and establish therapeutic vulnerabilities in esophageal adenocarcinoma. 2019 , 10, 3101	17
236	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. 2019 , 21, 3873-3884	11
235	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. 2019 , 1910, 605-634	3
234	High accuracy consol simulation method of bimorph cantilever for piezoelectric vibration energy harvesting. 2019 , 9, 095067	20
233	Coupling caging and proteomics on the European flounder (<i>Platichthys flesus</i>) to assess the estuarine water quality at micro scale. 2019 , 695, 133760	6
232	Transcriptome analysis to characterize the genes related to gonad growth and fatty acid metabolism in the sea urchin <i>Strongylocentrotus intermedius</i> . 2019 , 41, 1397-1415	4
231	RNA-seq analysis of local tissue of <i>Carassius auratus gibelio</i> with pharyngeal myxobolosis: Insights into the pharyngeal mucosal immune response in a fish-parasite dialogue. 2019 , 94, 99-112	13
230	The distinction of CPR bacteria from other bacteria based on protein family content. 2019 , 10, 4173	56
229	Accumulation mechanism of indigo and indirubin in <i>Polygonum tinctorium</i> revealed by metabolite and transcriptome analysis. 2019 , 141, 111783	7
228	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. 2019 , 8,	73
227	Dissecting the Evolutionary Development of the Species through Comparative Genomics Analyses. 2019 , 85,	7
226	Genomic and Metagenomic Insights Into the Microbial Community in the Regenerating Intestine of the Sea Cucumber. <i>Frontiers in Microbiology</i> , 2019 , 10, 1165	5-7 11
225	Global Structuring of Phylogenetic and Functional Diversity of Pelagic Fungi by Depth and Temperature. 2019 , 6,	17
224	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> , 2019 , 10, 834	5-7 16
223	Transcriptome analysis of activated sludge microbiomes reveals an unexpected role of minority nitrifiers in carbon metabolism. 2019 , 2, 179	20
222	Involvement of Salicylic Acid in Anthracnose Infection in Tea Plants Revealed by Transcriptome Profiling. 2019 , 20,	13

221	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. 2019 , 29, 1712-1720. e74		
220	Carbohydrate metabolism genes dominant in a subtropical marine mangrove ecosystem revealed by metagenomics analysis. 2019 , 57, 575-586		12
219	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. 2019 , 20, 228		0
218	Draft Genome Sequence of Broad-Spectrum Antibiotic-Producing Marine sp. Strain FIM060022. 2019 , 8,		
217	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous Fermentation of Riesling Must. <i>Frontiers in Microbiology</i> , 2019 , 10, 697	5-7	18
216	Comparative genomics reveals the unique evolutionary status of <i>Plasmodiophora brassicae</i> and the essential role of GPCR signaling pathways. 2019 , 1,		8
215	Transcriptional profiling of <i>Auricularia cornea</i> in selenium accumulation. 2019 , 9, 5641		7
214	GeM-Pro: a tool for genome functional mining and microbial profiling. 2019 , 103, 3123-3134		8
213	Unveiling Genomic Diversity among Members of the Species , a Widely Distributed Gut Commensal of the Animal Kingdom. 2019 , 85,		23
212	Man-made microbial resistances in built environments. 2019 , 10, 968		78
211	Transcriptome sequencing of a keystone aquatic herbivore yields insights on the temperature-dependent metabolism of essential lipids. 2019 , 20, 894		3
210	OrthoFinder: phylogenetic orthology inference for comparative genomics. 2019 , 20, 238		868
209	Transcriptomic analysis of β -synuclein knockdown after T3 spinal cord injury in rats. 2019 , 20, 851		1
208	Comparative transcriptome reveals the potential modulation mechanisms of estradiol affecting ovarian development of female <i>Portunus trituberculatus</i> . 2019 , 14, e0226698		6
207	Genomics of Foodborne Microorganisms. 2019 , 927-937		
206	A BONCAT-iTRAQ method enables temporally resolved quantitative profiling of newly synthesised proteins in <i>Leishmania mexicana</i> parasites during starvation. 2019 , 13, e0007651		6
205	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>). 2019 , 499, 109-118		42
204	A metagenomic analysis framework for characterization of antibiotic resistomes in river environment: Application to an urban river in Beijing. 2019 , 245, 398-407		34

203	Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community. 2019 , 10, 159	21
202	Multi-tissue transcriptomes of caecilian amphibians highlight incomplete knowledge of vertebrate gene families. 2019 , 26, 13-20	10
201	The antibiotic action of methylarsenite is an emergent property of microbial communities. 2019 , 111, 487-494	33
200	Exploring Microbial Diversity and Function in Petroleum Hydrocarbon Associated Environments Through Omics Approaches. 2019 , 171-194	5
199	Microbial genome analysis: the COG approach. 2019 , 20, 1063-1070	80
198	Reconstruction and in silico analysis of new <i>Marinobacter adhaerens</i> t76_800 with potential for long-chain hydrocarbon bioremediation associated with marine environmental lipases. 2020 , 49, 100685	3
197	Genome-wide functional association networks: background, data & state-of-the-art resources. 2020 , 21, 1224-1237	5
196	Characterization of an efficient estrogen-degrading bacterium <i>Stenotrophomonas maltophilia</i> SJTH1 in saline-, alkaline-, heavy metal-contained environments or solid soil and identification of four 17 β -estradiol-oxidizing dehydrogenases. 2020 , 385, 121616	11
195	Characterization of an 17 β -estradiol-degrading bacterium <i>Stenotrophomonas maltophilia</i> SJTL3 tolerant to adverse environmental factors. 2020 , 104, 1291-1305	8
194	Complete Genome Sequence of sp. Strain KCTC 42546, Isolated from a Reservoir in South Korea. 2020 , 9,	
193	Quantitative microbiome profiling links microbial community variation to the intestine regeneration rate of the sea cucumber <i>Apostichopus japonicus</i> . 2020 , 112, 5012-5020	4
192	Comparative transcriptome and co-expression analysis reveal key genes involved in leaf margin serration in <i>Perilla frutescens</i> . 2020 , 12, 265-272	0
191	Additives affect the distribution of metabolic profile, microbial communities and antibiotic resistance genes in high-moisture sweet corn kernel silage. 2020 , 315, 123821	13
190	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. <i>Frontiers in Microbiology</i> , 2020 , 11, 584222	5-7 5
189	Analysis of the vaginal microbiome of giant pandas using metagenomics sequencing. 2020 , 9, e1131	6
188	Coexistence of with the Gene in an Identical Plasmid of Indicates Their Synergistic Insecticidal Toxicity. 2020 , 68, 14081-14090	2
187	Clinical Reversion Analysis Identifies Hotspot Mutations and Predicted Neoantigens Associated with Therapy Resistance. 2020 , 10, 1475-1488	38
186	Complete genome sequence of butenyl-spinosyn-producing <i>Saccharopolyspora</i> strain ASAGF58. 2020 , 70,	1

185	Draft genome sequence data of strain TH2H2, isolated from a tomato flower in Korea. 2020 , 31, 105824		
184	Effects of Selenium- and Zinc-Enriched SeZi on Antioxidant Capacities and Gut Microbiome in an ICR Mouse Model. 2020 , 9,		3
183	Implementation of homology based and non-homology based computational methods for the identification and annotation of orphan enzymes: using Mycobacterium tuberculosis H37Rv as a case study. 2020 , 21, 466		1
182	Comparative Analysis of Soil Microbiome Profiles in the Companion Planting of White Clover and Orchard Grass Using 16S rRNA Gene Sequencing Data. 2020 , 11, 538311		1
181	Cell Plasticity and Genomic Structure of a Novel Filterable Bacterium that Belongs to a Widely Distributed Lineage. 2020 , 8,		2
180	Microbiome and nitrate removal processes by microorganisms on the ancient Preah Vihear temple of Cambodia revealed by metagenomics and N-15 isotope analyses. 2020 , 104, 9823-9837		13
179	Effects of Co-culture on Improved Productivity and Bioresource for Microalgal Biomass Using the Floc-Forming Bacteria. 2020 , 8, 588210		3
178	Accelerated bioremediation of petroleum refinery sludge through biostimulation and bioaugmentation of native microbiome. 2020 , 23-65		5
177	Parallel reductive genome evolution in Desulfovibrio ectosymbionts independently acquired by Trichonympha protists in the termite gut. 2020 , 14, 2288-2301		1
176	Regulation by fungal endophyte of Rhodiola crenulata from enzyme genes to metabolites based on combination of transcriptome and metabolome. 2020 , 100, 4483-4494		2
175	Characterization of the Phenanthrene-Degrading SJTF8 in Heavy Metal Co-Existing Liquid Medium and Analysis of Its Metabolic Pathway. 2020 , 8,		5
174	Molecular evolutionary and 3D protein structural analyses of Lactobacillus fermentum elongation factor Tu, a novel brain health promoting factor. 2020 , 112, 3915-3924		1
173	Macromolecular crowding links ribosomal protein gene dosage to growth rate in Vibrio cholerae. 2020 , 18, 43		3
172	Transcriptome Reveals Gene Changes in the Development of the Endosperm Chalazal Haustorium in (DC.) Danser. 2020 , 2020, 7871918		6
171	Complete genome sequence analysis of the Vibrio owensii strain SH-14 isolated from shrimp with acute hepatopancreatic necrosis disease. 2020 , 202, 1097-1106		1
170	Effects of spaceflight on the composition and function of the human gut microbiota. 2020 , 11, 807-819		11
169	The Wild Mouse (): Reservoir of a Novel Strain. <i>Frontiers in Microbiology</i> , 2019 , 10, 3066	5-7	4
168	De Novo Transcriptome Identifies Olfactory Genes in (Ashmead). <i>Genes</i> , 2020 , 11,	4-2	2

167	Metagenomics methods for the study of plant-associated microbial communities: A review. 2020 , 170, 105860		46
166	Integrated metabolomic and transcriptomic analyses identify critical genes in eicosapentaenoic acid biosynthesis and metabolism in the sea urchin <i>Strongylocentrotus intermedius</i> . 2020 , 10, 1697		6
165	Microbiome structure and function in rhizosphere of Jerusalem artichoke grown in saline land. 2020 , 724, 138259		19
164	The transcriptome of the newt <i>Cynops orientalis</i> provides new insights into evolution and function of sexual gene networks in sarcopterygians. 2020 , 10, 5445		9
163	WeiBI (web-based platform): Enriching integrated interaction network with increased coverage and functional proteins from genome-wide experimental OMICS data. 2020 , 10, 5618		1
162	Twitching and Swimming Motility Play a Role in <i>Ralstonia solanacearum</i> Pathogenicity. 2020 , 5,		16
161	The complex phylogenetic relationships of a 4mC/6mA DNA methyltransferase in prokaryotes. 2020 , 149, 106837		3
160	The preceding root system drives the composition and function of the rhizosphere microbiome. 2020 , 21, 89		27
159	A new genome allows the identification of genes associated with natural variation in aluminium tolerance in <i>Brachiaria</i> grasses. 2021 , 72, 302-319		8
158	How can accumulated organics and salts deteriorate the biological treatment unit in the printing and dyeing wastewater recycling system?. 2021 , 413, 127528		2
157	Long-Term Waterlogging as Factor Contributing to Hypoxia Stress Tolerance Enhancement in Cucumber: Comparative Transcriptome Analysis of Waterlogging Sensitive and Tolerant Accessions. <i>Genes</i> , 2021 , 12,	4.2	8
156	Metagenomics of Plant Rhizosphere and Endophytic Association: Concepts and Applications. <i>Rhizosphere Biology</i> , 2021 , 275-291		0.8
155	Comparative transcriptomics of a monocotyledonous geophyte reveals shared molecular mechanisms of underground storage organ formation. 2021 , 23, 155-173		1
154	Gut microbiome and its meta-omics perspectives: profound implications for cardiovascular diseases. 2021 , 13, 1936379		7
153	Genomic population structure of Shanghai isolates and identification of genomic features uniquely linked with pathogenicity. 2021 , 12, 1258-1270		2
152	ConVarT: a search tool for orthologous variants: A method and server for functional inference of human genetic variants.		0
151	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . 2021 , 38, 2240-2259		7
150	Informative Regions In Viral Genomes.		1

149	The effects of ALA-PDT on microbiota in pilosebaceous units of patients with severe acne: A metagenomic study. 2021 , 33, 102050		3
148	Longitudinal study of the scalp microbiome suggests coconut oil to enrich healthy scalp commensals. 2021 , 11, 7220		1
147	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male-heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> , 2021 , 21, 1966-1982	8.4	11
146	Intestinal microbiota and functional characteristics of black soldier fly larvae (<i>Hermetia illucens</i>). 2021 , 71,		6
145	The Composition and Primary Metabolic Potential of Microbial Communities Inhabiting the Surface Water in the Equatorial Eastern Indian Ocean. 2021 , 10,		2
144	Amoxicillin-Clavulanic Acid Resistance in the Genus. 2021 , 87,		3
143	Comparative genome analyses of isolated from different ecological niches reveal an environmental adaptation of this species to the human vaginal environment. 2021 ,		4
142	Reannotation of the cultivated strawberry genome and establishment of a strawberry genome database. 2021 , 8, 41		12
141	Comparative genomics and physiological investigation supported safety, cold adaptation, efficient hydrolytic and plant growth-promoting potential of psychrotrophic <i>Glutamicibacter arilaitensis</i> LJH19, isolated from night-soil compost. 2021 , 22, 307		7
140	Metatranscriptomic Analysis Reveals an Imbalance of Hepatopancreatic Flora of Chinese Mitten Crab with Hepatopancreatic Necrosis Disease. 2021 , 10,		1
139	Characterization of a new bifunctional endo-1,4- β -xylanase/esterase found in the rumen metagenome. 2021 , 11, 10440		1
138	Ketogenic diet-mediated steroid metabolism reprogramming improves the immune microenvironment and myelin growth in spinal cord injury rats according to gene and co-expression network analyses. 2021 , 13, 12973-12995		4
137	Microbial Ecological Mechanism for Long-Term Production of High Concentrations of ϵ -Caproate via Lactate-Driven Chain Elongation. 2021 , 87,		7
136	A primer on metagenomics and next-generation sequencing in fish gut microbiome research. 2021 , 52, 4574-4600		3
135	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. 2021 , 10,		114
134	A native conjugative plasmid confers potential selective advantages to plant growth-promoting <i>Bacillus velezensis</i> strain GH1-13. 2021 , 4, 582		1
133	Midgut transcriptome assessment of the cockroach-hunting wasp <i>Ampulex compressa</i> (Apoidea: Ampulicidae). 2021 , 16, e0252221		1
132	Draft genome assembly data of <i>Anoxybacillus</i> sp. strain MB8 isolated from Tattapani hot springs, India.		

131	Informative Regions In Viral Genomes. 2021 , 13,		2
130	Antimicrobial Resistance Determinants in Genomes and Plasmids from Clinical Isolates. 2021 , 10,		3
129	OCT1 - a yeast mitochondrial thiolase involved in the 3-oxoadipate pathway. 2021 , 21,		1
128	Fish diversity monitoring in Maninjau Lake, West Sumatra using the eDNA with the next generation sequencing (NGS) technique. 2021 , 819, 012045		
127	Genome-Wide Analysis and Expression Profile of Superoxide Dismutase (SOD) Gene Family in Rapeseed (L.) under Different Hormones and Abiotic Stress Conditions. 2021 , 10,		16
126	Mirage: Estimation of ancestral gene-copy numbers by considering different evolutionary patterns among gene families.		0
125	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. <i>Frontiers in Microbiology</i> , 2021 , 12, 711244	5-7	2
124	Diversity and function of culturable actinobacteria in the root-associated of Bunge. 2021 , 9, e11749		0
123	Dispersal strategies shape persistence and evolution of human gut bacteria. 2021 , 29, 1167-1176.e9		15
122	Rapid strain-specific identification of two <i>Lactobacillus rhamnosus</i> strains using PCR based on gene family analysis. 2021 , 146, 111395		1
121	Characterization of sp. nov., Isolated from a Mine Sediment. 2021 , 9,		0
120	Comparison of gene expression in the red imported fire ant (<i>Solenopsis invicta</i>) under different temperature conditions. 2021 , 11, 16476		4
119	High-Fat-Diet-Induced Oxidative Stress Linked to the Increased Colonization of <i>Lactobacillus sakei</i> in an Obese Population. 2021 , 9, e0007421		1
118	Transcriptomics analysis of the infected tissue of gibel carp (<i>Carassius auratus gibelio</i>) with liver myxobolosis infers the underlying defense mechanisms from the perspective of immune-metabolic interactions. 2021 , 542, 736867		1
117	Genome-Wide Characterization of Glutathione Peroxidase (GPX) Gene Family in Rapeseed (L.) Revealed Their Role in Multiple Abiotic Stress Response and Hormone Signaling. 2021 , 10,		11
116	Metagenomic Analysis Identifies Sex-Related Cecal Microbial Gene Functions and Bacterial Taxa in the Quail. 2021 , 8, 693755		0
115	Protein Bioinformatics Databases and Resources. 2017 , 1558, 3-39		119
114	Bioinformatics Analysis of Functional Associations of PTMs. 2017 , 1558, 303-320		3

113	Comparative Genomics Approaches to Identifying Functionally Related Genes. 2014 , 1-24	2
112	Transcriptional homogenization of <i>Lactobacillus rhamnosus</i> hsryfm 1301 under heat stress and oxidative stress. 2020 , 104, 2611-2621	4
111	Genomic and functional insights into the adaptation and survival of <i>Chryseobacterium</i> sp. strain PMSZPI in uranium enriched environment. 2020 , 191, 110217	9
110	A scored human protein-protein interaction network to catalyze genomic interpretation.	3
109	On phylogenetic branch lengths distribution and the late acquisition of mitochondria.	4
108	Taxon sampling unequally affects individual nodes in a phylogenetic tree: consequences for model gene tree construction in SwissTree.	3
107	Gut microbial ecology of <i>Xenopus</i> tadpoles across life stages.	0
106	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male-heterogametic sex determination system on chromosome 7.	2
105	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3.	22
104	Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community.	0
103	OrthoFinder: phylogenetic orthology inference for comparative genomics.	34
102	Quickly finding orthologs as reciprocal best hits with BLAT, LAST, and UBLAST: how much do we miss?. 2014 , 9, e101850	95
101	De novo assembly and annotation of the retinal transcriptome for the Nile grass rat (<i>Arvicanthis ansorgei</i>). 2017 , 12, e0179061	1
100	Phylen: automatic phylogenetic reconstruction using the EggNOG database. 2018 , 3, 593	4
99	Genome sequencing and analysis of the first complete genome of <i>Lactobacillus kunkeei</i> strain MP2, an <i>Apis mellifera</i> gut isolate. 2016 , 4, e1950	12
98	Speeding up all-against-all protein comparisons while maintaining sensitivity by considering subsequence-level homology. 2014 , 2, e607	6
97	ConVarT: a search engine for matching human genetic variants with variants from non-human species. <i>Nucleic Acids Research</i> , 2021 ,	20.1 2
96	Pan-Genome Analysis of Effectors in Korean Strains of the Soybean Pathogen pv.. 2021 , 9,	1

95	Characterization of the First Cultured Psychrotolerant Representative of from Antarctica Reveals Its Unique Genome Structure. 2021 , 9, e0042421		2
94	Comparative RNA-Seq Analyses of (Hymenoptera: Formicidae) Reveal Gene in Response to Cold Stress. <i>Genes</i> , 2021 , 12,	4.2	3
93	Probiotic effects of the <i>Bacillus velezensis</i> GY65 strain in the mandarin fish, <i>Siniperca chuatsi</i> . 2021 , 21, 100902		2
92	De novo transcriptome sequencing and comparative analysis of midgut tissues of four non-model insects pertaining to Hemiptera, Coleoptera, Diptera and Lepidoptera.		
91	Phylostratigraphic analysis of tumor and developmental transcriptomes reveals relationship between oncogenesis, phylogenesis and ontogenesis.		
90	The Response to Past Climate Perturbations Explains Extremely Low Genetic Diversity in the Genome of an Abundant Ice-Age Remnant, the Alpine Marmot.		
89	Patient-specific detection of cancer genes reveals recurrently perturbed processes in esophageal adenocarcinoma.		1
88	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies.		
87	Physiological genomics of dietary adaptation in a marine herbivorous fish.		
86	Macromolecular crowding links ribosomal protein gene dosage to growth rate in <i>Vibrio cholerae</i> .		
85	A BONCAT-iTRAQ method enables temporally resolved quantitative profiling of newly synthesised proteins in <i>Leishmania mexicana</i> parasites during starvation.		
84	A new genome allows the identification of genes associated with natural variation in aluminium tolerance in <i>Brachiaria</i> grasses.		0
83	Comparative transcriptomics of a monocotyledonous geophyte reveals shared molecular mechanisms of underground storage organ formation.		
82	Characterization of <i>gen. nov., sp. nov.</i> , isolated from human faeces, and proposal for the reclassification of within the genus. 2020 , 70, 2988-2997		2
81	Comparative genomics and proposal of <i>Streptomyces radicis</i> sp. nov., an endophytic actinomycete from roots of plants in Thailand. 2022 , 254, 126889		
80	Investigation of a night soil compost psychrotrophic bacterium <i>Glutamicibacter arilaitensis</i> LJH19 for its safety, efficient hydrolytic and plant growth-promoting potential.		0
79	Withering syndrome induced gene expression changes and a de-novo transcriptome for the Pinto abalone, <i>Haliotis kamtschatkana</i> . 2021 , 41, 100930		0
78	Metagenomic analysis of microbial communities and antibiotic resistance genes in spoiled household chemicals. 2021 , 132766		0

77	In Vitro Study of Biocontrol Potential of Rhizospheric against Pathogenic Fungi of Saffron (L.). 2021 , 10,		1
76	Mirage: A phylogenetic mixture model to reconstruct gene-content evolutionary history using a realistic evolutionary rate model.		
75	Comparative Genomic Analysis of Streptococcus pneumoniae Strains: Penicillin Non-susceptible Multi-drug-Resistant Serotype 19A Isolates.. 2022 , 79, 49		0
74	Genome insights into the pharmaceutical and plant growth promoting features of the novel species Nocardia alni sp. nov.. 2022 , 23, 70		4
73	Differential Transcriptome Analysis Reveals Genes Related to Low- and High-Temperature Stress in the Fall Armyworm, .. 2021 , 12, 827077		1
72	MCycDB: a curated database for comprehensively profiling methane cycling processes of environmental microbiomes.. <i>Molecular Ecology Resources</i> , 2022 ,	8.4	2
71	Comparative Genomic Analysis of Pathogenic Factors of Pectobacterium Species Isolated in South Korea Using Whole-Genome Sequencing.. <i>Plant Pathology Journal</i> , 2022 , 38, 12-24	2.5	
70	Dynamic Gene Expression and Alternative Splicing Events Demonstrate Co-Regulation of Testicular Differentiation and Maturation by the Brain and Gonad in Common Carp.. <i>Frontiers in Endocrinology</i> , 2021 , 12, 820463	5.7	
69	Scope of Actinobacteria in Bioengineering. <i>Rhizosphere Biology</i> , 2021 , 181-198	0.8	1
68	Taxonomic and Functional Diversity of Dendrobium Officinale Microbiome in Danxia Habitat.. <i>Journal of Applied Microbiology</i> , 2022 ,	4.7	0
67	Identification and Characterization of GYUN-300: An Antagonistic Bacterium Against Red Pepper Anthracnose Caused by in Korea.. <i>Frontiers in Microbiology</i> , 2022 , 13, 826827	5.7	1
66	Effects of Short-Chain Fatty Acid Modulation on Potentially Diarrhea-Causing Pathogens in Yaks Through Metagenomic Sequencing.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 805481	5.9	0
65	Antimicrobial resistance patterns and genetic elements associated with the antibiotic resistance of Helicobacter pylori strains from Shanghai.. <i>Gut Pathogens</i> , 2022 , 14, 14	5.4	1
64	Comparative Metagenomic and Metabolomic Profiling of Rhizospheres of Panax notoginseng Grown under Forest and Field Conditions. <i>Agronomy</i> , 2021 , 11, 2488	3.6	3
63	Data_Sheet_1.DOCX. 2018 ,		
62	Table_1.docx. 2018 ,		
61	Table_2.xlsx. 2018 ,		
60	Table_3.docx. 2018 ,		

59 Table_4.xlsx. **2018**,

58 Table_5.xlsx. **2018**,

57 Data_Sheet_1.pdf. **2020**,

56 Data_Sheet_1.docx. **2019**,

55 Data_Sheet_1.PDF. **2019**,

54 Table_1.XLS. **2019**,

53 Table_2.XLSX. **2019**,

52 Table_3.xlsx. **2019**,

51 Table_4.xlsx. **2019**,

50 Table_5.xls. **2019**,

49 Data_Sheet_1.docx. **2020**,

48 Table_1.xlsx. **2020**,

47 Data_Sheet_1.pdf. **2019**,

46 Image_1.tiff. **2019**,

45 Image_2.TIFF. **2019**,

44 Image_3.TIFF. **2019**,

43 Image_4.TIFF. **2019**,

42 Image_5.TIFF. **2019**,

41	Table_1.xlsx. 2019 ,		
40	Data_Sheet_1.PDF. 2019 ,		
39	Table_1.XLSX. 2019 ,		
38	Image_1.pdf. 2020 ,		
37	Table_1.xlsx. 2020 ,		
36	Metagenomics Reveals the Diversity and Taxonomy of Carbohydrate-Active Enzymes and Antibiotic Resistance Genes in Suancai Bacterial Communities. <i>Genes</i> , 2022 , 13, 773	4.2	○
35	Potential Use of Microbial Community Genomes in Various Dimensions of Agriculture Productivity and Its Management: A Review. <i>Frontiers in Microbiology</i> , 2022 , 13,	5.7	○
34	Parallel meta-transcriptome analysis reveals degradation of plant secondary metabolites by beetles and their gut symbionts. <i>Molecular Ecology</i> ,	5.7	
33	Characterization and Functional Studies of a Novel Depolymerase Against K19-Type <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 13,	5.7	1
32	Plasmidome analysis of a hospital effluent biofilm: Status of antibiotic resistance. <i>Plasmid</i> , 2022 , 122, 102638	3.3	
31	Isolation, Identification, and Investigation of Pathogenic Bacteria From Common Carp (<i>Cyprinus carpio</i>) Naturally Infected With <i>Plesiomonas shigelloides</i> . <i>Frontiers in Immunology</i> , 13,	8.4	○
30	Genome-Wide Characterization of Ascorbate Peroxidase Gene Family in Peanut (<i>Arachis hypogea</i> L.) Revealed Their Crucial Role in Growth and Multiple Stress Tolerance. 13,		1
29	Dynamic succession of microbial compost communities and functions during <i>Pleurotus ostreatus</i> mushroom cropping on a short composting substrate. 13,		
28	<i>Alkalibacter rhizosphaerae</i> sp. nov., a CO-utilizing bacterium isolated from tidal flat sediment, and emended description of the genus <i>Alkalibacter</i> . 2022 , 72,		
27	Synthesizing glycine betaine via choline oxidation pathway as an osmoprotectant strategy in <i>Haloferacales</i> . 2022 , 847, 146886		1
26	Structural and functional dysbiosis of gut microbiota in Tibetan subjects with coronary heart disease. 2022 , 110483		○
25	Niche specialization and ecophysiological adaptation strategies of salt-tolerant nitrite oxidizers in soil. 2022 , 58, 815-825		○
24	Complete Genome Sequence of a Novel <i>Lactobacillus paracasei</i> TK1501 and Its Application in the Biosynthesis of Isoflavone Aglycones. 2022 , 11, 2807		○

- 23 Metagenomic analysis reveals the microbiome and antibiotic resistance genes in indigenous Chinese yellow-feathered chickens. 13,
- 22 Microbial diversity and functional genes of red vinasse acid based on metagenome analysis. 13,
- 21 Genomic Analysis of Halotolerant Bacterial Strains *Marteella soudanensis* NC18T and NC20. **2022**,
- 20 Metagenomic Insights into Microbial Community Structure, Function, and Salt Adaptation in Saline Soils of Arid Land, China. **2022**, 10, 2183
- 19 Identification of a 17 β -Estradiol-degrading Microbacterium hominis SJTG1 With High Adaptability and Characterization of the Genes for Estrogen Degradation. **2022**, 130371
- 18 Integrative Systems Biology. **2016**, 484-491
- 17 Multi-omics analyses reveal that the gut microbiome and its metabolites promote milk fat synthesis in Zhongdian yak cows. 10, e14444
- 16 Host metabolic benefits of prebiotic exopolysaccharides produced by *Leuconostoc mesenteroides*. **2023**, 15,
- 15 Towards understanding the mechanism of n-hexane tolerance in *Synechocystis* sp. PCC 6803. **2023**,
- 14 Comparative analysis of physiological variations and genetic architecture for cold stress response in soybean germplasm. 13,
- 13 Potential virulence factors of *Nocardia seriolae* AHLQ20-01 based on whole-genome analysis and its pathogenicity to largemouth bass (*Micropterus salmoides*).
- 12 The molecular clock in long-lived tropical trees is independent of growth rate.
- 11 Integration of environmental signatures and omics-based approaches on the European flounder to assist with health assessment of estuarine ecosystems in Brittany, France. **2023**, 878, 163195
- 10 Genomic insights into secondary metabolites of pharmaceutical utility for *Hyphococcus flavus* MCCC 1K03223T, isolated from bathypelagic seawater. **2023**, 69, 101031
- 9 Function of CAZymes encoded by highly abundant genes in rhizosphere microbiome of *Moringa oleifera*. **2023**, 30, 103578
- 8 Gut microbiome variations in *Rhinopithecus roxellanae* caused by changes in the environment. **2023**, 24,
- 7 Effects of levodopa on gut bacterial antibiotic resistance in Parkinson's disease rat. 15,
- 6 Seasonal Changes in the Structure and Function of Gut Microbiota in the Muskrat (*Ondatra zibethicus*). **2023**, 13, 248

- 5 Trait biases in microbial reference genomes. **2023**, 10,
- 4 Taxonomic and enzymatic basis of the cellulolytic microbial consortium KKU-MC1 and its application in enhancing biomethane production. **2023**, 13,
- 3 Deciphering the gut microbiome of grass carp through multi-omics approach.
- 2 Genome-Wide Identification of Superoxide Dismutase and Expression in Response to Fruit Development and Biological Stress in Akebia trifoliata: A Bioinformatics Study. **2023**, 12, 726
- 1 Graph Visualization: Alternative Models Inspired by Bioinformatics. **2023**, 23, 3747