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Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes

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636	Antibiotic resistance in biofilm-forming pathogenic Coliforms & the role of membrane proteins. **2022**, 273-287	0
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626	Reactive oxygen species-based sensing by a single chemoreceptor controls bacterial chemotaxis to copper.	
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611	De Novo Transcriptome Assembly and Analysis of the Flat Oyster Pathogenic Protozoa Bonamia Ostreae. 12,	
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586	Multi-epitope-based vaccine design by exploring antigenic potential among leptospiral lipoproteins using comprehensive immunoinformatics and structure-based approaches.	0
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484	Exploring Optimal Taxol CYP725A4 Activity in Saccharomyces cerevisiae.	0
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434	High-Quality Genome Sequence Resource of Lasiodiplodia theobromae JMB122, a Fungal Pathogen Causing Peach Gummosis.	0
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.	0
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431	Immunoinformatics Approach to Design Novel Subunit Vaccine against the Epstein-Barr Virus.	0
430	Functional Identification of Arthrinium phaeospermum Effectors Related to Bambusa pervariabilis Dendrocalamopsis grandis Shoot Blight. **2022**, 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).	0
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.	0
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.	0
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419	Designing mRNA- and Peptide-Based Vaccine Construct against Emerging Multidrug-Resistant Citrobacter freundii: A Computational-Based Subtractive Proteomics Approach. **2022**, 58, 1356	1
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414	Involvement of glucose in freeze tolerance in the Japanese tree frog Hyla japonica.	1

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412	Structure of the two-component S-layer of the archaeon Sulfolobus acidocaldarius.	0
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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.	0

395	Tissue-specific transcriptomes reveal mechanisms of microbiome regulation in an ancient fish.	0
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392	Isolation and characterization of a neoxanthin synthase gene functioning in fucoxanthin biosynthesis ofPhaeodactyum tricornutum.	0
391	Identification of Schistosoma mansoni miracidia attractant candidates in infected Biomphalaria glabrata using behaviour-guided comparative proteomics. 13,	0
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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
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370	Glycogen degrading activities of catalytic domains of □amylase and □amylase-pullulanase enzymes conserved inGardnerellaspp. from the vaginal microbiome.	1
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362	Functional characterization of FaMBL1, a G-type lectin gene family member, in response to fungal pathogens of strawberry.	0
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324	Prediction of Potential Drug Targets and Vaccine Candidates Against Antibiotic-Resistant Pseudomonas aeruginosa. **2022**, 28,	0

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31	Secretory and transcriptomic responses of mantle cells to low pH in the Pacific oyster (Crassostrea gigas). 10,	0
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3	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode Brugia malayi. **2023**, 13,	0
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