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227		
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205	A method for predicting linear and conformational B-cell epitopes in an antigen from its primary sequence.	О
204	Expanded MutaT7 toolkit efficiently and simultaneously accesses all possible transition mutations in bacteria.	O
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200	Genome Iwide Analysis and Characterization of Eucalyptus grandis TCP Transcription Factors.	Ο

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159	Targeting influenza A virus by splicing inhibitor herboxidiene reveals the importance of subtype-specific signatures around splice sites. 2023 , 30,	О
158	Genomic identification of cotton SAC genes branded ovule and stress-related key genes in Gossypium hirsutum. 14,	O
157	Roles and evolution of fourLEAFYhomologs in floral patterning and leaf development in woodland strawberry.	О
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150	Enzymatic reactions of AGO4 in RNA-directed DNA methylation: siRNA duplex loading, passenger strand elimination, target RNA slicing, and sliced target retention. 2023 , 37, 103-118	О
149	Combination of Experimental and Bioinformatic Approaches for Identification of Immunologically Relevant Protein Peptide Interactions. 2023 , 13, 310	О
148	Horizontal gene transfer and CRISPR targeting drive phage-bacterial host interactions and coevolution in pink berry marine microbial aggregates.	O
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143	Escherichia coli CspA stimulates translation in the cold of its own mRNA by promoting ribosome progression. 14,	О
142	Comparative Modeling and Analysis of Extremophilic D-Ala-D-Ala Carboxypeptidases. 2023 , 13, 328	O
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135	Genome-wide analysis of R2R3-MYB genes in cultivated peanut (Arachis hypogaea L.): Gene duplications, functional conservation, and diversification. 14,	O
134	Using High-Throughput Molecular Dynamics Simulation to Enhance the Computational Design of Kemp Elimination Enzymes. 2023 , 63, 1323-1337	O
133	Structural and Biochemical Insights into Post-Translational Arginine-to-Ornithine Peptide Modifications by an Atypical Arginase. 2023 , 18, 528-536	O
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128	Bipalium admarginatumde Beauchamp, 1933 (Platyhelminthes, Tricladida, Geoplanidae) in Malaysia, with molecular characterisation including the mitogenome.	O

127	Structural screens identify candidate human homologs of insect chemoreceptors and cryptic Drosophila gustatory receptor-like proteins. 12,	О
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125	Targeted Screening for Spontaneous Insertion Mutations in a Lactic Acid Bacterium, Tetragenococcus halophilus. 2023 , 89,	О
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123	Genome-wide analysis of R2R3-MYB transcription factors in Boehmeria nivea (L.) gaudich revealed potential cadmium tolerance and anthocyanin biosynthesis genes. 14,	О
122	Late Embryogenesis Abundant Proteins Contribute to the Resistance of Toxoplasma gondii Oocysts against Environmental Stresses.	O
121	Conservation of land plant-specific receptor-like cytoplasmic kinase subfamily XI possessing a unique kinase insert domain. 14,	О
120	Analysis of the phosphoproteome of CK2 印加/图 C2C12 myoblasts compared to the wild-type cells. 2023 , 13,	О
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116	Comparative phylogenomic and structural analysis of canonical secretory PLA2 and novel PLA2-like family in plants. 14,	O
115	Critical Residues Involved in the Coassembly of L1 and L2 Capsid Proteins of Human Papillomavirus 16. 2023 , 97,	О
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111	Long non-coding RNA-derived peptides are immunogenic and drive a potent anti-tumour response. 2023 , 14,	2
110	Ubiquitin-like conjugation by bacterial cGAS enhances anti-phage defence. 2023 , 616, 326-331	О

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107	Identification of Microorganisms that Bind Specifically to Target Materials of Interest Using a Magnetophoretic Microfluidic Platform. 2023 , 15, 11391-11402	О
106	Overlapping SigH and SigE sigma factor regulons in Corynebacterium glutamicum. 13,	О
105	Computational Insights into the Allosteric Modulation of a Phthalate-Degrading Hydrolase by Distal Mutations. 2023 , 13, 443	О
104	Genome-Wide Analysis of MYB Transcription Factors and Screening of MYBs Involved in the Red Color Formation in Rhododendron delavayi. 2023 , 24, 4641	O
103	Comparative analysis of SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) gene family between bryophytes and seed plants.	О
102	Phage T3 overcomes the BREX defence through SAM cleavage and inhibition of SAM synthesis.	O
101	Computational design of a cyclic peptide that inhibits the CTLA4 immune checkpoint.	О
100	Cloning, characterization, and inhibition of the novel 毗arbonic anhydrase from parasitic blood fluke, Schistosoma mansoni. 2023 , 38,	О
99	Phylogenetic analyses of 5-hydroxytryptamine 3 (5-HT3) receptors in Metazoa. 2023 , 18, e0281507	0
98	The two-component regulator WalKR provides an essential link between cell wall homeostasis with DNA replication inStaphylococcus aureus.	O
97	Relationship Between Genetic Polymorphisms in Cell Cycle Regulatory Gene TP53 and Polycystic Ovarian Syndrome: A Casefontrol Study and In Silico Analyses.	О
96	Comparative-genomic analysis reveals dynamic NLR gene loss and gain across Apiaceae species. 14,	О
95	Cryo-EM structure of gas vesicles for buoyancy-controlled motility. 2023, 186, 975-986.e13	О
94	Genome-Wide Identification and Characterisation of Abiotic Stress Responsive mTERF Gene Family in Amaranthus hypochondriacus. 2023 , 92, 1649-1664	o
93	Comparative structural analysis of plant uridine diphosphate (UDP)-dependent glycosyltransferases (UGTs) in plant specialized metabolism: structures of plant UGTs for biosynthesis of steviol glycosides.	О
92	Exploring microbial functional biodiversity at the protein family level from metagenomic sequence reads to annotated protein clusters. 3,	O

91	Developmental mRNA clearance by PIWI-bound endo-siRNAs in Paramecium. 2023, 42, 112213	O
90	Sequence-structural features and evolution of the famylase family GH119 revealed by the in silico analysis of its relatedness to the family GH57.	O
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88	T-Cell Repertoire Analysis in the Conjunctiva of Murine Dry Eye Model. 2023 , 64, 14	O
87	NMR structure of emfourin, a novel protein metalloprotease inhibitor: Insights into the mechanism of action. 2023 , 299, 104585	O
86	ORC1 binds tocis-transcribed RNAs for efficient activation of replication origins.	O
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84	Genomic Analysis, Evolution and Characterization of E3 Ubiquitin Protein Ligase (TRIM) Gene Family in Common Carp (Cyprinus carpio). 2023 , 14, 667	O
83	Identification of a pluripotency-inducing small compound, PLU, that induces callus formation via Heat Shock Protein 90-mediated activation of auxin signaling. 14,	O
82	The biosynthesis, degradation, and function of cell wall 歌ylosylated xyloglucan mirrors that of arabinoxyloglucan.	O
81	A broadly distributed predicted helicase/nuclease confers phage resistance via abortive infection. 2023 , 31, 343-355.e5	O
80	Site-directed mutagenesis improves the practical application of L-glutamic acid decarboxylase in Escherichia coli. 2023 , 23,	O
79	Accurate prediction by AlphaFold2 for ligand binding in a reductive dehalogenase and implications for PFAS (per- and polyfluoroalkyl substance) biodegradation. 2023 , 13,	O
78	Functional and Phylogenetic Diversity of Cas10 Proteins. 2023 , 6, 152-162	O
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76	Imaging of plant calcium-sensor kinase conformation monitors real time calcium decodingin planta.	O
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