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From genomics to chemical genomics: new developments in KEGG

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1135	An improved combinatorial biclustering algorithm. <b>2013</b> , 22, 293-302		
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1133	Whole-Genome Expression Analysis of Human Mesenchymal Stromal Cells Exposed to Ultrasmooth Tantalum vs. Titanium Oxide Surfaces. <b>2013</b> , 6, 199-209		4
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1131	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <b>2013</b> , 56, 1-12		33
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1129	Identification of genes associated with fruit ripening in <i>Ziziphus jujuba</i> using suppression subtractive hybridization approach. <b>2013</b> , 35, 1997-2008		2
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1120	Exploring the biologically relevant chemical space for drug discovery. <b>2013</b> , 53, 2820-8		33
1119	Heat stress effects on the cumulus cells surrounding the bovine oocyte during maturation: altered matrix metalloproteinase 9 and progesterone production. <b>2013</b> , 146, 193-207		34
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1116	Data visualization in environmental proteomics. <b>2013</b> , 13, 2805-21		17
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719	The harmful algae, and , elicit stronger transcriptomic and mortality response in larval bivalves ( ) than climate change stressors. <b>2019</b> , 9, 4931-4948	2
718	PTML Model of Enzyme Subclasses for Mining the Proteome of Biofuel Producing Microorganisms. <b>2019</b> , 18, 2735-2746	18
717	The evolution of proteome: From the primeval to the very dawn of LUCA. <b>2019</b> , 181, 1-10	5
716	Genomic characterization of <i>Kerstersia gyiorum</i> SWMUKG01, an isolate from a patient with respiratory infection in China. <b>2019</b> , 14, e0214686	1
715	Anticandidal Potential of Stem Bark Extract from and the Identification of Its Major Anticandidal Compound. <b>2019</b> , 24,	1
714	Genome-wide analyses and expression patterns under abiotic stress of NAC transcription factors in white pear ( <i>Pyrus bretschneideri</i> ). <b>2019</b> , 19, 161	21
713	Significant Down-Regulation of Urea Cycle Generates Clinically Relevant Proteomic Signature in Hepatocellular Carcinoma Patients with Macrovascular Invasion. <b>2019</b> , 18, 2032-2044	9
712	Exposure of low-dose fipronil enantioselectively induced anxiety-like behavior associated with DNA methylation changes in embryonic and larval zebrafish. <b>2019</b> , 249, 362-371	22
711	Plastid genome and composition analysis of two medical ferns: <i>Nakai</i> and <i>Thunb.</i> <b>2019</b> , 14, 9	5
710	Neuronal Apolipoprotein E4 Expression Results in Proteome-Wide Alterations and Compromises Bioenergetic Capacity by Disrupting Mitochondrial Function. <b>2019</b> , 68, 991-1011	29

709	Identification of Hfq-binding RNAs in <i>Caulobacter crescentus</i> . <b>2019</b> , 16, 719-726		6
708	Evaluation of synthetic gene encoding $\beta$ -galactosidase through metagenomic sequencing of paddy soil. <b>2019</b> , 128, 274-282		4
707	Independent Microevolution Mediated by Mobile Genetic Elements of Individual <i>Clostridium difficile</i> Isolates from Clade 4 Revealed by Whole-Genome Sequencing. <b>2019</b> , 4,		9
706	G-protein-coupled receptors function as logic gates for nanoparticle binding using systems and synthetic biology approach. <b>2019</b> , 34, 1854-1867		2
705	Candidate Gene Selection for Cytoplasmic Male Sterility in Pepper ( <i>L.</i> ) through Whole Mitochondrial Genome Sequencing. <b>2019</b> , 20,		15
704	NRLMF: Beta-distribution-rescored neighborhood regularized logistic matrix factorization for improving the performance of drug-target interaction prediction. <b>2019</b> , 18, 100615		11
703	Draft Genome Analysis Offers Insights Into the Mechanism by Which WZS021 Increases Drought Tolerance in Sugarcane. <b>2018</b> , 9, 3262		21
702	Novel Insights reveal Anti-microbial Gene Regulation of Piglet Intestine Immune in response to <i>Clostridium perfringens</i> Infection. <b>2019</b> , 9, 1963		10
701	Genome-Wide mRNA-Seq Profiling Reveals that LEF1 and SMAD3 Regulate Epithelial-Mesenchymal Transition Through the Hippo Signaling Pathway During Palatal Fusion. <b>2019</b> , 23, 197-203		2
700	Brain transcriptome of honey bees ( <i>Apis mellifera</i> ) exhibiting impaired olfactory learning induced by a sublethal dose of imidacloprid. <b>2019</b> , 156, 36-43		25
699	The complete chloroplast genome of a rare species <i>Capparis versicolor</i> Griff. (Rhoadales: Capparaceae). <b>2019</b> , 4, 527-529		
698	Herb Target Prediction Based on Representation Learning of Symptom related Heterogeneous Network. <b>2019</b> , 17, 282-290		8
697	Drug repositioning via matrix completion with multi-view side information. <b>2019</b> , 13, 267-275		2
696	IILLS: predicting virus-receptor interactions based on similarity and semi-supervised learning. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 651	3.6	5
695	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. <b>2019</b> ,		5
694	Drug-target interaction data cluster analysis based on improving the density peaks clustering algorithm. <b>2019</b> , 23, 1335-1353		3
693	Mental-Map Preserving Visualisation of Partitioned Networks in Vanted. <i>Journal of Integrative Bioinformatics</i> , <b>2019</b> , 16,	3.8	1
692	Systems and Synthetic Biotechnology for Production of Nutraceuticals. <b>2019</b> ,		2

691	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 574	3.6	7
690	Functional Characterization and Genomic Analysis of the Chlorantraniliprole-Degrading Strain Sp. GW13. <b>2019</b> , 6,		1
689	Transcriptional Profiles of Murine Bone Marrow-Derived Dendritic Cells in Response to Peste des Petits Ruminants Virus. <b>2019</b> , 6,		1
688	Predicting drug-target interactions from drug structure and protein sequence using novel convolutional neural networks. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 689	3.6	17
687	Global gene expression analysis of cell-free RNA in amniotic fluid from women destined to develop preeclampsia. <b>2019</b> , 98, e13971		5
686	Comparative analysis of the complete chloroplast genome sequences of six species of Miller, Ranunculaceae. <b>2019</b> , 14, 53		5
685	Characterization and sequence analysis of potential biofertilizer and biocontrol agent <i>Bacillus subtilis</i> strain SEM-9 from silkworm excrement. <b>2019</b> , 65, 45-58		6
684	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp ( <i>Litopenaeus vannamei</i> ). <b>2019</b> , 499, 109-118		42
683	Predicting drug-target interactions using Lasso with random forest based on evolutionary information and chemical structure. <b>2019</b> , 111, 1839-1852		73
682	Complete genome sequence unveiled cellulose degradation enzymes and secondary metabolic potentials in <i>Streptomyces</i> sp. CC0208. <b>2019</b> , 59, 267-276		3
681	A novel lncRNA-mediated trans-regulatory mechanism in the development of cleft palate in mouse. <b>2019</b> , 7, e00522		6
680	Pharmacodynamics simulation of HOEC by a computational model of arachidonic acid metabolic network. <b>2019</b> , 7, 30-41		1
679	Transcriptomic and evolutionary analyses of white pear ( <i>Pyrus bretschneideri</i> ) $\alpha$ -amylase genes reveals their importance for cold and drought stress responses. <b>2019</b> , 689, 102-113		11
678	TAZ activation by Hippo pathway dysregulation induces cytokine gene expression and promotes mesothelial cell transformation. <b>2019</b> , 38, 1966-1978		9
677	A Foodomics Approach: CE-MS for Comparative Metabolomics of Colon Cancer Cells Treated with Dietary Polyphenols. <b>2019</b> , 1855, 303-313		1
676	Complete genome sequence of marine <i>Bacillus</i> sp. Y-01, isolated from the plastics contamination in the Yellow Sea. <b>2019</b> , 43, 72-74		2
675	Live single cell mass spectrometry reveals cancer-specific metabolic profiles of circulating tumor cells. <b>2019</b> , 110, 697-706		51
674	Genome-wide identification, characterization and expression analysis of novel long non-coding RNAs that mediate IBA-induced adventitious root formation in apple rootstocks. <b>2019</b> , 87, 287-302		14

673	Strategies for Pathway Analysis Using GWAS and WGS Data. <b>2019</b> , 100, e79	17
672	T cell dysfunction in chronic hepatitis B infection and liver cancer: evidence from transcriptome analysis. <b>2019</b> , 56, 22-28	6
671	Transcriptome profiling and histology changes in juvenile blunt snout bream ( <i>Megalobrama amblycephala</i> ) liver tissue in response to acute thermal stress. <b>2019</b> , 111, 242-250	13
670	Mutations of <i>Mycobacterium tuberculosis</i> induced by anti-tuberculosis treatment result in metabolism changes and elevation of ethambutol resistance. <b>2019</b> , 72, 151-158	2
669	Data Curation can Improve the Prediction Accuracy of Metabolic Intrinsic Clearance. <b>2019</b> , 38, e1800086	14
668	Genome-wide identification and comprehensive analysis of Excretory/Secretory proteins in nematodes provide potential drug targets for parasite control. <b>2019</b> , 111, 297-309	6
667	Open-source chemogenomic data-driven algorithms for predicting drug-target interactions. <b>2019</b> , 20, 1465-1474	18
666	Artificial intelligence in drug combination therapy. <b>2019</b> , 20, 1434-1448	29
665	Molecular subtyping of cancer: current status and moving toward clinical applications. <b>2019</b> , 20, 572-584	35
664	Drug knowledge bases and their applications in biomedical informatics research. <b>2019</b> , 20, 1308-1321	17
663	Whole genome sequence of <i>Auricularia heimuer</i> (Basidiomycota, Fungi), the third most important cultivated mushroom worldwide. <b>2019</b> , 111, 50-58	28
662	Drug Target Prediction by Multi-View Low Rank Embedding. <b>2019</b> , 16, 1712-1721	9
661	Complete Genome of <i>Bacillus velezensis</i> CMT-6 and Comparative Genome Analysis Reveals Lipopeptide Diversity. <b>2020</b> , 58, 1-15	8
660	Predicting Drug Target Interaction by Integrating Drug Fingerprint and Drug Side Effect Using Machine Learning. <b>2020</b> , 281-290	0
659	Genome Resource for Barley Leaf Stripe Pathogen. <b>2020</b> , 104, 320-322	2
658	Relationships between hydrocarbon evolution and the geochemistry of solid bitumen in the Guanwushan Formation, NW Sichuan Basin. <b>2020</b> , 111, 116-134	36
657	Predicting human disease-associated circRNAs based on locality-constrained linear coding. <b>2020</b> , 112, 1335-1342	24
656	Identification of potential drug-targets by combining evolutionary information extracted from frequency profiles and molecular topological structures. <b>2020</b> , 96, 758-767	7

655	The complete genome sequence of <i>Bifidobacterium longum</i> LTBL16, a potential probiotic strain from healthy centenarians with strong antioxidant activity. <b>2020</b> , 112, 769-773	8
654	Complete genome sequence of <i>Paracoccus</i> sp. Arc7-R13, a silver nanoparticles synthesizing bacterium isolated from Arctic Ocean sediments. <b>2020</b> , 50, 100694	3
653	Artificial Intelligence in Drug Treatment. <b>2020</b> , 60, 353-369	11
652	Accessing <i>Cryptosporidium</i> Omic and Isolate Data via CryptoDB.org. <b>2020</b> , 2052, 139-192	2
651	Evaluation of bacterial association in methane generation pathways of an anaerobic digesting sludge via metagenomic sequencing. <b>2020</b> , 202, 31-41	12
650	<i>Cryptosporidium</i> . <b>2020</b> ,	1
649	Transcriptional patterns of <i>Emiliana huxleyi</i> in the North Pacific Subtropical Gyre reveal the daily rhythms of its metabolic potential. <b>2020</b> , 22, 381-396	7
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647	Identification of drug-target interactions via fuzzy bipartite local model. <b>2020</b> , 32, 10303-10319	60
646	Bioinformatics of excretory/secretory proteins of <i>Toxoplasma gondii</i> strain ME49. <b>2020</b> , 140, 103951	0
645	A deep learning architecture for metabolic pathway prediction. <b>2020</b> , 36, 2547-2553	25
644	Dissecting microbial community structure in sewage treatment plant for pathogens' detection using metagenomic sequencing technology. <b>2020</b> , 202, 825-833	6
643	Identification of neuropeptides from eyestalk transcriptome profiling analysis of female oriental river prawn ( <i>Macrobrachium nipponense</i> ) under hypoxia and reoxygenation conditions. <b>2020</b> , 241, 110392	3
642	Bacterial growth, morphology, and cell component changes in <i>Herbaspirillum</i> sp. WT00C exposed to high concentration of selenate. <b>2020</b> , 60, 304-321	4
641	Raman-deuterium isotope probing to study metabolic activities of single bacterial cells in human intestinal microbiota. <b>2020</b> , 13, 572-583	28
640	Identification and comprehensive characterization of lncRNAs with copy number variations and their driving transcriptional perturbed subpathways reveal functional significance for cancer. <b>2020</b> , 21, 2153-2166	2
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638	Whole metagenome sequencing of cecum microbiomes in Ethiopian indigenous chickens from two different altitudes reveals antibiotic resistance genes. <b>2020</b> , 112, 1988-1999	12

637	LC-MS and docking profiling reveals potential difference between the pure and crude fucoidan metabolites. <b>2020</b> , 143, 11-29		8
636	High-throughput small molecule screening reveals Nrf2-dependent and -independent pathways of cellular stress resistance. <b>2020</b> , 6,		5
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633	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. <b>2020</b> , 18, 489-500		2
632	Mutant Strains of <i>Escherichia coli</i> and Methicillin-Resistant <i>Staphylococcus aureus</i> Obtained by Laboratory Selection To Survive on Metallic Copper Surfaces. <b>2020</b> , 87,		2
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629	Metagenomic analysis reveals mechanisms of atrazine biodegradation promoted by tree species. <b>2020</b> , 267, 115636		9
628	Responses to iron oxide and zinc oxide nanoparticles in echinoderm embryos and microalgae: uptake, growth, morphology, and transcriptomic analysis. <b>2020</b> , 14, 1342-1361		4
627	Identification of Drug-Target Interactions via Dual Laplacian Regularized Least Squares with Multiple Kernel Fusion. <b>2020</b> , 204, 106254		63
626	Sanitary Conditions Affect the Colonic Microbiome and the Colonic and Systemic Metabolome of Female Pigs. <b>2020</b> , 7, 585730		4
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622	Differential proteomics study of postharvest <i>Volvariella volvacea</i> during storage at 4°C. <b>2020</b> , 10, 13134		2
621	Drug-target interactions prediction using marginalized denoising model on heterogeneous networks. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 330	3.6	1
620	Identification of a Recurrence Signature and Validation of Cell Infiltration Level of Thyroid Cancer Microenvironment. <b>2020</b> , 11, 467		6

619	Shotgun Proteomics of Ascidians Tunic Gives New Insights on Host-Microbe Interactions by Revealing Diverse Antimicrobial Peptides. <b>2020</b> , 18,	5
618	Draft Genome Sequence of the Bacterium Paraburkholderia aromaticivorans AR20-38, a Gram-Negative, Cold-Adapted Degrader of Aromatic Compounds. <b>2020</b> , 9,	2
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614	ASMT Regulates Tumor Metastasis Through the Circadian Clock System in Triple-Negative Breast Cancer. <b>2020</b> , 10, 537247	0
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611	Comparative genomic analysis reveals metabolic diversity of different Paenibacillus groups. <b>2020</b> , 104, 10133-10143	4
610	Prediction of Drug-Target Interactions by Ensemble Learning Method From Protein Sequence and Drug Fingerprint. <b>2020</b> , 8, 185465-185476	2
609	Genomic Analysis for Antioxidant Property of Lactobacillus plantarum FLPL05 from Chinese Longevity People. <b>2020</b> , 12, 1451-1458	7
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605	Inference of Subpathway Activity Profiles Reveals Metabolism Abnormal Subpathway Regions in Glioblastoma Multiforme. <b>2020</b> , 10, 1549	
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602	Characterization of a Protease Hyper-Productive Mutant of Bacillus pumilus by Comparative Genomic and Transcriptomic Analysis. <b>2020</b> , 77, 3612-3622	1

601	Comprehensive analysis of GTP cyclohydrolase I activity in <i>Mycobacterium tuberculosis</i> H Rv via in silico studies. <b>2021</b> , 68, 756-768	1
600	Metalloproteins and apolipoprotein C: candidate plasma biomarkers of T2DM screened by comparative proteomics and lipidomics in ZDF rats. <b>2020</b> , 17, 66	2
599	Ensemble Learning Prediction of Drug-Target Interactions Using GIST Descriptor Extracted from PSSM-Based Evolutionary Information. <b>2020</b> , 2020, 4516250	1
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597	Quantitative models of nitrogen-fixing organisms. <b>2020</b> , 18, 3905-3924	6
596	Antigen-stimulated PBMC transcriptional protective signatures for malaria immunization. <b>2020</b> , 12,	12
595	Lactic acid biosynthesis pathways and important genes of <i>Lactobacillus panis</i> L7 isolated from the Chinese liquor brewing microbiome. <b>2020</b> , 36, 100627	7
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589	Genome-Scale Metabolic Model Driven Design of a Defined Medium for M1cam. <b>2020</b> , 11, 1072	2
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583	Comparative genomics and association analysis identifies virulence genes of <i>Cercospora sojina</i> in soybean. <i>BMC Genomics</i> , <b>2020</b> , 21, 172	4-5	3
582	Systems biology-based approaches to summarize and identify novel genes and pathways associated with acute and chronic postsurgical pain. <b>2020</b> , 62, 109738		9
581	Proteomic analyses reveal that Orf virus induces the activation and maturation of mouse bone marrow-derived dendritic cells. <b>2020</b> , 132, 563-573		0
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579	Genes and novel sRNAs involved in PAHs degradation in marine bacteria sp. P14 revealed by the genome and transcriptome analysis. <b>2020</b> , 10, 140		11
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573	A Machine Learning Approach for Drug-target Interaction Prediction using Wrapper Feature Selection and Class Balancing. <b>2020</b> , 39, e1900062		17
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566	Identification of bacteria involved in the decomposition of lignocellulosic biomass treated with cow rumen fluid by metagenomic analysis. <b>2020</b> , 130, 137-141		4

565	Identification of FOS as a Candidate Risk Gene for Liver Cancer by Integrated Bioinformatic Analysis. <b>2020</b> , 2020, 6784138		5
564	Identifying GPCR-drug interaction based on wordbook learning from sequences. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 150	3.6	5
563	Identification and validation of metformin protects against PM-induced macrophages cytotoxicity by targeting toll like receptor pathway. <b>2020</b> , 251, 126526		2
562	Metagenome metabolic analysis revealing the mechanism of simultaneous methanogenesis, aerobic methane oxidation and denitrification (SMAMOD) in a microaerobic up-flow sludge bed biofilm reactor. <b>2020</b> , 95, 2229-2236		7
561	Complete genome sequence data of multidrug-resistant <i>Stenotrophomonas</i> sp. strain SXG-1. <b>2020</b> , 22, 206-209		2
560	Pharmacodynamics of Ceftiofur Selected by Genomic and Proteomic Approaches of Isolated from the Flounder,. <b>2020</b> , 2020, 4850290		0
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558	Modified linear regression predicts drug-target interactions accurately. <b>2020</b> , 15, e0230726		6
557	Machine learning approaches and databases for prediction of drug-target interaction: a survey paper. <b>2021</b> , 22, 247-269		66
556	Troponin T amino acid mutation (R210) knock-in mice as a neonatal dilated cardiomyopathy model. <b>2021</b> , 89, 846-857		0
555	A computational approach for predicting drug-target interactions from protein sequence and drug substructure fingerprint information. <b>2021</b> , 36, 593-609		7
554	Complete genome sequence of an Arctic Ocean bacterium <i>Shewanella</i> sp. Arc9-LZ with capacity of synthesizing silver nanoparticles in darkness. <b>2021</b> , 56, 100808		3
553	Semantic Technologies in Drug Discovery. <b>2021</b> , 129-144		1
552	Disequilibrium in chicken gut microflora with avian colibacillosis is related to microenvironment damaged by antibiotics. <b>2021</b> , 762, 143058		4
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549	Small molecule databases: A collection of promising bioactive molecules. <b>2021</b> , 65-88		
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544	Molecular docking and dynamics simulations of novel drug targets. <b>2021</b> , 79-131	0
543	A neighborhood-based global network model to predict drug-target interactions. <b>2021</b> , PP,	0
542	An Efficient Computational Method to Predict Drug-Target Interactions Utilizing Matrix Completion and Linear Optimization Method. <b>2021</b> , 603-614	
541	Drug-Target Interaction Prediction Based on Multi-Similarity Fusion and Sparse Dual-Graph Regularized Matrix Factorization. <b>2021</b> , 9, 99718-99730	0
540	Structural-Genetic Characterization Of Novel Butaryl co-A Dehydrogenase and Proposition of Butanol Biosynthesis Pathway in <i>Pusillimonas ginsengisoli</i> SBSA. <b>2021</b> , 89, 81-94	1
539	A review on compound-protein interaction prediction methods: Data, format, representation and model. <b>2021</b> , 19, 1541-1556	8
538	Drug-Target Interactions Prediction with Feature Extraction Strategy Based on Graph Neural Network. <b>2021</b> , 561-569	
537	Complete genome sequence of the LCL126. <b>2021</b> , 12, 745-754	3
536	Neural Networks for Modeling Metabolic Pathways. <b>2021</b> , 177-193	
535	Metagenomics survey unravels diversity of biogas microbiomes with potential to enhance productivity in Kenya. <b>2021</b> , 16, e0244755	4
534	Large-scale regulatory and signaling network assembly through linked open data. <b>2021</b> , 2021,	
533	First description of color variations in the annual killifish <i>Millerichthys robustus</i> , and preliminary observations about its geographical distribution. <b>2021</b> , 104, 293-307	0
532	Inheritance of chloroplast genomic DNA in interspecific hybrids. <b>2021</b> , 6, 351-357	3
531	Transcriptome profiling and differential expression analysis of the immune-related genes during the acute phase of infection with <i>Mycobacterium marinum</i> in the goldfish ( <i>Carassius auratus</i> L.). <b>2021</b> , 533, 736198	3
530	Analyses of transcriptomes and the first complete genome of <i>Leucocalocybe mongolica</i> provide new insights into phylogenetic relationships and conservation. <b>2021</b> , 11, 2930	0

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525	The first complete mitochondrial genome of eggplant (). <b>2021</b> , 6, 650-652	
524	Rapid molecular evolution of symbionts of. <b>2021</b> , 7,	8
523	BOW-GBDT: A GBDT Classifier Combining With Artificial Neural Network for Identifying GPCR-Drug Interaction Based on Wordbook Learning From Sequences. <b>2020</b> , 8, 623858	6
522	The influence of spaceflight and simulated microgravity on bacterial motility and chemotaxis. <b>2021</b> , 7, 7	7
521	Genomic Comparison of AP and DR131 with Emphasis on the Butyric Acid Biosynthetic Pathways. <b>2021</b> , 9,	2
520	De novo transcriptome assembly of transgenic tobacco ( NC89) with early senescence characteristic. <b>2021</b> , 27, 237-249	
519	<i>Herbidospira solisilvae</i> sp. nov., a novel cellulose-degrading actinobacterium isolated from forest soil. <b>2021</b> , 114, 581-590	0
518	Characterization and overexpression of esterases-encoding Lip900 and Lip3954 through metagenomic sequencing of paddy soil. <b>2021</b> , 1113, 012005	
517	Mass spectrometry based untargeted metabolomics for plant systems biology. <b>2021</b> , 5, 189-201	2
516	Integrated analysis of three newly sequenced fern chloroplast genomes: Genome structure and comparative analysis. <b>2021</b> , 11, 4550-4563	5
515	Collaborative Matrix Factorization with Soft Regularization for Drug-Target Interaction Prediction. <b>2021</b> , 36, 310-322	1
514	The factors for the early and late development of midbrain dopaminergic neurons segregate into two distinct evolutionary clusters. <b>2021</b> , 1, 100002	1
513	Discovery through Machine Learning and Preclinical Validation of Novel Anti-Diabetic Peptides. <b>2021</b> , 9,	5
512	Drug-Target Interaction Prediction via Dual Laplacian Graph Regularized Logistic Matrix Factorization. <b>2021</b> , 2021, 5599263	0

511	Transcriptomic Responses of Four Pelagophytes to Nutrient (N, P) and Light Stress. <b>2021</b> , 8,	1
510	Recent advances in systems and synthetic biology approaches for developing novel cell-factories in non-conventional yeasts. <b>2021</b> , 47, 107695	27
509	The effects of ALA-PDT on microbiota in pilosebaceous units of patients with severe acne: A metagenomic study. <b>2021</b> , 33, 102050	3
508	Necrotic enteritis challenge regulates peroxisome proliferator-1 activated receptors signaling and Ebxidation pathways in broiler chickens. <b>2021</b> , 7, 239-251	3
507	Homogentisic Acid-Based Whole-Cell Biosensor for Detection of Alkaptonuria Disease. <b>2021</b> , 93, 4521-4527	2
506	Comparative analysis of chloroplast genomes of kenaf cytoplasmic male sterile line and its maintainer line. <b>2021</b> , 11, 5301	0
505	Microsatellite polymorphism and genetic differentiation of different populations screened from genome survey sequencing in red-tail catfish ( <i>Hemibagrus wyckioides</i> ). <b>2021</b> , 19, 100614	1
504	Grassland fairy rings of <i>Leucocalocybe mongolica</i> represent the center of a rich soil microbial community. <b>2021</b> , 52, 1357-1369	0
503	Pharmacometabonomics: data processing and statistical analysis. <b>2021</b> , 22,	9
502	The Ion-Translocating NrfD-Like Subunit of Energy-Transducing Membrane Complexes. <b>2021</b> , 9, 663706	1
501	Complete chloroplast genome sequencing of Job's tears ( <i>L.</i> ): genome structure, comparative analysis, and phylogenetic relationships. <b>2021</b> , 6, 1399-1405	1
500	Recent Advances in Development, Validation, and Exploitation of QSAR Models. 1-30	1
499	A computational approach to aid clinicians in selecting anti-viral drugs for COVID-19 trials. <b>2021</b> , 11, 9047	7
498	Metatranscriptomic Analysis Reveals an Imbalance of Hepatopancreatic Flora of Chinese Mitten Crab with Hepatopancreatic Necrosis Disease. <b>2021</b> , 10,	1
497	Metagenomics Analysis Reveals the Microbial Communities, Antimicrobial Resistance Gene Diversity and Potential Pathogen Transmission Risk of Two Different Landfills in China. <b>2021</b> , 13, 230	1
496	Skeletal Muscle Gene Expression Profile in Response to Caloric Restriction and Aging: A Role for SirT1. <b>2021</b> , 12,	1
495	Microbial Ecological Mechanism for Long-Term Production of High Concentrations of -Caproate via Lactate-Driven Chain Elongation. <b>2021</b> , 87,	7
494	Phenotypic and genomic characterization of a strain causing disease in provides insights into its niche adaptation and pathogenic mechanism. <b>2021</b> , 7,	1

493	Enhanced Thermogenesis in Triple-Negative Breast Cancer Is Associated with Pro-Tumor Immune Microenvironment. <b>2021</b> , 13,	7
492	Complete genome sequence of <i>Metabacillus</i> sp. cB07, a bacterium inducing settlement and metamorphosis of coral larvae. <b>2021</b> , 60, 100877	0
491	Pan-Genome Analysis of and Strains Isolated From Migratory Birds at Dali Nouer Lake in Chifeng, China. <b>2021</b> , 8, 638820	2
490	Genomic Analysis of the <i>Mycoparasite</i> sp. PG52. <b>2021</b> , 70, 189-199	1
489	Predicting Drug-Target Interactions Based on the Ensemble Models of Multiple Feature Pairs. <b>2021</b> , 22,	
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486	Application of Machine Learning Techniques in Drug-target Interactions Prediction. <b>2021</b> , 27, 2076-2087	2
485	The extremely large chloroplast genome of the green alga <i>Haematococcus pluvialis</i> : Genome structure, and comparative analysis. <b>2021</b> , 56, 102308	2
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482	Genome Sequence Resource of Padwick Strain HN-1, a Causal Agent of Maize Stalk Rot Disease. <b>2021</b> ,	0
481	Analysis of the Genome Sequence of Strain GiC-126 of with Genetic Linkage Map. <b>2021</b> , 49, 406-420	
480	Genomic Analysis of Reveals the Basis of Its Medicinal Properties and Evolutionary Relationships. <b>2021</b> , 12, 652324	2
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474	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <b>2021</b> , 148, 111285	0
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471	Multimorbidity prediction using link prediction. <b>2021</b> , 11, 16392	2
470	Haloalkaliphilic denitrifiers-dependent sulfate-reducing bacteria thrive in nitrate-enriched environments. <b>2021</b> , 201, 117354	2
469	Hippocampal miR-211-5p regulates neurogenesis and depression-like behaviors in the rat. <b>2021</b> , 194, 108618	3
468	Using Continuous Directed Evolution to Improve Enzymes for Plant Applications.	
467	Complete Genome of Marine Microalgae Associated Algicidal Bacterium <i>Sulfitobacter pseudonitzschiae</i> H46 with Quorum Sensing System. <b>2021</b> , 78, 3741-3750	3
466	Machine learning methods, databases and tools for drug combination prediction. <b>2021</b> ,	5
465	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. <b>2021</b> , 11,	1
464	DNN-DTIs: Improved drug-target interactions prediction using XGBoost feature selection and deep neural network. <b>2021</b> , 136, 104676	4
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461	Genome mining reveals the genes of carboxypeptidase for OTA-detoxification in <i>Bacillus subtilis</i> CW14. <b>2021</b> , 186, 800-810	1
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459	In silico identification of excretory/secretory proteins and drug targets in monogenean parasites. <b>2021</b> , 93, 104931	3
458	Egg incubation and plasma proteome alterations in response to brood care in maternal crayfish ( <i>Procambarus clarkii</i> ). <b>2021</b> , 542, 736888	2

457	DTi2Vec: Drug-target interaction prediction using network embedding and ensemble learning. <b>2021</b> , 13, 71	4
456	Genome Sequence Resource for <i>Colletotrichum viniferum</i> , the cause of grapevine ripe rot in China. <b>2021</b> ,	0
455	Identification of drug-target interactions via multi-view graph regularized link propagation model. <b>2021</b> , 461, 618-631	8
454	Metagenomic Analysis Identifies Sex-Related Cecal Microbial Gene Functions and Bacterial Taxa in the Quail. <b>2021</b> , 8, 693755	0
453	Environmental DNA reveals aquatic biodiversity of an urban backwater area, southeast coast of India. <b>2021</b> , 171, 112786	1
452	TMT-based comparative proteomic analysis reveals regulatory pathways and protein targets associated with resin biosynthesis in <i>Pinus massoniana</i> . <b>2021</b> , 172, 114077	1
451	Three-compartment septic tanks as sustainable on-site treatment facilities? Watch out for the potential dissemination of human-associated pathogens and antibiotic resistance. <b>2021</b> , 300, 113709	1
450	Transcriptome profile analysis of the accompanying migratory parasitic wasp <i>Aenasius bambawalei</i> (= <i>Aenasius arizonensis girault</i> ) (Hymenoptera: Encyrtidae): Genes related to fertilization involved at different stage of ovary development. <b>2022</b> , 46, 195-205	0
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447	DPS1 regulates cuticle development and leaf senescence in rice. <b>2021</b> , 10, e273	4
446	Systems biology and bioinformatics approaches in leishmaniasis. <b>2021</b> , 509-548	1
445	A Survey of Computational Approaches to Reconstruct and Partition Biological Networks. 1-43	2
444	Modeling for Evolving Biological Networks. 77-108	1
443	Decomposing Metabolomic Isotope Patterns. <b>2006</b> , 12-23	12
442	Genome Analysis of Species of Agricultural Interest. <b>2009</b> , 385-402	1
441	Data Integration. <b>2009</b> , 151-171	2
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424	Phosphoproteome resource for systems biology research. <b>2011</b> , 694, 307-22	11
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422	Gene expression networks. <b>2013</b> , 930, 165-78	2

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417	An Ensemble Learning Approach for Improving Drug-Target Interactions Prediction. <b>2015</b> , 433-442	4
416	Structural Properties as Proxy for Semantic Relevance in RDF Graph Sampling. <b>2014</b> , 81-96	18
415	Mathematical Morphology on Soft Sets for Application to Metabolic Networks. <b>2015</b> , 209-218	1
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411	Reconstructing Metabolic Pathways by Bidirectional Chemical Search. <b>2007</b> , 217-232	1
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407	Boosting the Performance of Inference Algorithms for Transcriptional Regulatory Networks Using a Phylogenetic Approach. <b>2008</b> , 245-258	6
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405	Abstracts versus Full Texts and Patents: A Quantitative Analysis of Biomedical Entities. <b>2010</b> , 152-165	4
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402	Lagrangian Relaxation Applied to Sparse Global Network Alignment. <b>2011</b> , 225-236	21
401	Systems Biology and Integrative Omics in Breast Cancer. <b>2014</b> , 333-352	2
400	Omics Technology. <b>2010</b> , 11-31	7
399	Predicting Gene Function Using Omics Data: From Data Preparation to Data Integration. <b>2011</b> , 215-242	2
398	Advancement in Sustainable Agriculture: Computational and Bioinformatics Tools. <b>2019</b> , 465-547	4
397	<i>Halobasidium xiangyangense</i> gen. nov., sp. nov., a new xylose-utilizing yeast in the family Cystobasidiaceae, isolated from the pickling sauce used to make Datoucai, a high-salt fermented food. <b>2019</b> , 69, 139-145	5
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394	Advances in environmental genomics: towards an integrated view of micro-organisms and ecosystems. <b>2008</b> , 154, 347-359	24
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392	Rapid molecular evolution of <i>Spiroplasma</i> symbionts of <i>Drosophila</i> .	1
391	DNN-DTIs: improved drug-target interactions prediction using XGBoost feature selection and deep neural network.	3
390	Drug-Target Interaction prediction using Multi Graph Regularized Nuclear Norm Minimization.	2
389	Drug-Target Interaction prediction using Multi-Graph Regularized Deep Matrix Factorization.	2
388	Environment and host species identity shape gut microbiota diversity in sympatric herbivorous mammals. <b>2021</b> , 14, 1300-1315	5
387	Lignocellulosic Biomass Conversion to Ethanol by <i>Saccharomyces</i> . 17-36	15
386	Molecular Aspects of Butanol Fermentation. 321-334	1

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77	NNDSVD-GRMF: A Graph Dual Regularization Matrix Factorization Method Using Non-Negative Initialization for Predicting Drug-Target Interactions. <b>2022</b> , 10, 91235-91244	0
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75	Biological control and plant growth promotion properties of <i>Streptomyces albidoflavus</i> St-220 isolated from <i>Salvia miltiorrhiza</i> rhizosphere. 13,	2
74	Structural and functional dysbiosis of gut microbiota in Tibetan subjects with coronary heart disease. <b>2022</b> , 110483	0
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66	Description of <i>Halosolutus amylolyticus</i> gen. nov., sp. nov., <i>Halosolutus halophilus</i> sp. nov. and <i>Halosolutus gelatinilyticus</i> sp. nov., and genome-based taxonomy of genera <i>Natribaculum</i> and <i>Halovarius</i> . <b>2022</b> , 72,	0
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64	Functional Interpretation of Cross-Talking Pathways with Emphasis on Amino Acid Metabolism in Rhizosphere Microbiome of the Wild Plant <i>Moringa oleifera</i> . <b>2022</b> , 12, 1814	1
63	Cell Adhesion Molecules Affected by Ionizing Radiation and Estrogen in an Experimental Breast Cancer Model. <b>2022</b> , 23, 12674	0
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