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529	Molecular Basis of Inhibitory Mechanism of Naltrexone and Its Metabolites through Structural and Energetic Analyses. <b>2022</b> , 27, 4919	
529 528	Molecular Basis of Inhibitory Mechanism of Naltrexone and Its Metabolites through Structural and Energetic Analyses. <b>2022</b> , 27, 4919  Sulfur and methane oxidation by a single microorganism. <b>2022</b> , 119,	O
529 528 527	Molecular Basis of Inhibitory Mechanism of Naltrexone and Its Metabolites through Structural and Energetic Analyses. 2022, 27, 4919  Sulfur and methane oxidation by a single microorganism. 2022, 119,  Chimeric GPCRs mimic distinct signaling pathways and modulate microglia responses. 2022, 13,  Transcription factor NTL9 negatively regulates Arabidopsis vascular cambium development during	0
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521	High Nucleotide Substitution Rates Associated with Retrotransposon Proliferation Drive Dynamic Secretome Evolution in Smut Pathogens.	
520	Complete Genome Sequencing of Polar Arthrobacter sp. PAMC25284, Copper Tolerance Potential Unraveled with Genomic Analysis. <b>2022</b> , 2022, 1-12	О
519	Genomic characterization and phylogenetic analysis of a novel Nairobi sheep disease genogroup Orthonairovirus from ticks, Southeastern China. 13,	
518	Comprehensive characterization of Cysteine-rich protein-coding genes of Giardia lamblia and their role during antigenic variation. <b>2022</b> , 110462	o
517	Genome-wide identification of myeloblastosis gene family and its response to cadmium stress in Ipomoea aquatica. 13,	1
516	Complete Genome Sequence of the Gordonia Bacteriophage BiggityBass.	
515	Exploring the medicinally important secondary metabolites landscape through the lens of transcriptome data in fenugreek (Trigonella foenum graecum L.). <b>2022</b> , 12,	O
514	Transcriptional analysis of Ceratopteris richardii young sporophyte reveals conservation of stem cell factors in the root apical meristem. 13,	O
513	Transcriptomic analysis of the tick midgut and salivary gland responses upon repeated blood-feeding on a vertebrate host. 12,	0
512	Study of determined and AlphaFold2 predicted molecular structures of 13 human solute carrier transporters and their water-soluble QTY variants.	
511	Mass spectrometry-based immunopeptidomics and computational vaccinology strategies for the identification of universal Shigella immunogenic candidates. <b>2022</b> , 148, 105900	
510	A different transcriptional landscape sheds light on Russian sturgeon (Acipenser gueldenstaedtii) mechanisms to cope with bacterial infection and chronic heat stress. <b>2022</b> , 128, 505-522	О
509	Investigating the conformational dynamics of Zika virus NS4B protein. <b>2022</b> , 575, 20-35	0
508	Gene expression in the sugar metabolism between <b>G</b> uanxilþummelo and its early-ripening mutant <b>G</b> liuyuezao <b>[]2022</b> , 305, 111435	
507	Evaluation of indirect-ELISA using eluted antigens from Trichinella spiralis muscle larvae for diagnosis of swine trichinellosis. <b>2022</b> , 235, 106644	
506	Analysis of Crassostrea gasar transcriptome reveals candidate genes involved in metal metabolism. <b>2022</b> , 307, 136009	
505	Vaccinomics to Design a Multiepitope Vaccine against Legionella pneumophila. <b>2022</b> , 2022, 1-17	0
504	Bioinformatics analysis of Muscovy duck parvovirus REP and VP1 proteins. 1-16	О

503	Roles of Species-Specific Legumains in Pathogenicity of the Pinewood Nematode Bursaphelenchus xylophilus. <b>2022</b> , 23, 10437	O
502	Genome-Wide Identification and Expression Patterns of the SWEET Gene Family in Bletilla striata and its Responses to Low Temperature and Oxidative Stress. <b>2022</b> , 23, 10057	O
501	Family dinner: Transcriptional plasticity of five Noctuidae (Lepidoptera) feeding on three host plant species. <b>2022</b> , 12,	О
500	The necrosis- and ethylene-inducing peptide 1-like protein (NLP) gene family of the plant pathogen Corynespora cassiicola.	0
499	Complete Genome Sequences of the Novel Cluster BP Phages Infecting Streptomyces sanglieri, AxeJC, Cumberbatch, Eastland, Eklok, HFrancette, Ignacio, Piccadilly, and Vondra.	O
498	Using machine learning to predict protein-protein interactions between a zombie ant fungus and its carpenter ant host.	0
497	The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences. <b>2021</b> , 8, 1024-1037	1
496	Small secreted peptides encoded on the wheat (triticum aestivum L.) genome and their potential roles in stress responses. 13,	0
495	Sex-biased proteomic response to tomato spotted wilt virus infection of the salivary glands of Frankliniella occidentalis, the western flower thrips. <b>2022</b> , 149, 103843	O
494	Designing a vaccine-based therapy against Epstein-Barr virus-associated tumors using immunoinformatics approach. <b>2022</b> , 150, 106128	0
493	Modular structure of complex II: An evolutionary perspective. <b>2023</b> , 1864, 148916	0
492	The Swiss army knife of SARS-CoV-2: the structures and functions of NSP3. <b>2022</b> , 28, 39-61	O
491	Characterization and Structural Prediction of Proteins in SARS-CoV-2 Bangladeshi Variant Through Bioinformatics. <b>2022</b> , 15, 117863612211155	О
490	In Vivo and In Vitro Characterization of Cyclase and Phosphodiesterase Rhodopsins. 2022, 325-338	O
489	Ottowia massiliensis sp. nov., a new bacterium isolated from a fresh, healthy human fecal sample. <b>2022</b> , 369,	1
488	Prevotella merdae sp. nov., a new bacterial species isolated from human faeces. <b>2022</b> , 369,	1
487	Evolutionary history of plant receptor-like kinases. <b>2023</b> , 25-37	О
486	Genomic and phenotypic evolution of nematode-infecting microsporidia.	O

485	Isolation of Saccharibacillus WB17 strain from wheat bran phyllosphere and genomic insight into the cellulolytic and hemicellulolytic complex of the Saccharibacillus genus.	Ο
484	Exploring Optimal Taxol CYP725A4 Activity in Saccharomyces cerevisiae.	Ο
483	Analysis of lineage-specific protein family variability in prokaryotes combined with evolutionary reconstructions. <b>2022</b> , 17,	0
482	Genome Sequence of a Cluster CR2 Gordonia terrae Phage, StarStruck.	Ο
481	Lack of a Zn/Co substitution ability in the polar diatom Chaetoceros neogracile RS19. <b>2022</b> , 67, 2265-2280	Ο
480	A TAle of Two Pathways: Tail-Anchored Protein Insertion at the Endoplasmic Reticulum. a041252	Ο
479	Biocomputational characterisation of MBO_200107 protein of Mycobacterium tuberculosis variant caprae: a molecular docking and simulation study. 1-20	Ο
478	Identification and Characterization of the Larval Settlement Pheromone Protein Components in Adult Shells of Crassostrea gigas: A Novel Function of Shell Matrix Proteins. <b>2022</b> , 23, 9816	Ο
477	Immunoinformatic analysis of the whole proteome for vaccine design: An application to Clostridium perfringens. 13,	0
476	Genome-Wide Identification and Expression Analysis of the PIN Auxin Transporter Gene Family in Zanthoxylum armatum DC. <b>2022</b> , 12, 1318	Ο
475	In silico designing of a novel epitope-based candidate vaccine against Streptococcus pneumoniae with introduction of a new domain of PepO as adjuvant. <b>2022</b> , 20,	0
474	Isolation, characterization, and genome sequencing of a novel chitin deacetylase producing Bacillus aryabhattai TCI-16. 13,	О
473	Host-delivered RNAi-mediated silencing of the root-knot nematode (Meloidogyne incognita) effector genes, Mi-msp10 and Mi-msp23, confers resistance in Arabidopsis and impairs reproductive ability of the root-knot nematode. <b>2022</b> , 256,	0
472	Identification of Candidate Chemosensory Gene Families by Head Transcriptomes Analysis in the Mexican Fruit Fly, Anastrepha ludens Loew (Diptera: Tephritidae). <b>2022</b> , 23, 10531	Ο
471	Exploring optimal Taxol CYP725A4 activity in Saccharomyces cerevisiae. <b>2022</b> , 21,	0
470	Systematic Analysis of Copy Number Variations in the Pathogenic Yeast Candida parapsilosis Identifies a Gene Amplification in RTA3 That is Associated with Drug Resistance.	1
469	Toward the Complete Functional Characterization of a Minimal Bacterial Proteome. 2022, 126, 6820-6834	0
468	Expansion of the global RNA virome reveals diverse clades of bacteriophages. 2022,	2

467	Evaluating complete surface-associated and secretory proteome of Leishmania donovani for discovering novel vaccines and diagnostic targets. <b>2022</b> , 204,	0
466	Detoxification Gene Families at the Genome-Wide Level of Rhus Gall Aphid Schlechtendalia chinensis. <b>2022</b> , 13, 1627	Ο
465	A specialized tyrosine-based endocytosis signal in MR1 controls antigen presentation to MAIT cells. <b>2022</b> , 221,	1
464	Enterobacteria Phage Ac3's Genome Annotation and Host Range Analysis Against the ECOR Reference Library. <b>2022</b> , 3, 165-170	O
463	Genomic Profiling of Non-O157 Shiga Toxigenic Escherichia coli-Infecting Bacteriophages from South Africa.	O
462	The colonization of land was a likely driving force for the evolution of mitochondrial retrograde signalling in plants.	O
461	Membrane Localized GbTMEM214s Participate in Modulating Cotton Resistance to Verticillium Wilt. <b>2022</b> , 11, 2342	O
460	Complete Genome Sequence of Cluster C Mycobacteriophage McGee.	O
459	An integrative reverse vaccinology, immunoinformatic, docking and simulation approaches towards designing of multi-epitopes based vaccine against monkeypox virus. 1-14	1
458	Genome-Wide Identification of Histone Modification (HM) Gene Family and Their Expression Patterns Under Abiotic Stress and Different Developmental Stages of Tea (Camellia assamica).	O
457	Immune Isoform Atlas: Landscape of alternative splicing in human immune cells.	0
456	Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. <b>2022</b> ,	1
455	Weizmannia faecalis sp. nov., isolated from a human stool sample. <b>2022</b> , 204,	1
454	The human MRS2 magnesium binding domain is a regulatory feedback switch for channel activity.	O
453	Regulation of membrane protein structure and function by their lipid nano-environment.	3
452	Molecular characterisation of a novel pathogenic avipoxvirus from an Australian little crow (Corvus bennetti) directly from the clinical sample. <b>2022</b> , 12,	1
451	Culexarchaeia, a novel archaeal class of anaerobic generalists inhabiting geothermal environments. <b>2022</b> , 2,	О
450	Comparative study of neuropeptide signaling systems in Hemiptera.	O

449	First Report and Comparative Genomic Analysis of a Mycoplasma mycoides Subspecies capri HN-A in Hainan Island. <b>2022</b> , 10, 1908	O
448	Genomic features predict bacterial life history strategies in soil, as identified by metagenomic stable isotope probing.	o
447	Unique Evolution of Antiviral Tetherin in Bats.	2
446	Draft genomes and descriptions of Urmitella timonensis gen. nov., sp. nov. and Marasmitruncus massiliensis gen. nov., sp. nov., isolated from severely malnourished African children using culturomics.	O
445	Proteomic analysis provides insights into the function of Polian vesicles in the sea cucumber Apostichopus japonicus post-evisceration. <b>2022</b> , 40, 2028-2041	0
444	Complete Genome Sequences of Cluster A Mycobacteriophages Kenmech and Peterson and Cluster F Mycobacteriophage Rockne.	O
443	RcgA and RcgR, Two Novel Proteins Involved in the Conjugative Transfer of Rhizobial Plasmids.	0
442	Genome-wide identification and expression analysis of the calmodulin-binding transcription activator (CAMTA) family genes in tea plant. <b>2022</b> , 23,	o
441	Localized cardiolipin synthesis is required for the assembly of MreB during the polarized cell division of Chlamydia trachomatis. <b>2022</b> , 18, e1010836	1
440	Identification of Putative Neuropeptides That Alter the Behaviour of Schistosoma mansoni Cercariae. <b>2022</b> , 11, 1344	1
439	Farnesyl pyrophosphate compartmentalization in the green microalga Chlamydomonas reinhardtii during heterologous (E)-bisabolene production. <b>2022</b> , 21,	1
438	Homokaryotic High-Quality Genome Assembly of Medicinal Fungi Wolfiporia hoelen Reveals Auto-Regulation and High-Temperature Adaption of Probable Two-Speed Genome. <b>2022</b> , 23, 10484	0
437	Loss of the first Estrand of human prion protein generates an aggregation-competent partially Bpenlform.	0
436	Mutation in Transmembrane Domain 8 of Human Urate Transporter 1 Disrupts Uric Acid Recognition and Transport. <b>2022</b> , 7, 34621-34631	o
435	Identification, Characterization, and Detection of a Novel Strawberry Cytorhabdovirus.	0
434	High-Quality Genome Sequence Resource of Lasiodiplodia theobromae JMB122, a Fungal Pathogen Causing Peach Gummosis.	O
433	A Bioinformatics Analysis Reveals that the Transcription Levels of Cell Surface Receptor Encoding Genes are Associated with the Drug Response of Breast Cancer Cells and the Drug Off-Target Effects.	О
432	Genomic Characterization of the Cluster CZ4 Gordonia terrae Phage Oregano.	O

431	Immunoinformatics Approach to Design Novel Subunit Vaccine against the Epstein-Barr Virus.	O
430	Functional Identification of Arthrinium phaeospermum Effectors Related to Bambusa pervariabilis [Dendrocalamopsis grandis Shoot Blight. <b>2022</b> , 12, 1264	1
429	Genomic footprints related with adaptation and fumonisins production in Fusarium proliferatum. 13,	0
428	Genome-wide identification and functional prediction of silicon (Si) transporters in poplar (Populus trichocarpa).	O
427	Whole-Genome Sequence Resource of Phytophthora pini, the Causal Pathogen of Foliage Blight and Shoot Dieback of Rhododendron pulchrum.	0
426	FAS: Assessing the similarity between proteins using multi-layered feature architectures.	O
425	Genome Sequence of the Cluster CD Gordonia Phage Widow.	0
424	Crystal structure and sugar-binding ability of the C-terminal domain of N-acetylglucosaminyltransferase IV establish a new carbohydrate-binding module family.	O
423	Recent advances in liposome development for studying protein-lipid interactions. 1-14	1
422	Transmembrane helices mediate the formation of a stable ternary complex of b5R, cyt b5, and SCD1. <b>2022</b> , 5,	O
421	Expanding the Legionella pan-kinome.	0
420	OmicsIdata unveil early molecular response underlying limb regeneration in the Chinese mitten crab, Eriocheir sinensis. <b>2022</b> , 8,	O
419	Designing mRNA- and Peptide-Based Vaccine Construct against Emerging Multidrug-Resistant Citrobacter freundii: A Computational-Based Subtractive Proteomics Approach. <b>2022</b> , 58, 1356	1
418	Cloning and Functional Characterization of a Novel EGRP Gene From Melanotus cribricollis. <b>2022</b> , 22,	O
417	A novel strategy for developing vaccine candidate against Jaagsiekte sheep retrovirus from the envelope and gag proteins: an in-silico approach. <b>2022</b> , 18,	1
416	Ratchet effect modeling by method of paradoxical games for stochastic fluctuations of double-well potential. <b>2022</b> , 13, 338-348	O
415	The structure of a Plasmodium vivax Tryptophan Rich Antigen suggests a lipid binding function for a pan-Plasmodium multi-gene family.	0
414	Involvement of glucose in freeze tolerance in the Japanese tree frog Hyla japonica.	1

413	Species-specific transcriptomic changes upon respiratory syncytial virus infection in cotton rats. <b>2022</b> , 12,	Ο
412	Structure of the two-component S-layer of the archaeon Sulfolobus acidocaldarius.	O
411	Structural model for ligand binding and channel opening of an insect gustatory receptor. 2022, 102573	1
410	Al protein structure prediction-based modeling and mutagenesis of a protostome receptor and peptide ligands reveal key residues for their interaction. <b>2022</b> , 298, 102440	O
409	Bacterial Outer Membrane Polysaccharide Export (OPX) Proteins Occupy Three Structural Classes with Selective Barrel Porin Requirements for Polymer Secretion.	2
408	Structure and proteomic analysis of the crown-of-thorns starfish (Acanthaster planci cf. solaris) radial nerve cord.	O
407	Ribosome profiling reveals the translational landscape and allele-specific translational efficiency in rice. <b>2022</b> , 100457	0
406	Lysosomal enzyme trafficking factor LYSET enables nutritional usage of extracellular proteins. <b>2022</b> , 378,	2
405	Probing the sORF-encoded peptides of Deinococcus radiodurans in response to extreme stress. <b>2022</b> , 100423	Ο
404	A candidate multi-epitope vaccine against Lumpy Skin Disease.	Ο
403	Genome-Wide Investigation and Expression Analysis of the Nitraria sibirica Pall. CIPK Gene Family. <b>2022</b> , 23, 11599	0
402	The C-terminal stretch of glycine-rich proline-rich protein (SbGPRP1) from Sorghum bicolor serves as an antimicrobial peptide by targeting the bacterial outer membrane protein.	O
401	A Genomics Resource for 12 Edible Seaweeds to Predict Seaweed-Secreted Peptides with Potential Anti-Cancer Function. <b>2022</b> , 11, 1458	0
400	Retinal Cone Mosaic in sws1-Mutant Medaka (Oryzias latipes), A Teleost. <b>2022</b> , 63, 21	O
399	Intergenic regions of Saccharomycotina yeasts are enriched in potential to form transmembrane domains.	0
398	The GPI-anchored Ly6 protein Belly roll regulatesDrosophila melanogasterescape behaviors by modulating the excitability of nociceptive peptidergic interneurons.	O
397	Cyclic phosphatidic acid is produced by GDE7 in the ER lumen as a lysophospholipid mediator.	0
396	Transcriptomic analysis of lignocellulose degradation by Streptomyces coelicolor A3(2) and elicitation of secondary metabolites production.	O

395	Tissue-specific transcriptomes reveal mechanisms of microbiome regulation in an ancient fish.	O
394	Population genomics of Puccinia graminis f.sp. tritici highlights the role of admixture in the origin of virulent wheat rust races. <b>2022</b> , 13,	o
393	A fast-killing tyrosine amide ((S)-SW228703) with blood and liver-stage antimalarial activity associated with the Cyclic Amine Resistance Locus (PfCARL).	0
392	Isolation and characterization of a neoxanthin synthase gene functioning in fucoxanthin biosynthesis of Phaeodactyum tricornutum.	O
391	Identification of Schistosoma mansoni miracidia attractant candidates in infected Biomphalaria glabrata using behaviour-guided comparative proteomics. 13,	0
390	Core Proteomics and Immunoinformatic Approaches to Design a Multiepitope Reverse Vaccine Candidate against Chagas Disease. <b>2022</b> , 10, 1669	0
389	Concerted expansion and contraction of immune receptor gene repertoires in plant genomes. <b>2022</b> , 8, 1146-1152	2
388	Genome Resource of Rhizoctonia solani anastomosis group 4 strain AG4-JY, a pathomycete of sheath blight of foxtail millet.	o
387	MPAD: A database for binding affinity of membrane protein-protein complexes and their mutants. <b>2022</b> , 167870	О
386	A Candidatus Liberibacter asiaticus Esecreted polypeptide suppresses plant immune responses in Nicotiana benthamiana and Citrus sinensis. 13,	O
385	General control nonderepressible 1 interacts with cationic amino acid transporter 1 and affects Aedes aegypti fecundity. <b>2022</b> , 15,	О
384	Genomic Data Mining Reveals Abundant Uncharacterized Transporters in Coccidioides immitis and Coccidioides posadasii. <b>2022</b> , 8, 1064	O
383	The periplasmic chaperone Skp prevents misfolding of the secretory lipase A from Pseudomonas aeruginosa. 9,	1
382	The first transcriptomic analyses of fruits and cladodes for comparison between three species of Opuntia.	0
381	In silico functional annotation of hypothetical proteins from the Bacillus paralicheniformis strain Bac84 reveals proteins with biotechnological potentials and adaptational functions to extreme environments. <b>2022</b> , 17, e0276085	О
380	Quantification of cytosol and membrane proteins in rumen epithelium of sheep with low or high CH4 emission phenotype. <b>2022</b> , 17, e0273184	0
379	Functional Study on Cytochrome P450 in Response to L仰Carvone Stress in Bursaphelenchus xylophilus. <b>2022</b> , 13, 1956	1
378	Complete Genome Sequence and Characteristics of Mycobacteriophage IkeLoa.	O

377	A conserved protein disulfide isomerase enhances plant resistance against herbivores.	О
376	A contiguous de novo genome assembly of sugar beet EL10 (Beta vulgaris L.).	О
375	Post-translational modification by the Pgf glycosylation machinery modulatesStreptococcus mutansphysiology and virulence.	О
374	Challenges in the Heterologous Production of Furanocoumarins in Escherichia coli. <b>2022</b> , 27, 7230	O
373	Affine-mapping based variational ensemble Kalman filter. <b>2022</b> , 32,	О
372	TWO DISULFIDE-REDUCING PATHWAYS ARE REQUIRED FOR THE MATURATION OF PLASTIDC-TYPE CYTOCHROMES INCHLAMYDOMONAS REINHARDTII.	O
371	Multigenic resistance to Xylella fastidiosa in wild grapes (Vitis sps.) and its implications within a changing climate.	O
370	Glycogen degrading activities of catalytic domains of \text{\text{\text{Bmylase}} and \text{\text{\text{Bmylase-pullulanase}}} enzymes conserved in Gardnerellaspp. from the vaginal microbiome.	1
369	Structural investigation of eukaryotic cells: From the periphery to the interior by cryo-electron tomography. <b>2022</b> , 100923	1
368	Genome-wide analysis of polyamine biosynthesis genes in wheat reveals gene expression specificity and involvement of STRE and MYB-elements in regulating polyamines under drought. <b>2022</b> , 23,	O
367	Phylogenomics and gene selection in Aspergillus welwitschiae: Possible implications in the pathogenicity in Agave sisalana. <b>2022</b> , 110517	0
366	Near-atomic, non-icosahedrally averaged structure of giant virus Paramecium bursaria chlorella virus 1. <b>2022</b> , 13,	O
365	The genome ofLactuca saligna, a wild relative of lettuce, provides insight into non-host resistance to the downy mildewBremia lactucae.	0
364	Genome Sequence of Cluster BI1 Streptomyces griseus Phage TaidaOne.	О
363	Alternative splicing reprogramming in fungal pathogen Sclerotinia sclerotiorum at different infection stages on Brassica napus. 13,	0
362	Functional characterization of FaMBL1, a G-type lectin gene family member, in response to fungal pathogens of strawberry.	О
361	The Venturia inaequalis effector repertoire is dominated by expanded families with predicted structural similarity, but unrelated sequence, to avirulence proteins from other plant-pathogenic fungi. <b>2022</b> , 20,	О
360	Chromosome-level assembly of the Phytophthora agathidicida genome reveals adaptation in effector gene families. 13,	Ο

359	Complete Genome Sequence of Gordonia rubripertincta Bacteriophage Hexbug Suggests Potential for a New CT Subcluster.	0
358	The Difference in Structural States between Canonical Proteins and Their Isoforms Established by Proteome-Wide Bioinformatics Analysis. <b>2022</b> , 12, 1610	O
357	Fungal Effectoromics: A World in Constant Evolution. <b>2022</b> , 23, 13433	1
356	Isolation and characterization of extracellular vesicles from biotechnologically important fungus Aureobasidium pullulans. <b>2022</b> , 9,	1
355	Genome-wide scan for potential CD4+ T-cell vaccine candidates in Candida auris by exploiting reverse vaccinology and evolutionary information. 9,	0
354	Immuno-informatics profiling of monkeypox virus cell surface binding protein for designing a next generation multi-valent peptide-based vaccine. 13,	2
353	Complete Genome Sequence of Arthrobacter Phage GantcherGoblin Exhibits Both Conservation with Subcluster AU6 Phages and Genetic Novelty.	0
352	Genomic insights into phage-host interaction in the deep-sea chemolithoautotrophic Campylobacterota, Nitratiruptor. <b>2022</b> , 2,	O
351	Molecular phenotyping uncovers differences in basic housekeeping functions among closely related species of hares ( Lepus spp., Lagomorpha: Leporidae).	0
350	Transcriptome analysis of flathead grey mullet (Mugil cephalus) ovarian development induced by recombinant gonadotropin hormones. 13,	O
349	A reverse vaccinology approach identifies putative vaccination targets in the zoonotic nematode Ascaris. 9,	O
348	Biochemical, genomic and structural characteristics of the Acr3 pump in Exiguobacterium strains isolated from arsenic-rich Salar de Huasco sediments. 13,	O
347	Deep into the apoplast: grapevine and Plasmopara viticola proteomes reveal the secret beneath host and pathogen communication at 6h after contact.	O
346	Comprehensive in silico analysis of Phospholipase D gene family in economically important orchids. <b>2022</b> , 151, 655-666	О
345	Dissecting the genome, secretome, and effectome repertoires of Monilinia spp.: The causal agent of brown rot disease: A comparative analysis. <b>2023</b> , 195, 112120	0
344	Advances in X-ray crystallography methods to study structural dynamics of macromolecules. <b>2023</b> , 309-355	O
343	Citrobacter portucalensis Sb-2 contains a metalloid resistance determinant transmitted by Citrobacter phage Chris1. <b>2023</b> , 443, 130184	0
342	De novo transcriptome assembly and identification of G-Protein-Coupled-Receptors (GPCRs) in two species of monogenean parasites of fish. <b>2022</b> , 29, 51	1

341	Molecular identification and phylogenetic analysis of putative senescence associated gene 21 in Stevia rebaudiana accession MS007. <b>2022</b> , 6, 35	0
340	Characterization of a Glycolipid Synthase Producing EGalactosylceramide in Bacteroides fragilis. <b>2022</b> , 23, 13975	О
339	SecReT6 update: a comprehensive resource of bacterial Type VI Secretion Systems.	О
338	The Role of Transmembrane Proteins in Plant Growth, Development, and Stress Responses. <b>2022</b> , 23, 13627	1
337	Characteristics and Comparative Genomic Analysis of a Novel Virus, VarioGold, the First Bacteriophage of Variovorax. <b>2022</b> , 23, 13539	0
336	Identification of potential candidate vaccines against Mycobacterium ulcerans based on the major facilitator superfamily transporter protein. 13,	o
335	A Balance between Transmembrane-Mediated ER/Golgi Retention and Forward Trafficking Signals in Glycophorin-Anion Exchanger-1 Interaction. <b>2022</b> , 11, 3512	0
334	WideEffHunter: An Algorithm to Predict Canonical and Non-Canonical Effectors in Fungi and Oomycetes. <b>2022</b> , 23, 13567	O
333	Pectobacterium carotovorum Phage vB_PcaM_P7_Pc Is a New Member of the Genus Certrevirus.	O
332	Proximity labeling facilitates defining the proteome neighborhood of photosystem II oxygen evolution complex in a model cyanobacterium. <b>2022</b> , 100440	O
331	LRG1 is an adipokine that promotes insulin sensitivity and suppresses inflammation. 11,	0
330	Reconciliation and Evolution of Penicillium rubens Genome-Scale Metabolic Networks LWhat about Specialised Metabolism?.	O
329	Transcriptomic responses of females to consumption of nuptial food gifts as a potential mediator of sexual conflict in decorated crickets.	O
328	An LH1 <b>R</b> C photocomplex from an extremophilic phototroph provides insight into origins of two photosynthesis proteins. <b>2022</b> , 5,	2
327	Hemocyte response to treatment of susceptible and resistant Asian corn borer (Ostrinia furnacalis) larvae with Cry1F toxin from Bacillus thuringiensis. 13,	0
326	InterPro in 2022.	10
325	Global analysis of common bean multidrug and toxic compound extrusion transporters (PvMATEs): PvMATE8 and pinto bean seed coat darkening. 13,	0
324	Prediction of Potential Drug Targets and Vaccine Candidates Against Antibiotic-Resistant Pseudomonas aeruginosa. <b>2022</b> , 28,	O

323	Genome Sequences of Two Gordonia rubripertincta Cluster DJ Bacteriophages, Pherobrine and Burley.	0
322	Complete Genome Sequence of Arthrobacter Phage ScienceWizSam.	O
321	Small proteome of the nitrogen-fixing plant symbiontSinorhizobium meliloti.	O
320	Design of a multi-epitope protein as a subunit vaccine against lumpy skin disease using an immunoinformatics approach. <b>2022</b> , 12,	2
319	PDIA3 Activity Promotes Extracellular Accumulation of Proteins Relevant to Basal Breast Cancer Outcomes in Human MDA-MB-A231 Breast Cancer Cells.	O
318	Complete Genome Sequence of Pythium oligandrum, Isolated from Rhizosphere Soils of Chinese Angelica sinensis.	O
317	Bioinformatics approach for the construction of multiple epitope vaccine against omicron variant of SARS-CoV-2. <b>2022</b> , 12,	O
316	Transcriptome Sequencing Provides Insights into Understanding the Infection Mechanism of Alternaria solani on Potato.	O
315	Distinct energy-coupling factor transporter subunits enable flavin acquisition and extracytosolic trafficking for extracellular electron transfer inListeria monocytogenes.	0
314	African Swine Fever Virus MGF110-7L Induces Host Cell Translation Suppression and Stress Granule Formation by Activating the PERK/PKR-eIF2Pathway.	3
313	Transcription Factor VdCf2 Regulates Growth, Pathogenicity, and the Expression of a Putative Secondary Metabolism Gene Cluster in Verticillium dahliae.	1
312	Computational Design of a Chimeric Vaccine against Plesiomonas shigelloides Using Pan-Genome and Reverse Vaccinology. <b>2022</b> , 10, 1886	O
311	The red seaweed Asparagopsis taxiformis genome and integrative -omics analysis.	1
310	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. <b>2022</b> , 8,	O
309	Identification of novel inhibitors of high affinity iron permease (FTR1) through implementing pharmacokinetics index to fight against black fungus: An in silico approach. <b>2022</b> , 106, 105385	1
308	Immunoinformatic analysis of proteins from DNA replication, repair, recombination, and restriction/modification pathway of Mycobacterium tuberculosis revealed the diagnostic potential of Rv0054 and Rv3644c. <b>2022</b> , 9, 190-201	O
307	Functional characterization of the sugarcane (Saccharum spp.) ammonium transporter AMT2;1 suggests a role in ammonium root-to-shoot translocation. 13,	О
306	Evidence for Widespread Class II Microcins in Enterobacterales Genomes.	O

305	Single-Step Protocol for Isolating the Recombinant Extracellular Domain of the Luteinizing Hormone Receptor from the Ovis aries Testis. <b>2022</b> , 44, 5718-5727	О
304	A widespread group of large plasmids in methanotrophic Methanoperedens archaea. <b>2022</b> , 13,	1
303	A NIT sensor domain containing chemoreceptor is required for a successful entry and virulence of Dickeya dadantii 3937 in potato plants.	0
302	Phylogeny, gene structures, and expression patterns of the auxin response factor (GhARF2) in upland cotton (Gossypium hirsutum L.).	Ο
301	Crystal structure of the OrfX1 IDrfX3 complex from the PMP1 neurotoxin gene cluster.	0
300	Combining IP3 affinity chromatography and bioinformatics reveals a novel protein-IP3 binding site on Plasmodium falciparum MDR1 transporter. <b>2023</b> , 4, 100179	O
299	Genes associated with desiccation stress in foodborne Staphylococcus aureus as revealed by transposon insertion mutagenesis. <b>2023</b> , 163, 112271	Ο
298	PGRMC1: An enigmatic heme-binding protein. <b>2023</b> , 241, 108326	1
297	Designing multi-epitope monkeypox virus-specific vaccine using immunoinformatics approach. <b>2023</b> , 16, 107-116	1
296	Huizhou GDP forecast based on fractional opposite-direction accumulating nonlinear grey bernoulli markov model. <b>2023</b> , 31, 947-960	O
295	Single-cell RNA sequencing uncovers dynamic roadmap and cell-cell communication during buffalo spermatogenesis. <b>2023</b> , 26, 105733	0
294	The plasma membrane magnesium transporter CsMGT5 mediates magnesium uptake and translocation under magnesium limitation in tea plants (Camellia sinensis L.). <b>2023</b> , 310, 111711	Ο
293	Trypanosoma evansi secretome carries potential biomarkers for Surra diagnosis. <b>2023</b> , 272, 104789	0
292	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. <b>2023</b> , 855, 147127	O
291	Molecular evolution and diversification of phytoene synthase (PSY) gene family. 2022, 45,	Ο
290	Predictive modeling of moonlighting DNA-binding proteins. <b>2022</b> , 4,	O
289	First Report and Comparative Genomic Analysis of Mycoplasma capricolum subsp. capricolum HN-B in Hainan Island, China. <b>2022</b> , 10, 2298	О
288	Characterization of Genomic Diversity In Bacteriophages InfectingRhodococcus.	Ο

287	Characterization and the comprehensive expression analysis of tobacco valine-glutamine genes in response to trichomes development and stress tolerance.	0
286	Immunophilin CYN28 is required for accumulation of photosystem II and thylakoid FtsH protease in Chlamydomonas.	Ο
285	Functional Analyses of a Small Secreted Cysteine-Rich Protein ThSCSP_14 in Tilletia horrida. <b>2022</b> , 23, 15042	0
284	Preliminary Characterization of Phage-Like Particles from the Male-Killing Mollicute Spiroplasma poulsonii (an Endosymbiont of Drosophila). <b>2023</b> , 80,	Ο
283	Multi-Omics of Corynebacterium Pseudotuberculosis 12CS0282 and an In Silico Reverse Vaccinology Approach Reveal Novel Vaccine and Drug Targets. <b>2022</b> , 10, 39	0
282	Extensive somatic nuclear exchanges shape global populations of the wheat leaf rust pathogenPuccinia triticina.	O
281	Genetic duplication of tissue factor reveals subfunctionalization in venous and arterial hemostasis. <b>2022</b> , 18, e1010534	O
280	Origin and Evolution of Pseudomurein Biosynthetic Gene Clusters.	O
279	Species-Specific Duplication of Surface Antigen Genes in Paramecium. <b>2022</b> , 10, 2378	1
278	Tetraspanner-based nanodomains modulate BAR domain-induced membrane curvature.	O
277	Sphingosine 1-phosphate mediates adiponectin receptor signaling essential for lipid homeostasis and embryogenesis. <b>2022</b> , 13,	1
276	Selenate and selenite transporters in proso millet: Genome extensive detection and expression studies under salt stress and selenium. 13,	Ο
275	ThSCSP_12: Novel Effector in Tilletia horrida That Induces Cell Death and Defense Responses in Non-Host Plants. <b>2022</b> , 23, 14752	0
274	Structural informatic study of determined and AlphaFold2 predicted molecular structures of 13 human solute carrier transporters and their water-soluble QTY variants. <b>2022</b> , 12,	Ο
273	Genomics of Preaxostyla Flagellates Illuminates Evolutionary Transitions and the Path Towards Mitochondrial Loss.	1
272	Antiviral signaling by a cyclic nucleotide activated CRISPR protease.	Ο
271	The extrachromosomal circular DNAs of the rice blast pathogen Magnaporthe oryzae contain a wide variety of LTR retrotransposons, genes, and effectors. <b>2022</b> , 20,	O
270	Evolutionary dynamics of transposable elements inMagnaporthe oryzaereveal evidence of genomic transfer and key differences between rice and wheat blast pathotypes.	O

269	CLSTN3Ienforces adipocyte multilocularity to facilitate lipid utilization.	1
268	Whole-genome sequencing reveals diverse mechanisms underlying quantitative pathogenicity and host adaptation in a fungal plant pathogen.	O
267	A regulatory hydrogenase gene cluster observed in the thioautotrophic symbiont of Bathymodiolus mussel in the East Pacific Rise. <b>2022</b> , 12,	О
266	Complete Genome Sequences of Septoria linicola: A Resource for Studying a Damaging Flax Pathogen.	O
265	Comparative genomics of five Valsa species gives insights on their pathogenicity evolution.	О
264	Oropouche Virus Glycoprotein Topology and Cellular Requirements for Glycoprotein Secretion.	1
263	Host-symbiont interactions in Angomonas deanei include the evolution of a host-derived dynamin ring around the endosymbiont division site. <b>2022</b> ,	O
262	Conserved degronome features governing quality control associated proteolysis. 2022, 13,	O
261	Characterization and Spatial Mapping of the Human Gut Metasecretome. 2022, 7,	О
260	Unsupervised Machine Learning Organization of the Functional Dark Proteome of Gram-Negative Buperbugs[ISix Protein Clusters Amenable for Distinct Scientific Applications. <b>2022</b> , 7, 46131-46145	O
259	Pan-kinome of Legionella expanded by a bioinformatics survey. <b>2022</b> , 12,	1
258	Mechanistic dissection of alga recognition and uptake in coral-algal endosymbiosis.	O
257	Sex-specific expression of pheromones and other signals in gravid starfish. 2022, 20,	O
256	Differential Virulence of Aggregatibacter actinomycetemcomitans Serotypes Explained by Exoproteome Heterogeneity.	O
255	Structural and functional mapping of ars gene cluster in Deinococcus indicus DR1. 2022,	О
254	Cellular production of ade novomembrane cytochrome.	O
253	Porcine antibody profiles of 33 Mycoplasma hyopneumoniae fusion proteins from M. hyopneumoniae natural infection but not vaccination.	О
252	A pathogen effector FOLD diversified in symbiotic fungi.	O

251	A chromosome level genome assembly of longnose gar,Lepisosteus osseus.	O
250	In silico investigation on structurefunction relationship of members belonging to the human SLC52 transporter family.	O
249	Census of exposed aggregation-prone regions in proteomes.	Ο
248	MembraneFold: Visualising transmembrane protein structure and topology.	O
247	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. <b>2022</b> , 8,	О
246	A selectivity filter in the EMC limits protein mislocalization to the ER.	O
245	A comparative analysis of mitochondrial ORFs provides new insights on expansion of mitochondrial genome size in Arcidae. <b>2022</b> , 23,	О
244	Euglenozoan kleptoplasty illuminates the early evolution of photoendosymbiosis.	O
243	Identification of Subunits for Novel Universal Vaccines against Three Predominant Serogroups and the Emerging O145 among Avian Pathogenic Escherichia coli by Pan-RV Pipeline.	О
242	EstG is a novel esterase required for cell envelope integrity in Caulobacter. <b>2022</b> ,	O
241	Predicting the Assembly of the Transmembrane Domains of Viral Channel Forming Proteins and Peptide Drug Screening Using a Docking Approach. <b>2022</b> , 12, 1844	О
240	Molecular Cloning and Characterization of a Fasciola gigantica Nuclear Receptor Subfamily 1 (FgNR1). <b>2022</b> , 11, 1458	2
239	ViralVar: A Web Tool for Multilevel Visualization of SARS-CoV-2 Genomes. 2022, 14, 2714	O
238	Exploring the role and expression pattern of WRKY transcription factor in the growth and development of Bletilla striata based on transcriptome. <b>2022</b> , 101730	O
237	Genome-wide characterization and comparative analysis of the OSCA gene family and identification of its potential stress-responsive members in legumes.	О
236	Uncovering a 500 million year old history and evidence of pseudogenization for TLR15. 13,	O
235	Parallel evolution of opsin visual pigments in hawkmoths by tuning of spectral sensitivities during transition from a nocturnal to a diurnal ecology. <b>2022</b> , 225,	О
234	Cloning and functional analysis of expansin TaEXPA9 orthologs in winter wheat in frigid regions. 66, 272-286	О

233	iORbase: a database for the prediction of the structures and functions of insect olfactory receptors.	О
232	Draft genome sequencing and secretome profiling of Sclerotinia sclerotiorum revealed effector repertoire diversity and allied broad-host range necrotrophy. <b>2022</b> , 12,	O
231	Genome-wide identification of Fagus sylvatica aquaporins and their comparative spring and summer expression profiles.	0
230	Large-scale analysis of the N-terminal regulatory elements of the kinase domain in plant receptor-like kinase family.	Ο
229	Genome-Wide Analysis and Evolutionary History of the Necrosis- and Ethylene-Inducing Peptide 1-Like Protein (NLP) Superfamily Across the Dothideomycetes Class of Fungi. <b>2023</b> , 80,	0
228	Haploid-resolved and chromosome-scale genome assembly in hexa-autoploid sweetpotato (Ipomoea batatas (L.) Lam).	O
227	Characterization of Pantoea ananatis from rice planthoppers reveals a clade of rice-associated P. ananatis undergoing genome reduction. <b>2022</b> , 8,	0
226	Multiple Receptors Contribute to the Attractive Response of Caenorhabditis elegans to Pathogenic Bacteria.	O
225	Genome Sequence of Gordonia rubripertincta Phage Survivors, a Cluster CT Siphovirus.	0
224	Whole genome resource and genetic analysis of Magnaporthe oryzae from two field isolates in northeast China.	O
223	Complete Genome Sequence of the Microbacterium Bacteriophage Chako.	0
222	Comparative transcriptome analyses of immune responses to LPS in peripheral blood mononuclear cells from the giant panda, human, mouse, and monkey. 13,	O
221	MYB Transcription Factor Family in Pearl Millet: Genome-Wide Identification, Evolutionary Progression and Expression Analysis under Abiotic Stress and Phytohormone Treatments. <b>2023</b> , 12, 355	1
220	The Genome of Fusarium oxysporum f. sp. phaseoli Provides Insight into the Evolution of Genomes and Effectors of Fusarium oxysporum Species. <b>2023</b> , 24, 963	O
219	Genome Sequence Resource of Ustilago crameri, a Fungal Pathogen Causing Millet Smut Disease of Foxtail Millet.	0
218	FAXC Proteins of Vertebrates and Invertebrates: Relationship to Metaxin Proteins.	O
217	Heterodera schachtii Bactericidal Permeability-increasing protein (Hs-BPI) is a parasitism-related gene.	0
216	COVID-19 Spread Detection and Controlling with Fog-based Infection Probability Evaluation Model. <b>2023</b> ,	O

215	Identification and characterization of novel compound heterozygous variants in FSHR causing primary ovarian insufficiency with resistant ovary syndrome. 13,	O
214	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle Peltogaster reticulata (Crustacea: Rhizocephala). 11, 583	O
213	Discovery and Characterization of Putative Glycoprotein-Encoding Mycoviruses in the Bunyavirales.	O
212	Stem transcriptome screen for selection in wild and cultivated pitahaya (Selenicereus undatus): an epiphytic cactus with edible fruit. 11, e14581	O
211	Endophytic fungi related to the ash dieback causal agent encode signatures of pathogenicity on European ash.	O
210	Conformational changes in the AdeB transmembrane efflux pump by amphiphilic peptide Mastoparan-B, down-regulates expression of theadeB Gene and restores antibiotics Susceptibility.	O
209	Prophage-Derived Regions in Curtobacterium Genomes: Good Things, Small Packages. <b>2023</b> , 24, 1586	1
208	A draft Diabrotica virgifera virgifera genome: insights into control and host plant adaption by a major maize pest insect. <b>2023</b> , 24,	O
207	Comprehensive Analysis and Functional Verification of the Pinus massoniana NBS-LRR Gene Family Involved in the Resistance to Bursaphelenchus xylophilus. <b>2023</b> , 24, 1812	О
206	Genome-wide identification and analysis of wheat LRR-RLK family genes following Chinese wheat mosaic virus infection. 13,	O
205	TransAAP: an automated annotation pipeline for membrane transporter prediction in bacterial genomes. <b>2023</b> , 9,	O
204	Prediction of effector protein structures from fungal phytopathogens enables evolutionary analyses. <b>2023</b> , 8, 174-187	1
203	Surfaceome mapping of primary human heart cells with CellSurfer uncovers cardiomyocyte surface protein LSMEM2 and proteome dynamics in failing hearts. <b>2023</b> , 2, 76-95	О
202	Three Phages One Host: Isolation and Characterization of Pantoea agglomerans Phages from a Grasshopper Specimen. <b>2023</b> , 24, 1820	O
201	Conserved orthology in termite chemosensory gene families. 10,	О
200	Pathogen-associated gene discovery workflows for novel antivirulence therapeutic development. <b>2023</b> , 88, 104429	O
199	Secretomic Insights into the Pathophysiology of Venturia inaequalis: The Causative Agent of Scab, a Devastating Apple Tree Disease. <b>2023</b> , 12, 66	О
198	High-Quality Genomes of Pangolins: Insights into the Molecular Basis of Scale Formation and Adaption to Myrmecophagous Diet. <b>2023</b> , 40,	1

197	Parallel evolution of two AIM24 protein subfamilies and their conserved functions in ER stress tolerance in land plants. <b>2022</b> , 100513	О
196	The Completed Genome Data of the Pathogenic Fungus Exobasidium cylindrosporum.	O
195	Functional, and phylogenetic analysis of maleylacetate reductase of Pseudomonas sp strain PNPG3: An in-silico approach. <b>2022</b> , 10, 1331-1343	0
194	Sugar concentrations and expression of SUTs suggest active phloem loading in tall trees of Fagus sylvatica and Quercus robur.	O
193	Characterization of a Potential Probiotic Strain in Koumiss. <b>2023</b> , 9, 87	О
192	TriTrypDB: An integrated functional genomics resource for kinetoplastida. <b>2023</b> , 17, e0011058	O
191	Identification and Functional Analysis of Acyl-Acyl Carrier Protein Desaturase from Nannochloropsis oceanica. <b>2023</b> , 61, 95-107	O
190	ProtRAP: Predicting Lipid Accessibility Together with Solvent Accessibility of Proteins in One Run.	О
189	VPg impact on Ryegrass mottle virus serine-like 3C protease proteolysis and structure.	О
188	Machine learning in computational modelling of membrane protein sequences and structures: From methodologies to applications. <b>2023</b> , 21, 1205-1226	O
187	Genome-Wide Analysis and Expression of Cyclic Nucleotide Lated Ion Channel (CNGC) Family Genes under Cold Stress in Mango (Mangifera indica). <b>2023</b> , 12, 592	0
186	Genome and Transcriptome Analysis of Ascochyta pisi Provides Insights into the Pathogenesis of Ascochyta Blight of Pea.	O
185	Tandem repeats in giant archaeal Borg elements undergo rapid evolution and create new intrinsically disordered regions in proteins. <b>2023</b> , 21, e3001980	0
184	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. <b>2023</b> , 33, 112-128	O
183	Aspartyl protease in the secretome of honey bee trypanosomatid parasite is essential for the efficient infection of host.	О
182	FT-GPI, a highly sensitive and accurate predictor of GPI-anchored proteins, reveals the composition and evolution of the GPI proteome in Plasmodium species. <b>2023</b> , 22,	O
181	The gene expression fluctuations of glyceraldehyde-3-phosphate dehydrogenase in drought-stressed-basil cultivars.	0
180	Genome sequencing and annotation of Cercospora sesami, a fungal pathogen causing leaf spot to Sesamum indicum. <b>2023</b> , 13,	O

179	Gapless Genome Assembly of Puccinia triticina Provides Insights into Chromosome Evolution in Pucciniales.	О
178	Secretory and transcriptomic responses of mantle cells to low pH in the Pacific oyster (Crassostrea gigas).	O
177	Prediction of protein solubility based on sequence physicochemical patterns and distributed representation information with DeepSoluE. <b>2023</b> , 21,	О
176	Evidence of a Set of Core-Function Genes in 16 Bacillus Podoviral Genomes with Considerable Genomic Diversity. <b>2023</b> , 15, 276	Ο
175	Structural and Functional Annotation of Hypothetical Proteins from the Microsporidia Species Vittaforma corneae ATCC 50505 Using in silico Approaches. <b>2023</b> , 24, 3507	О
174	Distinct Energy-Coupling Factor Transporter Subunits Enable Flavin Acquisition and Extracytosolic Trafficking for Extracellular Electron Transfer in Listeria monocytogenes. <b>2023</b> , 14,	O
173	Staphylococcus aureus Prophage-Encoded Protein Causes Abortive Infection and Provides Population Immunity against Kayviruses.	О
172	The effectiveness of selection in a species affects the direction of amino acid frequency evolution.	O
171	Screening of Candidate Effectors from Magnaporthe oryzae by In Vitro Secretomic Analysis. <b>2023</b> , 24, 3189	O
170	Widespread readthrough events in plants reveal unprecedented plasticity of stop codons.	O
169	Chromosome-level genome assembly provides insights into adaptive evolution of chromosome and important traits in the geckoGekko japonicus.	О
168	Amine recognizing domain in diverse receptors from bacteria and archaea evolved from the universal amino acid sensor.	O
167	A K-17 serotype specific Klebsiella phage JKP2 with biofilm reduction potential. <b>2023</b> , 329, 199107	О
166	Botryosphaeriaceae gene machinery: Correlation between diversity and virulence. <b>2023</b> , 127, 1010-1031	O
165	Immunogenic multi-epitope-based vaccine development to combat cyclosporiasis of immunocompromised patients applying computational biology method. <b>2023</b> , 248, 108497	О
164	Phylogenetic and functional properties of hagfish neurohypophysial hormone receptors distinct from their jawed vertebrate counterparts. <b>2023</b> , 336, 114257	O
163	Exploring particulate methane monooxygenase (pMMO) proteins using experimentation and computational molecular docking. <b>2023</b> , 35, 102634	0
162	Genome-wide investigation of aquaporin genes in Corchorus spp and their role in organ development and abiotic stress tolerance. <b>2023</b> , 34, 100410	O

161	Genome-wide analysis of ELOVL family genes in the Pacific oyster genome and functional characterization of CgELOVL2/5 and genomic variations in synthesis of polyunsaturated fatty acids. <b>2023</b> , 571, 739477	0
160	Characterization and genomic analysis of novel bacteriophage NK20 to revert colistin resistance and combat pandrug-resistant Klebsiella pneumoniae in a rat respiratory infection model. <b>2023</b> , 322, 121639	0
159	Evolution of cox2 introns in angiosperm mitochondria and efficient splicing of an elongated cox2i691 intron. <b>2023</b> , 869, 147393	О
158	A tell tail sign: a conserved C-terminal tail-anchor domain targets a subset of pathogen effectors to the plant endoplasmic reticulum.	O
157	Genome-wide identification of MATE, functional analysis and molecular dynamics of DcMATE21 involved in anthocyanin accumulation in Daucus carota. <b>2023</b> , 210, 113676	О
156	Systems vaccinology for the design of rational vaccines against protozoan parasites. <b>2022</b> , 297-334	O
155	Lysine-deficient proteome can be regulated through non-canonical ubiquitination and ubiquitin-independent proteasomal degradation.	О
154	Systematic analysis reveals novel insight into the molecular determinants of function, diversity and evolution of sweet taste receptors T1R2/T1R3 in primates. 10,	O
153	In silico design of a multi-epitope vaccine against the spike and the nucleocapsid proteins of the Omicron variant of SARS-CoV-2. 1-15	0
152	Lateral gene transfer leaves lasting traces in Rhizaria.	O
151	Development of stable HEK293T cell pools expressing CSFV E2 protein: A potential antigen expression platform. <b>2023</b> , 41, 1573-1583	0
150	Evolution of pathogenicity-associated genes in Rhizoctonia solani AG1-IA by genome duplication and transposon-mediated gene function alterations. <b>2023</b> , 21,	0
149	Computational models for prediction of proteinprotein interaction in rice and Magnaporthe grisea. 13,	0
148	A core UPS molecular complement implicates unique endocytic compartments at the parasiteflost interface in Giardia lamblia. <b>2023</b> , 14,	o
148		0
, The second sec	interface in Giardia lamblia. 2023, 14,  Characterization of an atypical but widespread type IV secretion system for transfer of the	
147	interface in Giardia lamblia. 2023, 14,  Characterization of an atypical but widespread type IV secretion system for transfer of the integrative and conjugative element (ICEclc) inPseudomonas putida. 2023, 51, 2345-2362  Protein Therapeutic Target Candidates Against Acinetobacter baumannii, a Pathogen of Concern to	0

143	Elevator Mechanism of Alternating Access in theEscherichia coliConcentrative Nucleoside Transporter NupC.	О
142	Proteome encoded determinants of protein sorting into extracellular vesicles.	O
141	Latent class analysis of psychotic-affective disorders with data-driven plasma proteomics. 2023, 13,	О
140	Glycogen-Degrading Activities of Catalytic Domains of Amylase and Amylase-Pullulanase Enzymes Conserved in Gardnerella spp. from the Vaginal Microbiome. <b>2023</b> , 205,	O
139	Contribution of Extracellular Membrane Vesicles To the Secretome of Staphylococcus aureus. <b>2023</b> , 14,	O
138	The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. 14,	O
137	Gene expression responses of Bactrocera tryoni larvae feeding on different ripening stages of tomato fruit. <b>2023</b> , 147, 205-230	О
136	The human MRS2 magnesium-binding domain is a regulatory feedback switch for channel activity. <b>2023</b> , 6, e202201742	O
135	⊞,6-fucosyltransferase plays a critical role during embryogenesis of the hemimetabolous insect Nilaparvata lugens. <b>2023</b> , 154, 103918	O
134	N-Linked Glycoproteome Analysis of Diosorea alata Tuber Shows Atypical Glycosylation and Indicates Central Role of Glycosylated Proteins in Tuber Maturation. <b>2023</b> , 42, 78-93	O
133	Uncovering the role of wheat magnesium transporter family genes in abiotic responses. 14,	1
132	Immunization of Mice with Virus-Like Vesicles of Kaposi Sarcoma-Associated Herpesvirus Reveals a Role for Antibodies Targeting ORF4 in Activating Complement-Mediated Neutralization. <b>2023</b> , 97,	O
131	Complement-mediated killing of Mycoplasma bovis does not play a role in the protection of animals against an experimental challenge. <b>2023</b> , 41, 1743-1752	O
130	Mechanism of signal-anchor triage during early steps of membrane protein insertion. <b>2023</b> , 83, 961-973.e7	O
129	Stepwise recombination suppression around the mating-type locus in an ascomycete fungus with self-fertile spores. <b>2023</b> , 19, e1010347	O
128	Fast-Killing Tyrosine Amide ((S)-SW228703) with Blood- and Liver-Stage Antimalarial Activity Associated with the Cyclic Amine Resistance Locus (PfCARL). <b>2023</b> , 9, 527-539	O
127	Genome-wide identification and skin expression of immunoglobulin superfamily in discus fish (Symphysodon aequifasciatus) reveal common genes associated with vertebrate lactation. <b>2023</b> , 862, 147260	O
126	Gaining Insight into Large Gene Families with the Aid of Bioinformatic Tools. <b>2023</b> , 173-191	O

125	Hope toward potent drug target using tertiary topological instances of Mycobacterial transmembrane protein. <b>2022</b> , 10, 69-75	О
124	Comparative Genomic Analysis of a Thermophilic Protease-Producing Strain Geobacillus stearothermophilus H6. <b>2023</b> , 14, 466	О
123	Design of multi-epitope based vaccine against Mycobacterium tuberculosis: a subtractive proteomics and reverse vaccinology based immunoinformatics approach. 1-19	О
122	Genome-Wide Identification of G Protein-Coupled Receptors in Ciliated Eukaryotes. <b>2023</b> , 24, 3869	O
121	Effect of PACAP/PAC1R on Follicle Development of Djungarian Hamster (Phodopus sungorus) with the Variation of Ambient Temperatures. <b>2023</b> , 12, 315	0
120	Insights into the ecological generalist lifestyle of Clonostachys fungi through analysis of their predicted secretomes. 14,	O
119	Genome-Wide Identification and Expression Analysis of the Ammonium Transporter Family Genes in Soybean. <b>2023</b> , 24, 3991	О
118	Virulence and pathogenicity determinants in whole genome sequence of Fusarium udum causing wilt of pigeon pea. 14,	О
117	Distinct genomic contexts predict gene presence-absence variation in different pathotypes of a fungal plant pathogen.	О
116	Deafness gene screening based on a multilevel cascaded BPNN model. <b>2023</b> , 24,	O
115	A guide to current methodology and usage of reverse vaccinology towardsin silicovaccine discovery. <b>2023</b> , 47,	0
115		0
	discovery. <b>2023</b> , 47,  Genomic Insights of Alnus-Infective Frankia Strains Reveal Unique Genetic Features and New	
114	discovery. 2023, 47,  Genomic Insights of Alnus-Infective Frankia Strains Reveal Unique Genetic Features and New Evidence on Their Host-Restricted Lifestyle. 2023, 14, 530  Structural Analysis of Genomic and Proteomic Signatures Reveal Dynamic Expression of Intrinsically	О
114	discovery. 2023, 47,  Genomic Insights of Alnus-Infective Frankia Strains Reveal Unique Genetic Features and New Evidence on Their Host-Restricted Lifestyle. 2023, 14, 530  Structural Analysis of Genomic and Proteomic Signatures Reveal Dynamic Expression of Intrinsically Disordered Regions in Breast Cancer and Tissue.  Immunoinformatics-aided design of a new multi-epitope vaccine adjuvanted with domain 4 of	0
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107	In Silico Characterization of the Secretome of the Fungal Pathogen Thielaviopsis punctulata, the Causal Agent of Date Palm Black Scorch Disease. <b>2023</b> , 9, 303	0
106	Metagenome diversity illuminates origins of pathogen effectors.	О
105	Damage activatesEVG1to suppress vascular differentiation during regeneration inArabidopsis thaliana.	0
104	Elucidation of the GAUT gene family in eight Rosaceae species and function analysis of PbrGAUT22 in pear pollen tube growth. <b>2023</b> , 257,	O
103	The vitellogenin receptor gene contributes to mating and host-searching behaviors in parasitoid wasps. <b>2023</b> , 26, 106298	О
102	Transcriptome sequencing leads to an improved understanding of the infection mechanism of Alternaria solani in potato. <b>2023</b> , 23,	O
101	Deep origins of eukaryotic multicellularity revealed by the Acrasis kona genome and developmental transcriptomes.	0
100	Genome Sequences of Five Microbacterium foliorum Phages, GaeCeo, NeumannU, Eightball, Chivey, and Hiddenleaf. <b>2023</b> , 12,	o
99	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode Brugia malayi.	0
98	Long-term and rapid evolution in powdery mildew fungi.	o
97	The salivary protein Saglin facilitates efficient midgut colonization of Anopheles mosquitoes by malaria parasites. <b>2023</b> , 19, e1010538	0
96	Heritability and gene functions associated with sclerotia formation of Rhizoctonia solani AG-7 using whole genome sequencing and genome-wide association study. <b>2023</b> , 9,	O
95	Exploring microbial functional biodiversity at the protein family level@rom metagenomic sequence reads to annotated protein clusters. 3,	0
94	SARS-CoV-2 ORF3c suppresses immune activation by inhibiting innate sensing.	O
93	Chemoreceptors from the commensal gut Roseburia rectibacter bind to mucin and trigger chemotaxis.	O
92	Novel phytochemical inhibitors targeting monkeypox virus thymidine and serine/threonine kinase: integrating computational modeling and molecular dynamics simulation. 1-17	O
91	Isolation and characterization of a novel Tenacibaculum species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of Tenacibaculum larymnensis sp. nov. and Tenacibaculum phage Larrie. 14,	0
90	Genomic Features Predict Bacterial Life History Strategies in Soil, as Identified by Metagenomic Stable Isotope Probing.	O

89	Zinc/iron-regulated transporter-like protein gene family in Theobroma cacao L: Characteristics, evolution, function and 3D structure analysis. 14,	О
88	Immunoselective progression of a multi-epitope-based subunit vaccine candidate to convey protection against the parasite Onchocerca lupi. <b>2023</b> , 38, 101209	Ο
87	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. <b>2023</b> , 8, 651-665	О
86	Tat-fimbriae (Eafi) Thovel type of haloarchaeal surface structures.	0
85	Unfolding Individual Domains of BmrA, a Bacterial ABC Transporter Involved in Multidrug Resistance. <b>2023</b> , 24, 5239	О
84	Discovery of an unrecognized nidovirus associated with granulomatous hepatitis in rainbow trout. <b>2023</b> , 26, 106370	O
83	Domain shuffling of a highly mutable ligand-binding fold drives adhesin generation across the bacterial kingdom.	О
82	VPg Impact on Ryegrass Mottle Virus Serine-like 3C Protease Proteolysis and Structure. <b>2023</b> , 24, 5347	Ο
81	The Sensory Histidine Kinase CusS of Escherichia coli Senses Periplasmic Copper Ions. 2023, 11,	О
80	Molecular mechanisms of functional impairment for active site mutations in glucose-6-phosphatase catalytic subunit 1 linked to glycogen storage disease type 1a.	Ο
79	Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. 2023, 8, 727-744	О
78	Spatial Proteome Reorganization of a Photosynthetic Model Cyanobacterium in Response to Abiotic Stresses. <b>2023</b> , 22, 1255-1269	Ο
77	Parallel evolution of fish bi-modal breathing and expansion of olfactory receptor (OR) genes: toward a universal ORs nomenclature. <b>2023</b> ,	1
76	Characterization of oil body-associated proteins obtained from oil bodies with different sizes in oleaginous diatom Fistulifera solaris. <b>2023</b> ,	O
75	Complete biosynthesis of the phenylethanoid glycoside verbascoside. 2023, 100592	О
74	Citrus Bright Spot Virus: A New Dichorhavirus, Transmitted by Brevipalpus azores, Causing Citrus Leprosis Disease in Brazil. <b>2023</b> , 12, 1371	О
73	Adaptive evolution in virulence effectors of the rice blast fungusPyricularia oryzae.	О
72	The Identification and Expression Analysis of the Liriodendron chinense (Hemsl.) Sarg. SOD Gene Family. <b>2023</b> , 14, 628	o

71	Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. <b>2023</b> , 12, 476	0
70	Transcriptome analysis of Lr19-virulent mutants provides clues for the AvrLr19 of Puccinia triticina.	O
69	Biology and Roles in Diseases of Selenoprotein I Characterized by Ethanolamine Phosphotransferase Activity and Antioxidant Potential. <b>2023</b> ,	O
68	Cryptosporidium uses multiple distinct secretory organelles to interact with and modify its host cell. <b>2023</b> , 31, 650-664.e6	O
67	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. <b>2023</b> , 3,	O
66	Spherical Body Protein 4 from Babesia bigemina: A Novel Gene That Contains Conserved B-Cell Epitopes and Induces Cross-Reactive Neutralizing Antibodies in Babesia ovata. <b>2023</b> , 12, 495	O
65	LSPpred Suite: Tools for Leaderless Secretory Protein Prediction in Plants. <b>2023</b> , 12, 1428	O
64	Computational Approaches for Peroxisomal Protein Localization. 2023, 405-411	O
63	Computational Methods to Predict Intrinsically Disordered Regions and Functional Regions in Them. <b>2023</b> , 231-245	0
62	RNA silencing proteins and small RNAs in oomycete plant pathogens and biocontrol agents. 14,	O
61	Computer-aided genomic data analysis of drug-resistant Neisseria gonorrhoeae for the Identification of alternative therapeutic targets. 13,	O
60	Genome-wide identification, expression analysis, and transcriptome analysis of the IAA gene family in Zoysia japonica.	O
59	De novo transcriptome assemblies of five major European oilseed rape insect pests. <b>2023</b> , 24,	0
58	Evolution of tetraspanin antigens in the zoonotic Asian blood fluke Schistosoma japonicum. <b>2023</b> , 16,	O
57	Pan-cancer analysis identifies tumor-specific antigens derived from transposable elements. <b>2023</b> , 55, 631-639	0
56	The root pathogen Aphanomyces euteiches secretes modular proteases in pea apoplast during host infection. 14,	O
55	Docking cholesterol to integral membrane proteins with Rosetta. 2023, 19, e1010947	0
54	A progestin regulates the prostaglandin pathway in the neuroendocrine system in female mudskipper Boleophthalmus pectinirostris. <b>2023</b> , 231, 106300	Ο

53	Functional characterization of the GhNRT2.1e gene reveals its significant role in improving nitrogen use efficiency in Gossypium hirsutum. 11, e15152	O
52	The genome of Lactuca saligna , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew Bremia lactucae.	O
51	The Core Technology of Electric Power Knowledge Graph and Its System Application. 2023, 87-94	0
50	Structural dynamics and functional analysis of Saprolegnia parasitica chitin synthases 5 in a phospholipid bilayer. 1-14	O
49	The Trypanosoma brucei MISP family of invariant proteins is co-expressed with BARP as triple helical bundle structures on the surface of salivary gland forms, but is dispensable for parasite development within the tsetse vector. <b>2023</b> , 19, e1011269	O
48	Ligand Partition to the Lipid Bilayer Should Be Accounted for When Estimating Their Affinity to Proteins. <b>2023</b> , 28, 3136	O
47	Comparative genomics reveals unique features of two Babesia motasi subspecies: Babesia motasi lintanensis and Babesia motasi hebeiensis. <b>2023</b> ,	0
46	Molecular Basis of Unequal Alternative Splicing of Human SCD5 and Its Alteration by Natural Genetic Variations. <b>2023</b> , 24, 6517	O
45	An intermembrane space protein facilitates completion of mitochondrial division in yeast.	O
44	Fascinating strategies of marine benthic organisms to cope with emerging pollutant: Titanium dioxide nanoparticles. <b>2023</b> , 121538	O
43	T9GPred: A Comprehensive Computational Tool for the Prediction of Type 9 Secretion System, Gliding Motility and the Associated Secreted Proteins.	O
42	LINC00493-encoded microprotein SMIM26 exerts anti-metastatic activity in renal cell carcinoma.	O
41	An Overview of the Putative Structural and Functional Properties of the GHBh1 Receptor through a Bioinformatics Approach. <b>2023</b> , 13, 926	0
40	Major proliferation of transposable elements shaped the genome of the soybean rust pathogen Phakopsora pachyrhizi. <b>2023</b> , 14,	O
39	Investigation of Peptidoglycan-Associated Lipoprotein of Acinetobacter baumannii and Its Interaction with Fibronectin To Find Its Therapeutic Potential.	O
38	Whole-genome sequencing and comparative genomic analysis of potential biotechnological strains of Trichoderma harzianum, Trichoderma atroviride, and Trichoderma reesei.	O
37	Identification of Potential Drug Targets in Erythrocyte Invasion Pathway of Plasmodium falciparum. <b>2023</b> , 80,	O
36	De novo full-length transcriptome analysis of two ecotypes of Phragmites australis (swamp reed and dune reed) provides new insights into the transcriptomic complexity of dune reed and its long-term adaptation to desert environments. <b>2023</b> , 24,	O

35	A Complete Genome Sequence of Podosphaera xanthii Isolate YZU573, the Causal Agent of Powdery Mildew Isolated from Cucumber in China. <b>2023</b> , 12, 561	0
34	Clean Production of l-Alanyl-l-glutamine by an Efficient Yeast Biocatalyst Expressing ⊞Amino Acid Ester Acyltransferase without N-Glycosylation.	О
33	Genomic insights into the c-di-GMP signaling and biofilm development in the saprophytic spirochete Leptospira biflexa. <b>2023</b> , 205,	0
32	Genome-wide characterization and comparative analysis of the OSCA gene family and identification of its potential stress-responsive members in legumes. <b>2023</b> , 13,	o
31	Secretory and transcriptomic responses of mantle cells to low pH in the Pacific oyster (Crassostrea gigas). 10,	0
30	Targeting Essential Hypothetical Proteins of Pseudomonas aeruginosa PAO1 for Mining of Novel Therapeutics: An In Silico Approach. <b>2023</b> , 2023, 1-28	o
29	Targeting advanced prostate cancer with STEAP1 chimeric antigen receptor T cell and tumor-localized IL-12 immunotherapy. <b>2023</b> , 14,	0
28	Genome-wide identification and expression profiling of snakin/GASA genes under drought stress in barley (Hordeum vulgare L.). <b>2023</b> , 13,	o
27	Near-atomic architecture of Singapore grouper iridovirus and implications for giant virus assembly. <b>2023</b> , 14,	0
26	A small cysteine-rich fungal effector, BsCE66 is essential for the virulence of Bipolaris sorokiniana on wheat plants. <b>2023</b> , 166, 103798	o
25	Immunoinformatics approach to design next-generation epitope-based peptide vaccine against Peste des Petits Ruminants Virus (PPRV). <b>2023</b> ,	0
24	In depth amino acid mutational analysis of the key interspecific incompatibility transmembrane factor Stigmatic Privacy 1.	O
23	Antigen discovery by bioinformatics analysis and peptide microarray for the diagnosis of cystic echinococcosis. <b>2023</b> , 17, e0011210	0
22	Systematic Analysis of NRAMP Family Genes in Areca catechu and Its Response to Zn/Fe Deficiency Stress. <b>2023</b> , 24, 7383	O
21	A pathogenicity locus of Streptococcus gallolyticus subspecies gallolyticus. 2023, 13,	0
20	A subunit vaccine against pneumonia: targeting Streptococcus pneumoniae and Klebsiella pneumoniae. <b>2023</b> , 12,	O
19	Identification and Evaluation of Novel Antigen Candidates against Salmonella Pullorum Infection Using Reverse Vaccinology. <b>2023</b> , 11, 865	0
18	Structure based virtual screening, molecular dynamic simulation to identify the oxadiazole derivatives as inhibitors of Enterococcus D-Ala-D-Ser ligase for combating vancomycin resistance. <b>2023</b> , 106965	О

17	Genetics Behind Sexual Incompatibility in Plants: How Much We Know and What More to Uncover?.	0
16	Attack of the clones: Population genetics reveals clonality of Colletotrichum lupini, the causal agent of lupin anthracnose.	O
15	Identification and analysis of the secretome of plant pathogenic fungi reveals lifestyle adaptation.	0
14	Integrating Metabolic Modeling and High-Throughput Data to Characterize Diatoms Metabolism. <b>2023</b> , 165-191	O
13	Extracellular Vesicles of the Plant Pathogen Botrytis cinerea. <b>2023</b> , 9, 495	O
12	Comparative genomics of the brown rot fungi Monilinia fructicola, M. laxa and M. fructigena. <b>2023</b> , 31-38	O
11	A novel cell division protein critical for the assembly of the bacterial divisome.	O
10	In silico structural and functional characterization of hypothetical proteins from Monkeypox virus. <b>2023</b> , 21,	O
9	slr2103, a homolog of type-2 diacylglycerol acyltransferase genes, for plastoquinone-related neutral lipid synthesis and NaCl-stress acclimatization in a cyanobacterium, Synechocystis sp. PCC 6803. 14,	0
8	Identifying sex-differential gene expression in the antennal gland of the swimming crab by transcriptomic analysis. <b>2023</b> , 46, 101087	O
7	Molecular cloning and in silico analysis of chalcone isomerase from Polygonum minus.	O
6	Genome-wide identification and expression profile analysis of metal tolerance protein gene family in Eucalyptus grandis under metal stresses. <b>2023</b> , 23,	O
5	Pyruvate orthophosphate dikinase is required for the acclimation to high bicarbonate concentrations in Phaeodactylum tricornutum. <b>2023</b> , 72, 103131	O
4	GDE7 produces cyclic phosphatidic acid in the ER lumen functioning as a lysophospholipid mediator. <b>2023</b> , 6,	O
3	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode Brugia malayi. <b>2023</b> , 13,	0
2	Complete genome analysis of Tequatrovirus ufvareg1, a Tequatrovirus species inhibiting Escherichia coli O157:H7. 13,	O
1	Complete Genome Assembly and Annotation of Escherichia coli Bacteriophage 107.	О