

UniProt: the universal protein knowledgebase

Nucleic Acids Research

45, D158-D169

DOI: [10.1093/nar/gkw1099](https://doi.org/10.1093/nar/gkw1099)

Citation Report

#	ARTICLE	IF	CITATIONS
8	The BRENDA enzyme information systemâ€œFrom a database to an expert system. Journal of Biotechnology, 2017, 261, 194-206.	3.8	136
9	agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. Nucleic Acids Research, 2017, 45, W122-W129.	14.5	1,872
10	Protein composition of the hepatitis A virus quasi-envelope. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6587-6592.	7.1	78
11	The Proteins API: accessing key integrated protein and genome information. Nucleic Acids Research, 2017, 45, W539-W544.	14.5	69
12	Differential redox sensitivity of cathepsin B and L holds the key to autophagy-apoptosis interplay after Thioredoxin reductase inhibition in nutritionally stressed SH-SY5Y cells. Free Radical Biology and Medicine, 2017, 108, 819-831.	2.9	26
13	The EBI search engine: EBI search as a serviceâ€œmaking biological data accessible for all. Nucleic Acids Research, 2017, 45, W545-W549.	14.5	30
14	HLA class I binding prediction via convolutional neural networks. Bioinformatics, 2017, 33, 2658-2665.	4.1	99
15	Identification of a target protein of Hydra actinoporin-like toxin-1 (HALT-1) using GST affinity purification and SILAC-based quantitative proteomics. Toxicon, 2017, 133, 153-161.	1.6	6
16	Subcellular locations of potential cell wall proteins in plants: predictors, databases and cross-referencing. Briefings in Bioinformatics, 2018, 19, 1130-1140.	6.5	10
17	Ca ²⁺ signaling machinery is present at intercellular junctions and structures associated with junction turnover in rat Sertoli cellsâ€œ. Biology of Reproduction, 2017, 96, 1288-1302.	2.7	26
18	RegulatorTrail: a web service for the identification of key transcriptional regulators. Nucleic Acids Research, 2017, 45, W146-W153.	14.5	21
19	Large differences in proportions of harmful and benign amino acid substitutions between proteins and diseases. Human Mutation, 2017, 38, 839-848.	2.5	17
20	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. Molecular Cell, 2017, 67, 214-227.e7.	9.7	533
21	Proteomic features linked to tenderness of aged pork loins1. Journal of Animal Science, 2017, 95, 2533-2546.	0.5	16
22	RiPPMiner: a bioinformatics resource for deciphering chemical structures of RiPPs based on prediction of cleavage and cross-links. Nucleic Acids Research, 2017, 45, W80-W88.	14.5	100
23	Ptbp2 Controls an Alternative Splicing Network Required for Cell Communication during Spermatogenesis. Cell Reports, 2017, 19, 2598-2612.	6.4	54
24	Phenotype databases for genetic screens in human cells. Journal of Biotechnology, 2017, 261, 63-69.	3.8	10
25	Novel Predators Reshape Holozoan Phylogeny and Reveal the Presence of a Two-Component Signaling System in the Ancestor of Animals. Current Biology, 2017, 27, 2043-2050.e6.	3.9	87

#	ARTICLE	IF	CITATIONS
26	Gene expression and adaptive noncoding changes during human evolution. BMC Genomics, 2017, 18, 435.	2.8	13
27	Characterization of Phormidium lacuna strains from the North Sea and the Mediterranean Sea for biotechnological applications. Process Biochemistry, 2017, 59, 194-206.	3.7	14
28	The third wave: Intermediate filaments in the maturing nervous system. Molecular and Cellular Neurosciences, 2017, 84, 68-76.	2.2	32
29	PMut: a web-based tool for the annotation of pathological variants on proteins, 2017 update. Nucleic Acids Research, 2017, 45, W222-W228.	14.5	184
30	Major hnRNP proteins act as general TDP-43 functional modifiers both in Drosophila and human neuronal cells. Nucleic Acids Research, 2017, 45, 8026-8045.	14.5	62
31	Identifying relationships between unrelated pharmaceutical target proteins on the basis of shared active compounds. Future Science OA, 2017, 3, FSO212.	1.9	4
32	Compound heterozygous KCNQ1 mutations (A300T/P535T) in a child with sudden unexplained death: Insights into possible molecular mechanisms based on protein modeling. Gene, 2017, 627, 40-48.	2.2	7
33	Crystal structure of the thioesterification conformation of Bacillus subtilis o-succinylbenzoyl-CoA synthetase reveals a distinct substrate-binding mode. Journal of Biological Chemistry, 2017, 292, 12296-12310.	3.4	6
34	Comparative genomics of free-living Gammaproteobacteria: pathogenesis-related genes or interaction-related genes?. Pathogens and Disease, 2017, 75, .	2.0	23
35	Hydroxyurea inhibits parvovirus B19 replication in erythroid progenitor cells. Biochemical Pharmacology, 2017, 136, 32-39.	4.4	24
36	Determining Cysteines Available for Covalent Inhibition Across the Human Kinome. Journal of Medicinal Chemistry, 2017, 60, 2879-2889.	6.4	104
37	Whole exome sequencing with genomic triangulation implicates <i>CDH2</i> -encoded N-cadherin as a novel pathogenic substrate for arrhythmogenic cardiomyopathy. Congenital Heart Disease, 2017, 12, 226-235.	0.2	46
38	Predicting "Hot" and "Warm" Spots for Fragment Binding. Journal of Medicinal Chemistry, 2017, 60, 4036-4046.	6.4	32
39	Transcriptome-based investigation of cirrus development and identifying microsatellite markers in rattan (<i>Daemonorops jenkinsiana</i>). Scientific Reports, 2017, 7, 46107.	3.3	16
40	A potent small-molecule inhibitor of the DCN1-UBC12 interaction that selectively blocks cullin 3 neddylation. Nature Communications, 2017, 8, 1150.	12.8	71
41	Site-specific identification and quantitation of endogenous SUMO modifications under native conditions. Nature Communications, 2017, 8, 1171.	12.8	92
42	The TPR domain of BepA is required for productive interaction with substrate proteins and the β -barrel assembly machinery complex. Molecular Microbiology, 2017, 106, 760-776.	2.5	26
43	Complete genomic characterisation of two novel poxviruses (WKPV and EKPV) from western and eastern grey kangaroos. Virus Research, 2017, 242, 106-121.	2.2	8

#	ARTICLE	IF	CITATIONS
44	Sequence composition predicts immunoglobulin superfamily members that could share the intrinsically disordered properties of antibody CH1 domains. <i>Scientific Reports</i> , 2017, 7, 12404.	3.3	7
45	Multi-Protease Strategy Identifies Three PE2 Missing Proteins in Human Testis Tissue. <i>Journal of Proteome Research</i> , 2017, 16, 4352-4363.	3.7	21
46	POTAGE: A Visualisation Tool for Speeding up Gene Discovery in Wheat. <i>Scientific Reports</i> , 2017, 7, 14315.	3.3	11
47	Mutations of PTPN23 in developmental and epileptic encephalopathy. <i>Human Genetics</i> , 2017, 136, 1455-1461.	3.8	15
48	Salivary Proteome Patterns Affecting Human Salt Taste Sensitivity. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 9275-9286.	5.2	25
49	Enhanced unbiased sampling of protein dynamics using evolutionary coupling information. <i>Scientific Reports</i> , 2017, 7, 12700.	3.3	47
50	First Biochemical Characterization of a Methylcitric Acid Cycle from <i>Bacillus subtilis</i> Strain 168. <i>Biochemistry</i> , 2017, 56, 5698-5711.	2.5	15
51	Proteomic analysis of the venom of the predatory ant <i>Pachycondyla striata</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT / Overlook	1.5	15
52	Differential oxidation of protein-tyrosine phosphatases during zebrafish caudal fin regeneration. <i>Scientific Reports</i> , 2017, 7, 8460.	3.3	10
53	Combination of C-H Hydrogen Bonds and van der Waals Packing Modulates the Stability of GxxxG-Mediated Dimers in Membranes. <i>Journal of the American Chemical Society</i> , 2017, 139, 15774-15783.	13.7	36
54	How Many Protein Sequences Fold to a Given Structure? A Coevolutionary Analysis. <i>Biophysical Journal</i> , 2017, 113, 1719-1730.	0.5	38
55	Friedreich Ataxia: Developmental Failure of the Dorsal Root Entry Zone. <i>Journal of Neuropathology and Experimental Neurology</i> , 2017, 76, 969-977.	1.7	43
56	SalmoNet, an integrated network of ten <i>Salmonella enterica</i> strains reveals common and distinct pathways to host adaptation. <i>Npj Systems Biology and Applications</i> , 2017, 3, 31.	3.0	28
57	Experimental design and metabolic flux analysis tools to optimize industrially relevant <i>Haemophilus influenzae</i> type b growth medium. <i>Biotechnology Progress</i> , 2017, 33, 1508-1519.	2.6	2
58	Mouse Genome Informatics (MGI) Resource: Genetic, Genomic, and Biological Knowledgebase for the Laboratory Mouse. <i>ILAR Journal</i> , 2017, 58, 17-41.	1.8	77
59	Ultracompact states of native proteins. <i>Biophysical Chemistry</i> , 2017, 230, 36-44.	2.8	1
60	LytM factors affect the recruitment of autolysins to the cell division site in <i>Caulobacter crescentus</i> . <i>Molecular Microbiology</i> , 2017, 106, 419-438.	2.5	26
61	DNA methyltransferase homologue TRDMT1 in <i>Plasmodium falciparum</i> specifically methylates endogenous aspartic acid tRNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1047-1057.	1.9	20

#	ARTICLE	IF	CITATIONS
62	Data Resources for the Computer-Guided Discovery of Bioactive Natural Products. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2099-2111.	5.4	131
63	Liver transcriptome analysis reveals important factors involved in the metabolic adaptation of the transition cow. <i>Journal of Dairy Science</i> , 2017, 100, 9311-9323.	3.4	24
64	The molecular basis for peptide repertoire selection in the human leukocyte antigen (HLA) C*06:02 molecule. <i>Journal of Biological Chemistry</i> , 2017, 292, 17203-17215.	3.4	34
65	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	3.8	107
66	Dissecting the CD93-Multimerin 2 interaction involved in cell adhesion and migration of the activated endothelium. <i>Matrix Biology</i> , 2017, 64, 112-127.	3.6	59
67	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
68	Near-atomic structure of jasplakinolide-stabilized malaria parasite F-actin reveals the structural basis of filament instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10636-10641.	7.1	64
69	Discovery of Variants Underlying Host Susceptibility to Virus Infection Using Whole-Exome Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1656, 209-227.	0.9	0
70	Characterization of the Gray Whale <i>Eschrichtius robustus</i> Genome and a Genotyping Array Based on Single-Nucleotide Polymorphisms in Candidate Genes. <i>Biological Bulletin</i> , 2017, 232, 186-197.	1.8	25
71	De novo transcriptome assembly for the spiny mouse (<i>Acomys cahirinus</i>). <i>Scientific Reports</i> , 2017, 7, 8996.	3.3	37
72	Cancer immunotherapy with recombinant poliovirus induces IFN-dominant activation of dendritic cells and tumor antigen-specific CTLs. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	180
73	Decoding the Effect of Isobaric Substitutions on Identifying Missing Proteins and Variant Peptides in Human Proteome. <i>Journal of Proteome Research</i> , 2017, 16, 4415-4424.	3.7	8
74	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. <i>Autophagy</i> , 2017, 13, 1969-1980.	9.1	48
75	Toward Neuropoteomics in Biological Psychiatry: A Systems Approach Unravels Okadaic Acid-Induced Alterations in the Neuronal Phosphoproteome. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 550-563.	2.0	8
76	Effects of genomic disruption of a guanine quadruplex in the 5' UTR of the Bcl-2 mRNA in melanoma cells. <i>FEBS Letters</i> , 2017, 591, 3649-3659.	2.8	17
77	Use of Single-Cysteine Variants for Trapping Transient States in DNA Mismatch Repair. <i>Methods in Enzymology</i> , 2017, 592, 77-101.	1.0	4
78	Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. <i>Genome Research</i> , 2017, 27, 1715-1729.	5.5	150
79	Human protein secretory pathway genes are expressed in a tissue-specific pattern to match processing demands of the secretome. <i>Npj Systems Biology and Applications</i> , 2017, 3, 22.	3.0	32

#	ARTICLE	IF	CITATIONS
80	Evolutionary dynamics of the kinetochore network in eukaryotes as revealed by comparative genomics. EMBO Reports, 2017, 18, 1559-1571.	4.5	206
81	Flexible small molecular anti-estrogens with N,N-dialkylated-2,5-diethoxy-4-morpholinoaniline scaffold targets multiple estrogen receptor conformations. Cell Cycle, 2017, 16, 1465-1477.	2.6	3
82	Multi-Target Fragments Display Versatile Binding Modes. Molecular Informatics, 2017, 36, 1700042.	2.5	7
83	The Disordered Linker in p53 Participates in Nonspecific Binding to and One-Dimensional Sliding along DNA Revealed by Single-Molecule Fluorescence Measurements. Biochemistry, 2017, 56, 4134-4144.	2.5	23
84	Molecular modeling and molecular dynamics simulation study of archaeal leucyl-tRNA synthetase in complex with different mischarged tRNA in editing conformation. Journal of Molecular Graphics and Modelling, 2017, 76, 289-295.	2.4	4
85	Membrane-bound human orphan cytochrome P450 2U1: Sequence singularities, construction of a full 3D model, and substrate docking. Biochimie, 2017, 140, 166-175.	2.6	7
86	Comparative proteomics reveals recruitment patterns of some protein families in the venoms of Cnidaria. Toxicon, 2017, 137, 19-26.	1.6	24
87	Sorting without a Golgi complex. Traffic, 2017, 18, 637-645.	2.7	9
88	Dynamic regulation of lysine acetylation: the balance between acetyltransferase and deacetylase activities. American Journal of Physiology - Renal Physiology, 2017, 313, F842-F846.	2.7	34
89	multiplierz v2.0: A Python-based ecosystem for shared access and analysis of native mass spectrometry data. Proteomics, 2017, 17, 1700091.	2.2	40
90	Identification of Differentially Expressed Splice Variants by the Proteogenomic Pipeline Splicify. Molecular and Cellular Proteomics, 2017, 16, 1850-1863.	3.8	33
91	Probing Medin Monomer Structure and its Amyloid Nucleation Using ¹³ C-Direct Detection NMR in Combination with Structural Bioinformatics. Scientific Reports, 2017, 7, 45224.	3.3	13
92	Genetic Evidence for Erythrocyte Receptor Glycophorin B Expression Levels Defining a Dominant Plasmodium falciparum Invasion Pathway into Human Erythrocytes. Infection and Immunity, 2017, 85, .	2.2	19
93	Quantitative trait loci associated with agronomic traits and stripe rust in winter wheat mapping population using single nucleotide polymorphic markers. Molecular Breeding, 2017, 37, 1.	2.1	5
94	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49
95	Molecular Dynamics Simulations Reveal Key Roles of the Interleukin-6 Alpha Receptor in the Assembly of the Human Interleukin-6 Receptor Complex. Journal of Physical Chemistry B, 2017, 121, 8113-8122.	2.6	7
96	TITINdb—a computational tool to assess titin's role as a disease gene. Bioinformatics, 2017, 33, 3482-3485.	4.1	34
97	Conserved Gene Microsynteny Unveils Functional Interaction Between Protein Disulfide Isomerase and Rho Guanine-Dissociation Inhibitor Families. Scientific Reports, 2017, 7, 17262.	3.3	16

#	ARTICLE	IF	CITATIONS
98	Proteomic analyses identify ARH3 as a serine mono-ADP-ribosylhydrolase. Nature Communications, 2017, 8, 2055.	12.8	98
99	Ubiquitin-conjugating enzyme E2T (UBE2T) and denticleless protein homolog (DTL) are linked to poor outcome in breast and lung cancers. Scientific Reports, 2017, 7, 17530.	3.3	53
100	Dynamics of Intact MexAB-OprM Efflux Pump: Focusing on the MexA-OprM Interface. Scientific Reports, 2017, 7, 16521.	3.3	30
101	The WD40-domain containing protein CORO2B is specifically enriched in glomerular podocytes and regulates the ventral actin cytoskeleton. Scientific Reports, 2017, 7, 15910.	3.3	20
102	Taste-active peptides and amino acids of pork meat as components of dry-cured meat products: An <i>in silico</i> study. Journal of Sensory Studies, 2017, 32, e12301.	1.6	65
103	Proteomics of phosphorylation and protein dynamics during fertilization and meiotic exit in the <i>Xenopus</i> egg. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10838-E10847.	7.1	43
104	The structural basis of flagellin detection by NAIP5: A strategy to limit pathogen immune evasion. Science, 2017, 358, 888-893.	12.6	164
105	FMNH2-dependent monooxygenases initiate catabolism of sulfonamides in <i>Microbacterium</i> sp. strain BR1 subsisting on sulfonamide antibiotics. Scientific Reports, 2017, 7, 15783.	3.3	66
106	Binding of mycotoxins to proteins involved in neuronal plasticity: a combined <i>in silico</i> /wet investigation. Scientific Reports, 2017, 7, 15156.	3.3	14
107	Human primary liver cancer-derived organoid cultures for disease modeling and drug screening. Nature Medicine, 2017, 23, 1424-1435.	30.7	905
108	Safety evaluation of HOWARU® Restore (Lactobacillus acidophilus NCFM, Lactobacillus paracasei) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 genomic risk factors, and acute toxicity. Food and Chemical Toxicology, 2017, 110, 316-324.	3.6	40
109	iDNAProt-ES: Identification of DNA-binding Proteins Using Evolutionary and Structural Features. Scientific Reports, 2017, 7, 14938.	3.3	73
110	Personalized Cancer Therapy: A Publicly Available Precision Oncology Resource. Cancer Research, 2017, 77, e123-e126.	0.9	31
111	Sequence conservation of protein binding segments in intrinsically disordered regions. Biochemical and Biophysical Research Communications, 2017, 494, 602-607.	2.1	16
112	PIM kinases: From survival factors to regulators of cell motility. International Journal of Biochemistry and Cell Biology, 2017, 93, 74-85.	2.8	48
113	Pharmacophore modelling, virtual screening and molecular docking studies on PLD1 inhibitors. SAR and QSAR in Environmental Research, 2017, 28, 991-1009.	2.2	8
114	Chemical space guided discovery of antimicrobial bridged bicyclic peptides against <i>Pseudomonas aeruginosa</i> and its biofilms. Chemical Science, 2017, 8, 6784-6798.	7.4	42
115	Comparison of Protein Extracts from Various Unicellular Green Sources. Journal of Agricultural and Food Chemistry, 2017, 65, 7989-8002.	5.2	47

#	ARTICLE	IF	CITATIONS
116	Development of a methodological approach for the characterization of bioaerosols in exhaust air from pig fattening farms with MALDI-TOF mass spectrometry. <i>International Journal of Hygiene and Environmental Health</i> , 2017, 220, 974-983.	4.3	12
117	DeepLoc: prediction of protein subcellular localization using deep learning. <i>Bioinformatics</i> , 2017, 33, 3387-3395.	4.1	876
118	Peptides derived from plasma proteins released by bothropasin, a metalloprotease present in the <i>Bothrops jararaca</i> venom. <i>Toxicon</i> , 2017, 137, 65-72.	1.6	4
119	A new genome-scale metabolic model of <i>Corynebacterium glutamicum</i> and its application. <i>Biotechnology for Biofuels</i> , 2017, 10, 169.	6.2	74
120	Glycosylation of <scp>KEAP</scp> 1 links nutrient sensing to redox stress signaling. <i>EMBO Journal</i> , 2017, 36, 2233-2250.	7.8	82
121	Methods for the Development of In Silico GPCR Models. <i>Methods in Enzymology</i> , 2017, 593, 405-448.	1.0	17
122	Defective mitochondrial rRNA methyltransferase MRM2 causes MELAS-like clinical syndrome. <i>Human Molecular Genetics</i> , 2017, 26, 4257-4266.	2.9	63
123	Biogenesis and iron-dependency of ribosomal RNA hydroxylation. <i>Nucleic Acids Research</i> , 2017, 45, 12974-12986.	14.5	34
124	Cell Cycle Model System for Advancing Cancer Biomarker Research. <i>Scientific Reports</i> , 2017, 7, 17989.	3.3	7
125	The Role of Type VI Secretion System Effectors in Target Cell Lysis and Subsequent Horizontal Gene Transfer. <i>Cell Reports</i> , 2017, 21, 3927-3940.	6.4	121
126	Programmatic access to bioinformatics tools from EMBL-EBI update: 2017. <i>Nucleic Acids Research</i> , 2017, 45, W550-W553.	14.5	285
127	Bayes ANOVA <i>Euglena gracilis</i>		
128	RNA sequencing and proteomics approaches reveal novel deficits in the cortex of Mecp2-deficient mice, a model for Rett syndrome. <i>Molecular Autism</i> , 2017, 8, 56.	4.9	75
129	A novel expert system for the prediction of accurate multiple sequence alignment and phylogenetic tree construction algorithms. , 2017, , .		0
130	Potential Roles of Intrinsic Disorder in Maternal-Effect Proteins Involved in the Maintenance of DNA Methylation. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1898.	4.1	9
131	Molecular Connectivity Predefines Polypharmacology: Aliphatic Rings, Chirality, and sp ³ Centers Enhance Target Selectivity. <i>Frontiers in Pharmacology</i> , 2017, 8, 552.	3.5	16
132	Mapping X-Disease Phytoplasma Resistance in <i>Prunus virginiana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2057.	3.6	5
133	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. <i>Emerging Infectious Diseases</i> , 2017, 23, 1441-1445.	4.3	40

#	ARTICLE	IF	CITATIONS
134	Critical Roles of Dual-Specificity Phosphatases in Neuronal Proteostasis and Neurological Diseases. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1963.	4.1	20
135	A Protocol for Generating and Exchanging (Genome-Scale) Metabolic Resource Allocation Models. <i>Metabolites</i> , 2017, 7, 47.	2.9	25
136	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. <i>Molecules</i> , 2017, 22, 1057.	3.8	53
137	Annotation of Peptide Structures Using SMILES and Other Chemical Codes—Practical Solutions. <i>Molecules</i> , 2017, 22, 2075.	3.8	11
138	TRANSPARENT TESTA GLABRA 1-Dependent Regulation of Flavonoid Biosynthesis. <i>Plants</i> , 2017, 6, 65.	3.5	62
139	The human cytoplasmic dynein interactome reveals novel activators of motility. <i>ELife</i> , 2017, 6, .	6.0	120
140	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1838.	4.1	59
141	The TORC2-Dependent Signaling Network in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Biomolecules</i> , 2017, 7, 66.	4.0	56
142	Cell Line Secretome and Tumor Tissue Proteome Markers for Early Detection of Colorectal Cancer: A Systematic Review. <i>Cancers</i> , 2017, 9, 156.	3.7	13
143	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life. <i>Genes</i> , 2017, 8, 248.	2.4	40
144	Responsive Proteins in Wheat Cultivars with Contrasting Nitrogen Efficiencies under the Combined Stress of High Temperature and Low Nitrogen. <i>Genes</i> , 2017, 8, 356.	2.4	16
145	Cellular Consequences of Diminished Protein O-Mannosyltransferase Activity in Baker's Yeast. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1226.	4.1	6
146	Sequence Analysis and Phylogenetic Studies of Hypoxia-Inducible Factor-1 α . <i>Cancer Informatics</i> , 2017, 16, 117693511771224.	1.9	0
147	Interpreting T-Cell Cross-reactivity through Structure: Implications for TCR-Based Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2017, 8, 1210.	4.8	50
148	Multi-omics Analysis Sheds Light on the Evolution and the Intracellular Lifestyle Strategies of Spotted Fever Group Rickettsia spp.. <i>Frontiers in Microbiology</i> , 2017, 8, 1363.	3.5	11
149	HPV8-E6 Interferes with Syntenin-2 Expression through Deregulation of Differentiation, Methylation and Phosphatidylinositol-Kinase Dependent Mechanisms. <i>Frontiers in Microbiology</i> , 2017, 8, 1724.	3.5	5
150	Evolutionary Analysis of HIV-1 Pol Proteins Reveals Representative Residues for Viral Subtype Differentiation. <i>Frontiers in Microbiology</i> , 2017, 8, 2151.	3.5	13
151	The Sit-and-Wait Hypothesis in Bacterial Pathogens: A Theoretical Study of Durability and Virulence. <i>Frontiers in Microbiology</i> , 2017, 8, 2167.	3.5	24

#	ARTICLE	IF	CITATIONS
152	The Essential UPP Phosphatase Pair BcrC and UppP Connects Cell Wall Homeostasis during Growth and Sporulation with Cell Envelope Stress Response in <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2403.	3.5	16
153	Kinase-Centric Computational Drug Development. <i>Annual Reports in Medicinal Chemistry</i> , 2017, , 197-236.	0.9	9
154	Transcriptomic and proteomic landscape of mitochondrial dysfunction reveals secondary coenzyme Q deficiency in mammals. <i>ELife</i> , 2017, 6, .	6.0	169
155	HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. <i>BioMed Research International</i> , 2017, 2017, 1-10.	1.9	41
156	New Targets for Zika Virus Determined by Human-Viral Interactomic: A Bioinformatics Approach. <i>BioMed Research International</i> , 2017, 2017, 1-15.	1.9	16
157	Prediction of Metal Ion Binding Sites in Proteins from Amino Acid Sequences by Using Simplified Amino Acid Alphabets and Random Forest Model. <i>Genomics and Informatics</i> , 2017, 15, 162-169.	0.8	9
158	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. <i>PLoS ONE</i> , 2017, 12, e0176347.	2.5	30
159	Carbohydrate-mediated responses during zygotic and early somatic embryogenesis in the endangered conifer, <i>Araucaria angustifolia</i> . <i>PLoS ONE</i> , 2017, 12, e0180051.	2.5	41
160	Transcriptomic profiling in muscle and adipose tissue identifies genes related to growth and lipid deposition. <i>PLoS ONE</i> , 2017, 12, e0184120.	2.5	25
161	SWI/SNF Infobase—An exclusive information portal for SWI/SNF remodeling complex subunits. <i>PLoS ONE</i> , 2017, 12, e0184445.	2.5	18
162	A deep transcriptomic resource for the copepod crustacean <i>Labidocera madurae</i> : A potential indicator species for assessing near shore ecosystem health. <i>PLoS ONE</i> , 2017, 12, e0186794.	2.5	17
163	Daily rhythms and enrichment patterns in the transcriptome of the behavior-manipulating parasite <i>Ophiocordyceps kimflamingiae</i> . <i>PLoS ONE</i> , 2017, 12, e0187170.	2.5	24
164	Comparison of histone-like HU protein DNA-binding properties and HU/IHF protein sequence alignment. <i>PLoS ONE</i> , 2017, 12, e0188037.	2.5	37
165	Inferring repeat-protein energetics from evolutionary information. <i>PLoS Computational Biology</i> , 2017, 13, e1005584.	3.2	11
166	Decoding the similarities and differences among mycobacterial species. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005883.	3.0	37
167	Interferon β induced compositional changes in human bone marrow derived mesenchymal stem/stromal cells. <i>Clinical Proteomics</i> , 2017, 14, 26.	2.1	30
168	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	3.8	114
169	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. <i>BMC Systems Biology</i> , 2017, 11, 132.	3.0	28

#	ARTICLE	IF	CITATIONS
170	Predicting drug-disease interactions by semi-supervised graph cut algorithm and three-layer data integration. BMC Medical Genomics, 2017, 10, 79.	1.5	23
171	Bacterial tail anchors can target to the mitochondrial outer membrane. Biology Direct, 2017, 12, 16.	4.6	9
172	Identification of a novel HERV-K(HML10): comprehensive characterization and comparative analysis in non-human primates provide insights about HML10 proviruses structure and diffusion. Mobile DNA, 2017, 8, 15.	3.6	38
173	Using semantics for representing experimental protocols. Journal of Biomedical Semantics, 2017, 8, 52.	1.6	8
174	Similarity Projection: A Geometric Measure for Comparison of Biological Sequences. , 2017, , .		0
175	Fast batch searching for protein homology based on compression and clustering. BMC Bioinformatics, 2017, 18, 508.	2.6	6
176	Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing. Genome Biology and Evolution, 2017, 9, 3328-3344.	2.5	26
177	Neural Mechanisms Underlying the Disruption of Male Courtship Behavior by Adult Exposure to Di(2-ethylhexyl) Phthalate in Mice. Environmental Health Perspectives, 2017, 125, 097001.	6.0	47
178	eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
179	Transcriptomics, metabolomics and histology indicate that high-carbohydrate diet negatively affects the liver health of blunt snout bream (Megalobrama amblycephala). BMC Genomics, 2017, 18, 856.	2.8	77
180	An overview of comparative modelling and resources dedicated to large-scale modelling of genome sequences. Acta Crystallographica Section D: Structural Biology, 2017, 73, 628-640.	2.3	46
181	Cross-Kingdom Regulation of Putative miRNAs Derived from Happy Tree in Cancer Pathway: A Systems Biology Approach. International Journal of Molecular Sciences, 2017, 18, 1191.	4.1	38
182	Functional Analysis of Human Hub Proteins and Their Interactors Involved in the Intrinsic Disorder-Enriched Interactions. International Journal of Molecular Sciences, 2017, 18, 2761.	4.1	85
183	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	4.1	91
184	Genome-wide identification of miRNAs and lncRNAs in Cajanus cajan. BMC Genomics, 2017, 18, 878.	2.8	40
185	Identification and analysis of mutational hotspots in oncogenes and tumour suppressors. Oncotarget, 2017, 8, 21290-21304.	1.8	23
186	Improved Prediction of Eukaryotic Protein Subcellular Localization Using Particle Swarm Optimization of Multiple Classifiers. , 2017, , .		1
187	De Novo Assembly of Lucina pectinata Genome using Ion Torrent Reads. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
188	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. <i>Biotechnology Advances</i> , 2018, 36, 894-904.	11.7	20
189	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	46.4	263
190	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018, 359, 930-935.	12.6	51
191	Differential Responses of Amino Acids and Soluble Proteins to Heat Stress Associated with Genetic Variations in Heat Tolerance for Hard Fescue. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 45-55.	1.0	36
192	Morphological and transcriptomic analyses reveal three discrete primary stages of postembryonic development in the common fire salamander, <i>Salamandra salamandra</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 96-108.	1.3	10
193	The H-subunit of the restriction endonuclease CgII contains a prototype DEAD-Z1 helicase-like motor. <i>Nucleic Acids Research</i> , 2018, 46, 2560-2572.	14.5	1
194	Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. <i>Journal of Proteome Research</i> , 2018, 17, 1383-1396.	3.7	16
195	Single and multiple phenotype QTL analyses of downy mildew resistance in interspecific grapevines. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1133-1143.	3.6	58
196	Aspirin-induced attenuation of adipogenic differentiation of bone marrow mesenchymal stem cells is accompanied by the disturbed epigenetic modification. <i>International Journal of Biochemistry and Cell Biology</i> , 2018, 98, 29-42.	2.8	15
197	Mechanisms of TPGS and its derivatives inhibiting P-glycoprotein efflux pump and application for reversing multidrug resistance in hepatocellular carcinoma. <i>Polymer Chemistry</i> , 2018, 9, 1827-1839.	3.9	32
198	Structural Principles Analysis of Host-Pathogen Protein-Protein Interactions: A Structural Bioinformatics Survey. <i>IEEE Access</i> , 2018, 6, 11760-11771.	4.2	12
199	Cheminformatics Analysis of Dynamic WNK-Inhibitor Interactions. <i>Molecular Informatics</i> , 2018, 37, e1700138.	2.5	7
200	Proteomic approaches to identify blood-based biomarkers for depression and bipolar disorders. <i>Expert Review of Proteomics</i> , 2018, 15, 325-340.	3.0	30
201	Screening, large-scale production and structure-based classification of cystine-dense peptides. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 270-278.	8.2	44
202	A monoclonal antibody against SV40 large T antigen (PAb416) does not label Merkel cell carcinoma. <i>Histopathology</i> , 2018, 73, 162-166.	2.9	4
203	Investigation on the metal binding sites of a putative Zn(II) transporter in opportunistic yeast species <i>Candida albicans</i> . <i>New Journal of Chemistry</i> , 2018, 42, 8123-8130.	2.8	6
204	A global view of structure-function relationships in the tautomerase superfamily. <i>Journal of Biological Chemistry</i> , 2018, 293, 2342-2357.	3.4	39
205	Characterization of a novel thermotolerant NAD ⁺ -dependent formate dehydrogenase from hot climate plant cotton (<i>Gossypium hirsutum</i> L.). <i>3 Biotech</i> , 2018, 8, 175.	2.2	3

#	ARTICLE	IF	CITATIONS
206	Neuropeptidomics of the Rat Habenular Nuclei. <i>Journal of Proteome Research</i> , 2018, 17, 1463-1473.	3.7	20
207	Spatiotemporal compartmentalization of hepatic NADH and NADPH metabolism. <i>Journal of Biological Chemistry</i> , 2018, 293, 7508-7516.	3.4	81
208	TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA-binding protein association. <i>BMC Bioinformatics</i> , 2018, 19, 41.	2.6	8
209	Rapid and robust MALDI-TOF MS techniques for microbial identification: a brief overview of their diverse applications. <i>Journal of Microbiology</i> , 2018, 56, 209-216.	2.8	99
210	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	12.8	405
211	MoonProt 2.0: an expansion and update of the moonlighting proteins database. <i>Nucleic Acids Research</i> , 2018, 46, D640-D644.	14.5	86
212	Crystal structure of Bâ€cell coâ€receptor CD19 in complex with antibody B43 reveals an unexpected fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 495-500.	2.6	31
213	Computational Analysis of LOX1 Inhibition Identifies Descriptors Responsible for Binding Selectivity. <i>ACS Omega</i> , 2018, 3, 2261-2272.	3.5	3
214	The fumarylacetoacetate hydrolase (FAH) superfamily of enzymes: multifunctional enzymes from microbes to mitochondria. <i>Biochemical Society Transactions</i> , 2018, 46, 295-309.	3.4	30
215	The OMA orthology database in 2018: retrieving evolutionary relationships among all domains of life through richer web and programmatic interfaces. <i>Nucleic Acids Research</i> , 2018, 46, D477-D485.	14.5	231
216	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	5.5	163
217	Cladogenesis and Genomic Streamlining in Extracellular Endosymbionts of Tropical Stink Bugs. <i>Genome Biology and Evolution</i> , 2018, 10, 680-693.	2.5	21
218	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	14.5	489
219	Interleukins and their signaling pathways in the Reactome biological pathway database. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1411-1416.	2.9	11
220	Guiding Mitotic Progression by Crosstalk between Post-translational Modifications. <i>Trends in Biochemical Sciences</i> , 2018, 43, 251-268.	7.5	43
221	Cancer cells biomineralize ionic gold into nanoparticles-microplates via secreting defense proteins with specific gold-binding peptides. <i>Acta Biomaterialia</i> , 2018, 71, 61-71.	8.3	45
222	Modification of the interfacial properties of sodium caseinate using a commercial peptidase preparation from <i>Geobacillus stearothermophilus</i> . <i>Food Hydrocolloids</i> , 2018, 81, 60-70.	10.7	11
223	Development of a Neo-Epitope Specific Assay for Serological Assessment of Type VII Collagen Turnover and Its Relevance in Fibroproliferative Disorders. <i>Assay and Drug Development Technologies</i> , 2018, 16, 123-131.	1.2	9

#	ARTICLE	IF	CITATIONS
224	Protein S100-A8: A potential metastasis-associated protein for breast cancer determined via iTRAQ quantitative proteomic and clinicopathological analysis. <i>Oncology Letters</i> , 2018, 15, 5285-5293.	1.8	17
225	Proteome-wide analysis of cysteine oxidation reveals metabolic sensitivity to redox stress. <i>Nature Communications</i> , 2018, 9, 1581.	12.8	178
226	<i>Toxoplasma gondii</i> infection induces the formation of hostâ€™s nuclear granules containing poly(A)-binding proteins. <i>Canadian Journal of Microbiology</i> , 2018, 64, 551-558.	1.7	2
227	Comparative qualitative phosphoproteomics analysis identifies shared phosphorylation motifs and associated biological processes in evolutionary divergent plants. <i>Journal of Proteomics</i> , 2018, 181, 152-159.	2.4	20
228	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. <i>Structure</i> , 2018, 26, 894-904.e2.	3.3	81
229	Whole-Genome Analysis of an Extensively Drug-Resistance <i>Empedobacter falsenii</i> Strain Reveals Distinct Features and the Presence of a Novel Metallo- β -Lactamase (EBR-2). <i>Current Microbiology</i> , 2018, 75, 1084-1089.	2.2	6
230	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761.	14.5	2,710
231	Comparative proteomic analysis of human malignant ascitic fluids for the development of gastric cancer biomarkers. <i>Clinical Biochemistry</i> , 2018, 56, 55-61.	1.9	17
232	Neural/Bayes network predictor for inheritable cardiac disease pathogenicity and phenotype. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 119, 19-27.	1.9	17
233	Structural dynamics is a determinant of the functional significance of missense variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4164-4169.	7.1	76
234	Identification of human glycosyltransferase genes expressed in erythroid cells predicts potential carbohydrate blood group loci. <i>Scientific Reports</i> , 2018, 8, 6040.	3.3	13
235	Dosage Compensation of the X Chromosome: A Complex Epigenetic Assignment Involving Chromatin Regulators and Long Noncoding RNAs. <i>Annual Review of Biochemistry</i> , 2018, 87, 323-350.	11.1	106
236	Exploring the Sea Urchin Neuropeptide Landscape by Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 923-934.	2.8	10
237	Searching and Extracting Data from the EMBL-EBI Complex Portal. <i>Methods in Molecular Biology</i> , 2018, 1764, 377-390.	0.9	7
238	ProtaBank: A repository for protein design and engineering data. <i>Protein Science</i> , 2018, 27, 1113-1124.	7.6	47
239	Ferritin from the haemolymph of adult ants: an extraction method for characterization and a ferromagnetic study. <i>European Biophysics Journal</i> , 2018, 47, 641-653.	2.2	6
240	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
241	Terminal Uridyltransferases Execute Programmed Clearance of Maternal Transcriptome in Vertebrate Embryos. <i>Molecular Cell</i> , 2018, 70, 72-82.e7.	9.7	87

#	ARTICLE	IF	CITATIONS
242	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science & Technology</i> , 2018, 52, 5386-5397.	10.0	52
243	MOCASSIN-prot: a multi-objective clustering approach for protein similarity networks. <i>Bioinformatics</i> , 2018, 34, 1270-1277.	4.1	2
244	DDX49 is an RNA helicase that affects translation by regulating mRNA export and the levels of pre-ribosomal RNA. <i>Nucleic Acids Research</i> , 2018, 46, 6304-6317.	14.5	29
245	Protein Tertiary Structure by Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018, 43, 157-169.	7.5	77
246	Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 1801-1811.	3.7	17
247	Dopamine-mediated calcium channel regulation in synaptic suppression in <i>L. stagnalis</i> interneurons. <i>Channels</i> , 2018, 12, 153-173.	2.8	6
248	Structural basis of noncanonical polyphenol oxidase activity in DLLA: A lectin from <i>Dolichos lablab</i> . <i>Biotechnology and Applied Biochemistry</i> , 2018, 65, 701-717.	3.1	1
249	Computational Systems Biology of Metabolism in Infection. <i>Experientia Supplementum</i> (2012), 2018, 109, 235-282.	0.9	6
250	A plasmid borne, functionally novel glycoside hydrolase family 30 subfamily 8 endoxylanase from solventogenic <i>Clostridium</i> . <i>Biochemical Journal</i> , 2018, 475, 1533-1551.	3.7	20
251	Archaeal and eukaryal translation initiation factor 1 differ in their RNA interacting loops. <i>FEBS Letters</i> , 2018, 592, 1602-1610.	2.8	2
252	A sequence family database built on ECOD structural domains. <i>Bioinformatics</i> , 2018, 34, 2997-3003.	4.1	5
253	Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. <i>Methods in Molecular Biology</i> , 2018, 1762, 51-69.	0.9	4
254	The solution structure of monomeric CCL5 in complex with a doubly sulfated N-terminal segment of CCR5. <i>FEBS Journal</i> , 2018, 285, 1988-2003.	4.7	35
255	From HSV infection to erythema multiforme through autoimmune crossreactivity. <i>Autoimmunity Reviews</i> , 2018, 17, 576-581.	5.8	18
256	Improving the genetic signature of prostate cancer, the somatic mutations. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2018, 36, 312.e17-312.e23.	1.6	6
257	Sertoli Cells. <i>Methods in Molecular Biology</i> , 2018, , .	0.9	1
258	Peptide identifications and false discovery rates using different mass spectrometry platforms. <i>Talanta</i> , 2018, 182, 456-463.	5.5	17
259	A scalable approach to the computation of invariant measures for high-dimensional Markovian systems. <i>Scientific Reports</i> , 2018, 8, 1796.	3.3	6

#	ARTICLE	IF	CITATIONS
260	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. Scientific Reports, 2018, 8, 1794.	3.3	99
261	<i>TEOSINTE BRANCHED1</i> Regulates Inflorescence Architecture and Development in Bread Wheat (<i>Triticum aestivum</i>). Plant Cell, 2018, 30, 563-581.	6.6	215
262	The Role of Self-Assembling Lipid Molecules in Vaccination. Advances in Biomembranes and Lipid Self-Assembly, 2018, 27, 1-37.	0.6	1
263	Mechanism and Catalytic Site Atlas (M-CSA): a database of enzyme reaction mechanisms and active sites. Nucleic Acids Research, 2018, 46, D618-D623.	14.5	151
264	Dual transcriptomics reveals co- evolutionary mechanisms of intestinal parasite infections in blue mussels <i>Mytilus edulis</i>. Molecular Ecology, 2018, 27, 1505-1519.	3.9	15
265	Computational Methods Involved in Evaluating the Toxicity of the Reproductive Toxicants in Sertoli Cell. Methods in Molecular Biology, 2018, 1748, 253-277.	0.9	2
266	TDP-43 post-translational modifications in health and disease. Expert Opinion on Therapeutic Targets, 2018, 22, 279-293.	3.4	110
267	ASCA-PSO: Adaptive sine cosine optimization algorithm integrated with particle swarm for pairwise local sequence alignment. Expert Systems With Applications, 2018, 99, 56-70.	7.6	129
268	Molecular dialogues between Trichoderma and roots: Role of the fungal secretome. Fungal Biology Reviews, 2018, 32, 62-85.	4.7	183
269	New Insights into the Function and Global Distribution of Polyethylene Terephthalate (PET)-Degrading Bacteria and Enzymes in Marine and Terrestrial Metagenomes. Applied and Environmental Microbiology, 2018, 84, .	3.1	259
270	Lose it or keep it: (how bivalves can provide) insights into mitochondrial inheritance mechanisms. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 41-51.	1.3	12
271	Quantitative proteomics and SWATH-MS to elucidate peri-receptor mechanisms in human salt taste sensitivity. Food Chemistry, 2018, 254, 95-102.	8.2	16
272	AIMOES: Archive information assisted multi-objective evolutionary strategy for ab initio protein structure prediction. Knowledge-Based Systems, 2018, 146, 58-72.	7.1	46
273	Protein Profile of the Acquired Enamel Pellicle after Rinsing with Whole Milk, Fat-Free Milk, and Water: An in vivo Study. Caries Research, 2018, 52, 288-296.	2.0	21
274	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. Journal of Molecular Biology, 2018, 430, 1024-1050.	4.2	32
275	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
276	Gene annotation bias impedes biomedical research. Scientific Reports, 2018, 8, 1362.	3.3	125
277	Inhibition of Human Tyrosinase Requires Molecular Motifs Distinctively Different from Mushroom Tyrosinase. Journal of Investigative Dermatology, 2018, 138, 1601-1608.	0.7	141

#	ARTICLE	IF	CITATIONS
278	Proteome Data Improves Protein Function Prediction in the Interactome of <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 961-973.	3.8	8
279	Cell growth inhibition and apoptosis in breast cancer cells induced by anti-FZD7 scFvs: involvement of bioinformatics-based design of novel epitopes. <i>Breast Cancer Research and Treatment</i> , 2018, 169, 427-436.	2.5	12
280	Identification of cisapride as new inhibitor of putrescine uptake in <i>Trypanosoma cruzi</i> by combined ligand- and structure-based virtual screening. <i>European Journal of Medicinal Chemistry</i> , 2018, 149, 22-29.	5.5	15
281	Proteomic response of <i>Streptococcus pneumoniae</i> to iron limitation. <i>International Journal of Medical Microbiology</i> , 2018, 308, 713-721.	3.6	26
282	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
283	Comparative analysis of Salivette® and paraffin gum preparations for establishment of a metaproteomics analysis pipeline for stimulated human saliva. <i>Journal of Oral Microbiology</i> , 2018, 10, 1428006.	2.7	10
284	Transcriptome analysis reveals TMPRSS6 isoforms with distinct functionalities. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2498-2509.	3.6	11
285	Genomewide Transcriptional Responses of Iron-Starved <i>Chlamydia trachomatis</i> Reveal Prioritization of Metabolic Precursor Synthesis over Protein Translation. <i>MSystems</i> , 2018, 3, .	3.8	38
286	NLSdb™ major update for database of nuclear localization signals and nuclear export signals. <i>Nucleic Acids Research</i> , 2018, 46, D503-D508.	14.5	61
287	G2S: a web-service for annotating genomic variants on 3D protein structures. <i>Bioinformatics</i> , 2018, 34, 1949-1950.	4.1	10
288	Deciphering the Link between Doubly Uniparental Inheritance of mtDNA and Sex Determination in Bivalves: Clues from Comparative Transcriptomics. <i>Genome Biology and Evolution</i> , 2018, 10, 577-590.	2.5	32
289	A presumed homologue of the regulatory subunits of eIF2B functions as ribose-1,5-bisphosphate isomerase in <i>Pyrococcus horikoshii</i> OT3. <i>Scientific Reports</i> , 2018, 8, 1891.	3.3	5
290	Ancient Diversification of Three-Finger Toxins in <i>Micrurus</i> Coral Snakes. <i>Journal of Molecular Evolution</i> , 2018, 86, 58-67.	1.8	30
291	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	3.3	215
292	Homology modelling and <i>in silico</i> substrate-binding analysis of a <i>Rhizobium</i> sp. RC1 haloalkanoic acid permease. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 339-349.	1.3	4
293	3Dâ€Chem: Structural Cheminformatics Workflows for Computerâ€Aided Drug Discovery. <i>ChemMedChem</i> , 2018, 13, 614-626.	3.2	17
294	Interactome Mapping Uncovers a General Role for Numb in Protein Kinase Regulation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2216-2228.	3.8	10
295	The OncoPPI Portal: an integrative resource to explore and prioritize proteinâ€protein interactions for cancer target discovery. <i>Bioinformatics</i> , 2018, 34, 1183-1191.	4.1	41

#	ARTICLE	IF	CITATIONS
296	ProteomicsDB. Nucleic Acids Research, 2018, 46, D1271-D1281.	14.5	197
297	Antibiotic resistance ABCF proteins reset the peptidyl transferase centre of the ribosome to counter translational arrest. Nucleic Acids Research, 2018, 46, 3753-3763.	14.5	71
298	Atomic structures of low-complexity protein segments reveal kinked β^2 sheets that assemble networks. Science, 2018, 359, 698-701.	12.6	376
299	Coarse-grained molecular dynamics simulations reveal lipid access pathways in P-glycoprotein. Journal of General Physiology, 2018, 150, 417-429.	1.9	31
300	First homology model of Plasmodium falciparum glucose-6-phosphate dehydrogenase: Discovery of selective substrate analog-based inhibitors as novel antimalarial agents. European Journal of Medicinal Chemistry, 2018, 146, 108-122.	5.5	9
301	The unique fold and lability of the [2Fe-2S] clusters of NEET proteins mediate their key functions in health and disease. Journal of Biological Inorganic Chemistry, 2018, 23, 599-612.	2.6	52
302	Structural and functional characterization of the Vindoline biosynthesis pathway enzymes of Catharanthus roseus. Journal of Molecular Modeling, 2018, 24, 53.	1.8	8
303	Molecular Pathways for Immune Recognition of Preproinsulin Signal Peptide in Type 1 Diabetes. Diabetes, 2018, 67, 687-696.	0.6	35
304	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. Nucleic Acids Research, 2018, 46, D726-D735.	14.5	175
305	Structural Characterization and Function Prediction of Immunoglobulin-like Fold in Cell Adhesion and Cell Signaling. Journal of Chemical Information and Modeling, 2018, 58, 532-542.	5.4	14
306	Remarkable similarity in Plasmodium falciparum and Plasmodium vivax geranylgeranyl diphosphate synthase dynamics and its implication for antimalarial drug design. Chemical Biology and Drug Design, 2018, 91, 1068-1077.	3.2	5
307	Peptide selection for the quantification of P α CH α NP in human serum by mass spectrometry. Rapid Communications in Mass Spectrometry, 2018, 32, 535-542.	1.5	6
308	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. Nature, 2018, 554, 118-122.	27.8	160
309	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. Journal of Bacteriology, 2018, 200, .	2.2	41
310	Ca ²⁺ -Induced Two-Component System CvsSR Regulates the Type III Secretion System and the Extracytoplasmic Function Sigma Factor AlgU in Pseudomonas syringae pv. tomato DC3000. Journal of Bacteriology, 2018, 200, .	2.2	40
311	Proteome-scale identification of Leishmania infantum for novel vaccine candidates: A hierarchical subtractive approach. Computational Biology and Chemistry, 2018, 72, 16-25.	2.3	18
312	Emerging whole-cell modeling principles and methods. Current Opinion in Biotechnology, 2018, 51, 97-102.	6.6	57
313	Dissecting and analyzing key residues in protein-DNA complexes. Journal of Molecular Recognition, 2018, 31, e2692.	2.1	7

#	ARTICLE	IF	CITATIONS
314	Temperature dependent cellulase adsorption on lignin from sugarcane bagasse. <i>Bioresource Technology</i> , 2018, 252, 143-149.	9.6	37
315	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. <i>Genome</i> , 2018, 61, 241-247.	2.0	15
316	Objective, Quantitative, Data-Driven Assessment of Chemical Probes. <i>Cell Chemical Biology</i> , 2018, 25, 194-205.e5.	5.2	71
317	An isotope dilution model for partitioning of phenylalanine and tyrosine uptake by the liver of lactating dairy cows. <i>Journal of Theoretical Biology</i> , 2018, 444, 100-107.	1.7	4
318	Expression system for structural and functional studies of human glycosylation enzymes. <i>Nature Chemical Biology</i> , 2018, 14, 156-162.	8.0	182
319	e Repo-ORP: Exploring the Opportunity Space to Combat Orphan Diseases with Existing Drugs. <i>Journal of Molecular Biology</i> , 2018, 430, 2266-2273.	4.2	10
320	A noncoding variant in <i>GANAB</i> explains isolated polycystic liver disease (PCLD) in a large family. <i>Human Mutation</i> , 2018, 39, 378-382.	2.5	21
321	Mol2vec: Unsupervised Machine Learning Approach with Chemical Intuition. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 27-35.	5.4	398
322	Gene-specific Variant Classifier (DPYD-Varifier) to Identify Deleterious Alleles of Dihydropyrimidine Dehydrogenase. <i>Clinical Pharmacology and Therapeutics</i> , 2018, 104, 709-718.	4.7	43
323	X-ray Structures of Target-Ligand Complexes Containing Compounds with Assay Interference Potential. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 1276-1284.	6.4	22
324	The eukaryotic linear motif resource – 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	14.5	183
325	Hypoxia-inducible lipid droplet-associated protein inhibits adipose triglyceride lipase. <i>Journal of Lipid Research</i> , 2018, 59, 531-541.	4.2	60
326	PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. <i>Nucleic Acids Research</i> , 2018, 46, D1197-D1201.	14.5	135
327	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. <i>Nucleic Acids Research</i> , 2018, 46, D624-D632.	14.5	1,234
328	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. <i>Scientific Reports</i> , 2018, 8, 678.	3.3	26
329	Systematic Identification of Lysine 2-hydroxyisobutyrylated Proteins in <i>Proteus mirabilis</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 482-494.	3.8	43
330	Muscle molecular adaptations to endurance exercise training are conditioned by glycogen availability: a proteomics-based analysis in the McArdle mouse model. <i>Journal of Physiology</i> , 2018, 596, 1035-1061.	2.9	26
331	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	14.5	57

#	ARTICLE	IF	CITATIONS
332	Monoclonal antibody-based ELISA for the quantification of porcine hemoglobin in meat products. Food Chemistry, 2018, 250, 170-179.	8.2	30
333	CHCHD10 mutations p.R15L and p.G66V cause motoneuron disease by haploinsufficiency. Human Molecular Genetics, 2018, 27, 706-715.	2.9	30
334	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	14.5	48
335	The European Bioinformatics Institute in 2017: data coordination and integration. Nucleic Acids Research, 2018, 46, D21-D29.	14.5	56
336	Impact of cycling cells and cell cycle regulation on Hydra regeneration. Developmental Biology, 2018, 433, 240-253.	2.0	28
337	eRAM: encyclopedia of rare disease annotations for precision medicine. Nucleic Acids Research, 2018, 46, D937-D943.	14.5	56
338	Microbial and viral chitinases: Attractive biopesticides for integrated pest management. Biotechnology Advances, 2018, 36, 818-838.	11.7	107
339	Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. Genome Biology and Evolution, 2018, 10, 166-188.	2.5	61
340	X-ray-Structure-Based Identification of Compounds with Activity against Targets from Different Families and Generation of Templates for Multitarget Ligand Design. ACS Omega, 2018, 3, 106-111.	3.5	19
341	TFClass: expanding the classification of human transcription factors to their mammalian orthologs. Nucleic Acids Research, 2018, 46, D343-D347.	14.5	112
342	G Protein-Coupled Receptors as Targets for Approved Drugs: How Many Targets and How Many Drugs?. Molecular Pharmacology, 2018, 93, 251-258.	2.3	825
343	Impact of diet-induced obesity on the mouse brain phosphoproteome. Journal of Nutritional Biochemistry, 2018, 58, 102-109.	4.2	22
344	Quantifying the Evolutionary Conservation of Genes Encoding Multidrug Efflux Pumps in the ESKAPE Pathogens To Identify Antimicrobial Drug Targets. MSystems, 2018, 3, .	3.8	20
345	Cross-linking BioThings APIs through JSON-LD to facilitate knowledge exploration. BMC Bioinformatics, 2018, 19, 30.	2.6	24
346	Alignment-free clustering of large data sets of unannotated protein conserved regions using minhashing. BMC Bioinformatics, 2018, 19, 83.	2.6	10
347	Building protein-protein interaction networks for Leishmania species through protein structural information. BMC Bioinformatics, 2018, 19, 85.	2.6	20
348	Diapause in a tropical oil-collecting bee: molecular basis unveiled by RNA-Seq. BMC Genomics, 2018, 19, 305.	2.8	39
349	The use of whole exome sequencing and murine patient derived xenografts as a method of chemosensitivity testing in sarcoma. Clinical Sarcoma Research, 2018, 8, 4.	2.3	4

#	ARTICLE	IF	CITATIONS
350	Complete genome sequence of <i>Pseudomonas alcaliphila</i> JAB1 (=DSM 26533), a versatile degrader of organic pollutants. <i>Standards in Genomic Sciences</i> , 2018, 13, 3.	1.5	36
351	Regulation of Clusterin Gene Expression. <i>Current Protein and Peptide Science</i> , 2018, 19, 612-622.	1.4	19
352	GROOLS: reactive graph reasoning for genome annotation through biological processes. <i>BMC Bioinformatics</i> , 2018, 19, 132.	2.6	2
353	In vitro gentamicin exposure alters caveolae protein profile in cochlear spiral ligament pericytes. <i>Proteome Science</i> , 2018, 16, 7.	1.7	1
354	Identification of Cyclin-dependent Kinase 1 Specific Phosphorylation Sites by an <i>In Vitro</i> Kinase Assay. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	8
355	Toward clinical and molecular understanding of pathogenic variants in the <i>ZBTB18</i> gene. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 393-400.	1.2	22
356	Diet Impacts Pre-implantation Histotroph Proteomes in Beef Cattle. <i>Journal of Proteome Research</i> , 2018, 17, 2144-2155.	3.7	7
357	Horizons of Systems Biocatalysis and Renaissance of Metabolite Synthesis. <i>Biotechnology Journal</i> , 2018, 13, 1700620.	3.5	19
358	Structural principles of distinct assemblies of the human $\alpha 4\beta 2$ nicotinic receptor. <i>Nature</i> , 2018, 557, 261-265.	27.8	177
359	Accessing Expert-Curated Pharmacological Data in the IUPHAR/BPS Guide to PHARMACOLOGY. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 1.34.1-1.34.46.	25.8	13
360	Waterlogging affects plant morphology and the expression of key genes in <i>tef</i> (<i>Eragrostis tef</i>). <i>Plant Direct</i> , 2018, 2, e00056.	1.9	24
361	Structure and properties of AB21, a novel <i>Agaricus bisporus</i> protein with structural relation to bacterial pore-forming toxins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 897-911.	2.6	3
362	Necklace: combining reference and assembled transcriptomes for more comprehensive RNA-Seq analysis. <i>GigaScience</i> , 2018, 7, .	6.4	9
363	Structure and hydrodynamics of a DNA G-quadruplex with a cytosine bulge. <i>Nucleic Acids Research</i> , 2018, 46, 5319-5331.	14.5	44
364	Human transbodies that interfere with the functions of Ebola virus VP35 protein in genome replication and transcription and innate immune antagonism. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-15.	6.5	32
365	hpLysis Database-Engine: A New Data-Scheme for Fast Semantic Queries in Biomedical Databases. , 2018, , .		1
366	In vitro screening, homology modeling and molecular docking studies of some pyrazole and imidazole derivatives. <i>Biomedicine and Pharmacotherapy</i> , 2018, 103, 653-661.	5.6	60
367	Precision Profiling of the Cardiovascular Post-Translationally Modified Proteome. <i>Circulation Research</i> , 2018, 122, 1221-1237.	4.5	33

#	ARTICLE	IF	CITATIONS
368	Targeted data-independent acquisition for mass spectrometric detection of RAS mutations in formalin-fixed, paraffin-embedded tumor biopsies. <i>Journal of Proteomics</i> , 2018, 189, 91-96.	2.4	12
369	The Rosa genome provides new insights into the domestication of modern roses. <i>Nature Genetics</i> , 2018, 50, 772-777.	21.4	344
370	A New Database for Drug Discovery Through Application of Data-Integration and Semantics. , 2018, , .		1
371	Kinetic Characterization of PA1225 from <i>Pseudomonas aeruginosa</i> PAO1 Reveals a New NADPH:Quinone Reductase. <i>Biochemistry</i> , 2018, 57, 3050-3058.	2.5	7
372	Recessive variants of <i>MuSK</i> are associated with late onset CMS and predominant limb girdle weakness. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1594-1601.	1.2	25
373	Targeting of epigenetic regulators in neuroblastoma. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-12.	7.7	34
374	Comparative systems analysis of the secretome of the opportunistic pathogen <i>Aspergillus fumigatus</i> and other <i>Aspergillus</i> species. <i>Scientific Reports</i> , 2018, 8, 6617.	3.3	42
375	Urinary CE-MS peptide marker pattern for detection of solid tumors. <i>Scientific Reports</i> , 2018, 8, 5227.	3.3	28
376	New Frontiers in Mining Complex Patterns. <i>Lecture Notes in Computer Science</i> , 2018, , .	1.3	0
377	Computational Modelling of Protein Complex Structure and Assembly. <i>Methods in Molecular Biology</i> , 2018, 1764, 347-356.	0.9	2
378	Evolution of photosynthetic reaction centers: insights from the structure of the heliobacterial reaction center. <i>Photosynthesis Research</i> , 2018, 138, 11-37.	2.9	53
379	A pathway for every product? Tools to discover and design plant metabolism. <i>Plant Science</i> , 2018, 273, 61-70.	3.6	18
380	Decreased PECAM1-mediated TGF- β 1 expression in the mid-secretory endometrium in women with recurrent implantation failure. <i>Human Reproduction</i> , 2018, 33, 832-843.	0.9	59
381	Molecular Insights into the Mechanisms of SUN1 Oligomerization in the Nuclear Envelope. <i>Biophysical Journal</i> , 2018, 114, 1190-1203.	0.5	35
382	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. <i>Molecular Cell</i> , 2018, 70, 327-339.e5.	9.7	356
383	HMDB 4.0: the human metabolome database for 2018. <i>Nucleic Acids Research</i> , 2018, 46, D608-D617.	14.5	2,805
384	Systematic characterization of pan-cancer mutation clusters. <i>Molecular Systems Biology</i> , 2018, 14, e7974.	7.2	39
385	Transcriptomic characterization of MRI contrast with focus on the T1-w/T2-w ratio in the cerebral cortex. <i>NeuroImage</i> , 2018, 174, 504-517.	4.2	51

#	ARTICLE	IF	CITATIONS
386	Glycan affinity magnetic nanoplatfoms for urinary glycobimarkers discovery in bladder cancer. Talanta, 2018, 184, 347-355.	5.5	29
387	Proteomic Characterization of the Neural Ectoderm Fated Cell Clones in the <i>Xenopus laevis</i> Embryo by High-Resolution Mass Spectrometry. ACS Chemical Neuroscience, 2018, 9, 2064-2073.	3.5	19
388	Succinate-acetate permease from <i>Citrobacter koseri</i> is an anion channel that unidirectionally translocates acetate. Cell Research, 2018, 28, 644-654.	12.0	15
389	Structure of the peptidoglycan polymerase RodA resolved by evolutionary coupling analysis. Nature, 2018, 556, 118-121.	27.8	110
390	ADPredict: ADP-ribosylation site prediction based on physicochemical and structural descriptors. Bioinformatics, 2018, 34, 2566-2574.	4.1	17
391	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic β Cell. Cell, 2018, 173, 11-19.	28.9	179
393	Learned protein embeddings for machine learning. Bioinformatics, 2018, 34, 2642-2648.	4.1	223
394	An orphan G-protein-coupled receptor causes human gigantism and/or acromegaly: Molecular biology and clinical correlations. Best Practice and Research in Clinical Endocrinology and Metabolism, 2018, 32, 125-140.	4.7	26
395	Deciphering metabonomics biomarkers-targets interactions for psoriasis vulgaris by network pharmacology. Annals of Medicine, 2018, 50, 323-332.	3.8	10
396	Redundancy in two major compound databases. Drug Discovery Today, 2018, 23, 1183-1186.	6.4	8
397	Cross-linked peptide identification: A computational forest of algorithms. Mass Spectrometry Reviews, 2018, 37, 738-749.	5.4	27
398	Refined ab initio gene predictions of <i>Heterorhabditis bacteriophora</i> using RNA-seq. International Journal for Parasitology, 2018, 48, 585-590.	3.1	6
399	Fsr1, a striatin homologue, forms an endomembrane-associated complex that regulates virulence in the maize pathogen <i>Fusarium verticillioides</i> . Molecular Plant Pathology, 2018, 19, 812-826.	4.2	25
400	Genome-wide linkage and sequence analysis challenge <i>CCDC66</i> as a human retinal dystrophy candidate gene and support a distinct <i>NMNAT1</i> -related fundus phenotype. Clinical Genetics, 2018, 93, 149-154.	2.0	13
401	Rapid detection of milk adulteration using intact protein flow injection mass spectrometric fingerprints combined with chemometrics. Food Chemistry, 2018, 240, 573-578.	8.2	23
402	Genomewide identification of genes involved in the potato response to drought indicates functional evolutionary conservation with <i>Arabidopsis</i> plants. Plant Biotechnology Journal, 2018, 16, 603-614.	8.3	42
403	Proteomic analysis of sweet algerian apricot kernels (<i>Prunus armeniaca</i> L.) by combinatorial peptide ligand libraries and LC-MS/MS. Food Chemistry, 2018, 239, 935-945.	8.2	15
404	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Science, 2018, 27, 14-25.	7.6	3,377

#	ARTICLE	IF	CITATIONS
405	The transcriptome, extracellular proteome and active secretome of agroinfiltrated <i>Nicotiana benthamiana</i> uncover a large, diverse protease repertoire. <i>Plant Biotechnology Journal</i> , 2018, 16, 1068-1084.	8.3	54
406	Computational design of new protein kinase D 1 (PKD1) inhibitors: homology-based active site prediction, energy-optimized pharmacophore, docking and database screening. <i>Molecular Diversity</i> , 2018, 22, 47-56.	3.9	3
407	BioPlex Display: An Interactive Suite for Large-Scale AP-MS Protein-Protein Interaction Data. <i>Journal of Proteome Research</i> , 2018, 17, 722-726.	3.7	59
408	Mobi 2.0: an improved method to define intrinsic disorder, mobility and linear binding regions in protein structures. <i>Bioinformatics</i> , 2018, 34, 122-123.	4.1	24
409	20 years of the SMART protein domain annotation resource. <i>Nucleic Acids Research</i> , 2018, 46, D493-D496.	14.5	1,525
410	The online Tabloid Proteome: an annotated database of protein associations. <i>Nucleic Acids Research</i> , 2018, 46, D581-D585.	14.5	6
411	RCSB Protein Data Bank: Sustaining a living digital data resource that enables breakthroughs in scientific research and biomedical education. <i>Protein Science</i> , 2018, 27, 316-330.	7.6	219
412	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , 2018, 46, D213-D217.	14.5	134
413	Machine learning provides predictive analysis into silver nanoparticle protein corona formation from physicochemical properties. <i>Environmental Science: Nano</i> , 2018, 5, 64-71.	4.3	75
414	Human CCDC47 sandwich immunoassay development with electrochemiluminescence technology. <i>Journal of Immunological Methods</i> , 2018, 452, 12-19.	1.4	1
415	dbCAN-seq: a database of carbohydrate-active enzyme (CAZyme) sequence and annotation. <i>Nucleic Acids Research</i> , 2018, 46, D516-D521.	14.5	224
416	BtsT, a Novel and Specific Pyruvate/H ⁺ Symporter in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	36
417	Comparative proteomic profiling of myofibrillar proteins in dry-cured ham with different proteolysis indices and adhesiveness. <i>Food Chemistry</i> , 2018, 244, 238-245.	8.2	57
418	Gene of the month: SDH. <i>Journal of Clinical Pathology</i> , 2018, 71, 95-97.	2.0	28
419	Synaptic proteomics as a means to identify the molecular basis of mental illness: Are we getting there?. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 84, 353-361.	4.8	23
420	The evolution of a Web resource: The Galactosemia Proteins Database 2.0. <i>Human Mutation</i> , 2018, 39, 52-60.	2.5	13
421	Applications of sequence coevolution in membrane protein biochemistry. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 895-908.	2.6	27
422	Spatial features of proteins related to their phosphorylation and associated structural changes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 13-20.	2.6	7

#	ARTICLE	IF	CITATIONS
423	Computational characterization of substrate and product specificities, and functionality of Sâ€œadenosylmethionine binding pocket in histone lysine methyltransferases from Arabidopsis, rice and maize. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 21-34.	2.6	8
424	PDBsum: Structural summaries of PDB entries. <i>Protein Science</i> , 2018, 27, 129-134.	7.6	910
425	Quantitative phosphoproteomic analysis of acquired cancer drug resistance to pazopanib and dasatinib. <i>Journal of Proteomics</i> , 2018, 170, 130-140.	2.4	27
426	Microbial ecologyâ€based engineering of Microbial Electrochemical Technologies. <i>Microbial Biotechnology</i> , 2018, 11, 22-38.	4.2	27
427	Chemical shift assignments and the secondary structure of the Est3 telomerase subunit in the yeast <i>Hansenula polymorpha</i> . <i>Biomolecular NMR Assignments</i> , 2018, 12, 57-62.	0.8	3
428	Correlation of pheromone-binding proteinâ€™ligand equilibrium dissociation constants with electroantennogram response patterns. <i>Canadian Journal of Chemistry</i> , 2018, 96, 168-177.	1.1	5
429	Liposome encapsulation of anionic and cationic whey peptides: Influence of peptide net charge on properties of the nanovesicles. <i>LWT - Food Science and Technology</i> , 2018, 87, 40-46.	5.2	36
430	CHEMGENIE: integration of chemogenomics data for applications in chemical biology. <i>Drug Discovery Today</i> , 2018, 23, 151-160.	6.4	13
431	Investigation of the Perilipin 5 gene expression and association study of its sequence polymorphism with meat and carcass quality traits in different pig breeds. <i>Animal</i> , 2018, 12, 1135-1143.	3.3	7
432	Engineering peptide ligase specificity by proteomic identification of ligation sites. <i>Nature Chemical Biology</i> , 2018, 14, 50-57.	8.0	80
433	Bad phosphorylation as a target of inhibition in oncology. <i>Cancer Letters</i> , 2018, 415, 177-186.	7.2	58
434	14â€3â€3 proteins mediate inhibitory effects of <scp>cAMP</scp> on saltâ€inducible kinases (<scp>SIK</scp>s). <i>FEBS Journal</i> , 2018, 285, 467-480.	4.7	49
435	Structural changes of homodimers in the PDB. <i>Journal of Structural Biology</i> , 2018, 202, 42-50.	2.8	3
436	Race Disparities in the Contribution of miRNA Isoforms and tRNA-Derived Fragments to Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2018, 78, 1140-1154.	0.9	90
437	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus â€Candidatus <i>Sulfobium</i> â€. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	83
438	Design, synthesis, and biological evaluation of polo-like kinase 1/eukaryotic elongation factor 2 kinase (PLK1/EEF2K) dual inhibitors for regulating breast cancer cells apoptosis and autophagy. <i>European Journal of Medicinal Chemistry</i> , 2018, 144, 517-528.	5.5	31
439	A Structural Framework for GPCR Chemogenomics: Whatâ€™s In a Residue Number?. <i>Methods in Molecular Biology</i> , 2018, 1705, 73-113.	0.9	6
440	Varieties of charge distributions in coat proteins of ssRNA+â€™%â€™%viruses. <i>Journal of Physics Condensed Matter</i> , 2018, 30, 024001.	1.8	10

#	ARTICLE	IF	CITATIONS
441	Metabolic versatility of a novel <i>N-fixing</i> Alphaproteobacterium isolated from a marine oxygen minimum zone. <i>Environmental Microbiology</i> , 2018, 20, 755-768.	3.8	29
442	Molecular Recognition Features in Zika Virus Proteome. <i>Journal of Molecular Biology</i> , 2018, 430, 2372-2388.	4.2	58
443	Structure-based statistical modeling and analysis of peptide affinity and cross-reactivity to human senile osteoporosis <sc>OSF SH3</sc> domain. <i>Journal of Chemometrics</i> , 2018, 32, e2967.	1.3	0
444	Characterization of cysteine thiol modifications based on protein microenvironments and local secondary structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 192-209.	2.6	16
445	Viral Short ORFs and Their Possible Functions. <i>Proteomics</i> , 2018, 18, e1700255.	2.2	17
446	In silico approaches for unveiling novel glycomarkers in cancer. <i>Journal of Proteomics</i> , 2018, 171, 95-106.	2.4	14
447	Biochemical Characterization of Two Clinically-Relevant Human Fumarase Variants Defective for Oligomerization. <i>The Open Biochemistry Journal</i> , 2018, 12, 1-15.	0.5	15
448	A Phylogenetic Study of Monalysin Family of Proteobacterial Pore-Forming Toxins. , 2018, , .		0
449	Transcriptomic Characterization of the South American Freshwater Stingray <i>Potamotrygon motoro</i> Venom Apparatus. <i>Toxins</i> , 2018, 10, 544.	3.4	13
450	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
451	A partially function-to-topic model for protein function prediction. <i>BMC Genomics</i> , 2018, 19, 883.	2.8	3
452	Representativeness of variation benchmark datasets. <i>BMC Bioinformatics</i> , 2018, 19, 461.	2.6	18
453	Proteomics and multivariate modelling reveal sex-specific alterations in distinct regions of human carotid atheroma. <i>Biology of Sex Differences</i> , 2018, 9, 54.	4.1	12
454	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	1
455	End-to-end prediction of protein-protein interaction based on embedding and recurrent neural networks. , 2018, , .		18
456	Statistical-based database fingerprint: chemical space dependent representation of compound databases. <i>Journal of Cheminformatics</i> , 2018, 10, 55.	6.1	8
457	BASILIScan: a tool for high-throughput analysis of intrinsic disorder patterns in homologous proteins. <i>BMC Genomics</i> , 2018, 19, 902.	2.8	0
458	Comparative Analysis of Genomic Island Prediction Tools. <i>Frontiers in Genetics</i> , 2018, 9, 619.	2.3	29

#	ARTICLE	IF	CITATIONS
459	Accelerating annotation of articles via automated approaches: evaluation of the neXtA5 curation-support tool by neXtProt. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	6
460	NommPred: Prediction of Mitochondrial and Mitochondrion-Related Organelle Proteins of Nonmodel Organisms. Evolutionary Bioinformatics, 2018, 14, 117693431881983.	1.2	17
461	Integrative Gene Selection on Gene Expression Data: Providing Biological Context to Traditional Approaches. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	15
462	Hybrid natural language processing for high-performance patent and literature mining in IBM Watson for Drug Discovery. IBM Journal of Research and Development, 2018, 62, 8:1-8:12.	3.1	5
463	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	9
464	NeVOmics: An Enrichment Tool for Gene Ontology and Functional Network Analysis and Visualization of Data from OMICs Technologies. Genes, 2018, 9, 569.	2.4	16
465	Expert curation for building network-based dynamical models: a case study on atherosclerotic plaque formation. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	6
466	Targeting HCV polymerase: a structural and dynamic perspective into the mechanism of selective covalent inhibition. RSC Advances, 2018, 8, 42210-42222.	3.6	14
467	Protein structure networks provide insight into active site flexibility in esterase/lipases from the carnivorous plant <i>Drosera capensis</i> . Integrative Biology (United Kingdom), 2018, 10, 768-779.	1.3	10
468	Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. Scientific Data, 2018, 5, 180117.	5.3	22
469	A de novo transcriptome assembly of the zebra bullhead shark, <i>Heterodontus zebra</i> . Scientific Data, 2018, 5, 180197.	5.3	11
470	Liberating links between datasets using lightweight data publishing: an example using plant names and the taxonomic literature. Biodiversity Data Journal, 2018, 6, e27539.	0.8	7
471	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. PeerJ, 2018, 6, e5298.	2.0	27
472	Protein database search using compressed k-mer vocabularies. , 2018, , .		0
473	Proteomic changes in traumatic brain injury: experimental approaches. Current Opinion in Neurology, 2018, 31, 709-717.	3.6	14
474	WDFY4 is required for cross-presentation in response to viral and tumor antigens. Science, 2018, 362, 694-699.	12.6	216
475	Transcriptomics of <i>Haemophilus (Glässerella) parasuis</i> serovar 5 subjected to culture conditions partially mimetic to natural infection for the search of new vaccine antigens. BMC Veterinary Research, 2018, 14, 326.	1.9	11
476	Design of metalloproteins and novel protein folds using variational autoencoders. Scientific Reports, 2018, 8, 16189.	3.3	82

#	ARTICLE	IF	CITATIONS
477	<i>PCNT</i> point mutations and familial intracranial aneurysms. <i>Neurology</i> , 2018, 91, e2170-e2181.	1.1	22
478	Genetic Characterization of Maximilian Sunflower for the Development of a Locally Adapted Perennial Grain Oilseed. <i>Crop Science</i> , 2018, 58, 2241-2260.	1.8	8
479	X-search: an open access interface for cross-cohort exploration of the National Sleep Research Resource. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 99.	3.0	11
480	A Pipeline for Classifying Deleterious Coding Mutations in Agricultural Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1734.	3.6	9
481	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. <i>Journal of Proteome Research</i> , 2018, 18, 426-435.	3.7	18
483	C.e.l Phosphatome: A Catalogue of Actual and Pseudo Phosphatases Based on In-Silico Studies in <i>Caenorhabditis elegans</i> . <i>Protein Journal</i> , 2018, 37, 572-580.	1.6	1
484	Enhancing the Production of the Fungal Pigment Aurofusarin in <i>Fusarium graminearum</i> . <i>Toxins</i> , 2018, 10, 485.	3.4	26
485	Genomic Deoxyxylulose Phosphate Reductoisomerase (DXR) Mutations Conferring Resistance to the Antimalarial Drug Fosmidomycin in <i>E.Âcoli</i>. <i>ACS Synthetic Biology</i> , 2018, 7, 2824-2832.	3.8	11
486	PPARÎ³ maintains the metabolic heterogeneity and homeostasis of renal tubules. <i>EBioMedicine</i> , 2018, 38, 178-190.	6.1	29
487	Population Genomics and Biogeography of the Northern Acorn Barnacle (<i>Semibalanus balanoides</i>) Using Pooled Sequencing Approaches. <i>Population Genomics</i> , 2018, , 139-168.	0.5	9
488	Loss of the Mia40a oxidoreductase leads to hepato-pancreatic insufficiency in zebrafish. <i>PLoS Genetics</i> , 2018, 14, e1007743.	3.5	10
489	Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. <i>PLoS Genetics</i> , 2018, 14, e1007807.	3.5	116
490	Supervised Approaches for Protein Function Prediction by Topological Data Analysis. , 2018, , .		15
491	Draft genome sequence and detailed characterization of biofuel production by oleaginous microalga <i>Scenedesmus quadricauda</i> LWC002611. <i>Biotechnology for Biofuels</i> , 2018, 11, 308.	6.2	15
492	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. <i>PLoS Genetics</i> , 2018, 14, e1007758.	3.5	144
493	Characterization of mitochondrial proteomes of nonbilaterian animals. <i>IUBMB Life</i> , 2018, 70, 1289-1301.	3.4	9
494	Chemical Profiling of the Endoplasmic Reticulum Proteome Using Designer Labeling Reagents. <i>Journal of the American Chemical Society</i> , 2018, 140, 17060-17070.	13.7	37
495	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	3.5	37

#	ARTICLE	IF	CITATIONS
496	Signalink: Multilayered Regulatory Networks. <i>Methods in Molecular Biology</i> , 2018, 1819, 53-73.	0.9	17
497	Association of Cystathionine β -Synthase Gene Polymorphisms With Preeclampsia. <i>Clinical and Applied Thrombosis/Hemostasis</i> , 2018, 24, 285S-293S.	1.7	4
498	Large-Scale Modeling Approach Reveals Functional Metabolic Shifts during Hepatic Differentiation. <i>Journal of Proteome Research</i> , 2019, 18, 204-216.	3.7	6
499	HaploSaurus computes protein haplotypes for use in precision drug design. <i>Nature Communications</i> , 2018, 9, 4128.	12.8	21
500	Structural Biology Helps Interpret Variants of Uncertain Significance in Genes Causing Endocrine and Metabolic Disorders. <i>Journal of the Endocrine Society</i> , 2018, 2, 842-854.	0.2	7
501	A bacteria-derived tail anchor localizes to peroxisomes in yeast and mammalian cells. <i>Scientific Reports</i> , 2018, 8, 16374.	3.3	7
502	Parasitic Nematodes Exert Antimicrobial Activity and Benefit From Microbiota-Driven Support for Host Immune Regulation. <i>Frontiers in Immunology</i> , 2018, 9, 2282.	4.8	57
503	Identification of neoepitopes recognized by tumor-infiltrating lymphocytes (TILs) from patients with glioma. <i>Oncotarget</i> , 2018, 9, 19469-19480.	1.8	10
504	Prediction of DNA-binding residues in local segments of protein sequences with Fuzzy Cognitive Maps. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	15
505	Diversification of DNA binding specificities enabled SREBP transcription regulators to expand the repertoire of cellular functions that they govern in fungi. <i>PLoS Genetics</i> , 2018, 14, e1007884.	3.5	14
506	Comparison of complex networks and tree-based methods of phylogenetic analysis and proposal of a bootstrap method. <i>PeerJ</i> , 2018, 6, e4349.	2.0	4
507	Comparative De Novo transcriptome analysis of the Australian black-lip and Sydney rock oysters reveals expansion of repetitive elements in <i>Saccostrea</i> genomes. <i>PLoS ONE</i> , 2018, 13, e0206417.	2.5	3
508	<i>Arabidopsis thaliana</i> responds to colonisation of <i>Piriformospora indica</i> by secretion of symbiosis-specific proteins. <i>PLoS ONE</i> , 2018, 13, e0209658.	2.5	17
509	Major histocompatibility complex class I in the horse (<i>Equus caballus</i>) placenta during pregnancy and parturition. <i>Placenta</i> , 2018, 74, 36-46.	1.5	5
510	YummyData: providing high-quality open life science data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	17
511	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. <i>BMC Genomics</i> , 2018, 19, 851.	2.8	59
512	Proteome Map of Pea (<i>Pisum sativum</i> L.) Embryos Containing Different Amounts of Residual Chlorophylls. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4066.	4.1	15
513	Analysis of protein features and machine learning algorithms for prediction of druggable proteins. <i>Quantitative Biology</i> , 2018, 6, 334-343.	0.5	11

#	ARTICLE	IF	CITATIONS
514	Improved Protein Residue-Residue Contact Prediction Using Image Denoising Methods. , 2018, , .		1
515	Genome of the small hive beetle (<i>Aethina tumida</i> , Coleoptera: Nitidulidae), a worldwide parasite of social bee colonies, provides insights into detoxification and herbivory. GigaScience, 2018, 7, .	6.4	49
516	Systematic characterization and prediction of post-translational modification cross-talk between proteins. Bioinformatics, 2019, 35, 2626-2633.	4.1	12
517	NLRP3 lacking the leucine-rich repeat domain can be fully activated via the canonical inflammasome pathway. Nature Communications, 2018, 9, 5182.	12.8	102
518	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. PLoS ONE, 2018, 13, e0208273.	2.5	41
519	The evolution of ependymin-related proteins. BMC Evolutionary Biology, 2018, 18, 182.	3.2	17
520	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	12.8	151
521	Comparative transcriptomics identifies genes differentially expressed in the intestine of a new fast-growing strain of common carp with higher unsaturated fatty acid content in muscle. PLoS ONE, 2018, 13, e0206615.	2.5	14
522	Different effects of long noncoding RNA <i>NDRG1-OT1</i> fragments on <i>NDRG1</i> transcription in breast cancer cells under hypoxia. RNA Biology, 2018, 15, 1487-1498.	3.1	20
523	Comparative Proteomic Analysis. , 2018, , .		2
524	RNA-Binding Proteomics Reveals MATR3 Interacting with lncRNA SNHG1 To Enhance Neuroblastoma Progression. Journal of Proteome Research, 2019, 18, 406-416.	3.7	21
525	Nonsense mutation in PMEL is associated with yellowish plumage colour phenotype in Japanese quail. Scientific Reports, 2018, 8, 16732.	3.3	16
526	Proteomic profiling of senescent human diploid fibroblasts treated with gamma-tocotrienol. BMC Complementary and Alternative Medicine, 2018, 18, 314.	3.7	4
527	A Systematic Overview of Type II and III Toxin-Antitoxin Systems with a Focus on Druggability. Toxins, 2018, 10, 515.	3.4	47
528	Clinical, Genetics, and Bioinformatic Characterization of Mutations Affecting an Essential Region of <i>PLS3</i> in Patients with BMND18. International Journal of Endocrinology, 2018, 2018, 1-9.	1.5	9
529	Automated selection of homologs to track the evolutionary history of proteins. BMC Bioinformatics, 2018, 19, 431.	2.6	7
530	Large-Scale Analyses of Site-Specific Evolutionary Rates across Eukaryote Proteomes Reveal Confounding Interactions between Intrinsic Disorder, Secondary Structure, and Functional Domains. Genes, 2018, 9, 553.	2.4	10
531	Both Intrinsically Disordered Regions and Structural Domains Evolve Rapidly in Immune-Related Mammalian Proteins. International Journal of Molecular Sciences, 2018, 19, 3860.	4.1	3

#	ARTICLE	IF	CITATIONS
532	Optimised Desorption Electrospray Ionisation Mass Spectrometry Imaging (DESI-MSI) for the Analysis of Proteins/Peptides Directly from Tissue Sections on a Travelling Wave Ion Mobility Q-ToF. Journal of the American Society for Mass Spectrometry, 2018, 29, 2456-2466.	2.8	78
533	Exon Skipping in a Dysf-Missense Mutant Mouse Model. Molecular Therapy - Nucleic Acids, 2018, 13, 198-207.	5.1	14
534	High-throughput in vivo mapping of RNA accessible interfaces to identify functional sRNA binding sites. Nature Communications, 2018, 9, 4084.	12.8	30
535	The intracellular proteome of African swine fever virus. Scientific Reports, 2018, 8, 14714.	3.3	59
536	Optimisation of a serum albumin removal protocol for use in a proteomic study to identify the protein biomarkers for silent gastric ulceration in horses. Journal of Equine Science, 2018, 29, 53-60.	0.8	4
537	Revisiting Chameleon Sequences in the Protein Data Bank. Algorithms, 2018, 11, 114.	2.1	6
538	Automatic Inference of Sequence from Low-Resolution Crystallographic Data. Structure, 2018, 26, 1546-1554.e2.	3.3	0
539	ProteomeGenerator: A Framework for Comprehensive Proteomics Based on de Novo Transcriptome Assembly and High-Accuracy Peptide Mass Spectral Matching. Journal of Proteome Research, 2018, 17, 3681-3692.	3.7	24
540	A Highly Bioactive Lys-Deficient IFN Leads to a Site-Specific Di-PEGylated IFN with Equivalent Bioactivity to That of Unmodified IFN- β 2b. ACS Synthetic Biology, 2018, 7, 2537-2546.	3.8	0
541	Fyn Regulates Binding Partners of Cyclic-AMP Dependent Protein Kinase A. Proteomes, 2018, 6, 37.	3.5	6
542	Infection-Induced Peroxisome Biogenesis Is a Metabolic Strategy for Herpesvirus Replication. Cell Host and Microbe, 2018, 24, 526-541.e7.	11.0	65
543	Analyzing the Structure of Pathways and Its Influence on the Interpretation of Biomedical Proteomics Data Sets. Journal of Proteome Research, 2018, 17, 3801-3809.	3.7	3
544	Genome sequence analysis of Zooshikella ganghwensis strain VG4 and its potential for the synthesis of antimicrobial metabolites. Biotechnology Reports (Amsterdam, Netherlands), 2018, 19, e00278.	4.4	4
545	Structure and Protein Interaction-Based Gene Ontology Annotations Reveal Likely Functions of Uncharacterized Proteins on Human Chromosome 17. Journal of Proteome Research, 2018, 17, 4186-4196.	3.7	27
546	THE-DB: a threading model database for comparative protein structure analysis of the E. coli K12 and human proteomes. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	6
547	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	5.1	20
548	Prediction and validation of the structural features of Ov58GPCR, an immunogenic determinant of Onchocerca volvulus. PLoS ONE, 2018, 13, e0202915.	2.5	7
549	Progress of analytical tools and techniques for human gut microbiome research. Journal of Microbiology, 2018, 56, 693-705.	2.8	49

#	ARTICLE	IF	CITATIONS
550	Newly-discovered enzymes that function in metabolite damage-control. <i>Current Opinion in Chemical Biology</i> , 2018, 47, 101-108.	6.1	30
551	Global Profiling of Lysine Acetylation in <i>Borrelia burgdorferi</i> B31 Reveals Its Role in Central Metabolism. <i>Frontiers in Microbiology</i> , 2018, 9, 2036.	3.5	29
552	A new tool for studying waterfowl immune and metabolic responses: Molecular level analysis using kinome profiling. <i>Ecology and Evolution</i> , 2018, 8, 8537-8546.	1.9	1
553	First draft genome sequencing of fennel (<i>Foeniculum vulgare</i> Mill.): identification of simple sequence repeats and their application in marker-assisted breeding. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	24
554	Large-Deviation Properties of Sequence Alignment of Correlated Sequences. <i>Journal of Computational Biology</i> , 2018, 25, 1339-1346.	1.6	0
555	Protein Language: Post-Translational Modifications Talking to Each Other. <i>Trends in Plant Science</i> , 2018, 23, 1068-1080.	8.8	199
556	CXCR5 overexpression in HL-60 cells enhances chemotaxis toward CXCL13 without anticipated interaction partners or enhanced MAPK signaling. <i>In Vitro Cellular and Developmental Biology - Animal</i> , 2018, 54, 725-735.	1.5	5
557	Subtractive proteomics and immunoinformatics revealed novel B-cell derived T-cell epitopes against <i>Yersinia enterocolitica</i> : An etiological agent of Yersiniosis. <i>Microbial Pathogenesis</i> , 2018, 125, 336-348.	2.9	22
558	Scalable Prediction of Intrinsically Disordered Protein Regions with Spark Clusters on Microsoft Azure Cloud. <i>Computational Biology</i> , 2018, , 215-247.	0.2	1
559	Pathogenic variants in glutamyl-tRNA ^{Gln} amidotransferase subunits cause a lethal mitochondrial cardiomyopathy disorder. <i>Nature Communications</i> , 2018, 9, 4065.	12.8	44
560	Conformational changes on substrate binding revealed by structures of <i>Methylobacterium extorquens</i> malate dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 610-616.	0.8	8
561	New N-(oxazolylmethyl)-thiazolidinedione Active against <i>Candida albicans</i> Biofilm: Potential Als Proteins Inhibitors. <i>Molecules</i> , 2018, 23, 2522.	3.8	22
562	Genetic conflicts with <i>Plasmodium</i> parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. <i>Scientific Reports</i> , 2018, 8, 14682.	3.3	2
563	<i>Yersinia pseudotuberculosis</i> BarA-UvrY Two-Component Regulatory System Represses Biofilms via CsrB. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 323.	3.9	9
564	Transcriptional and Functional Analysis of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Exposure to Tetracycline. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	22
565	Comprehensive Evolutionary Analysis of the Major RNA-Induced Silencing Complex Members. <i>Scientific Reports</i> , 2018, 8, 14189.	3.3	18
566	Biallelic mutations in human NHLRC2 enhance myofibroblast differentiation in FINCA disease. <i>Human Molecular Genetics</i> , 2018, 27, 4288-4302.	2.9	13
567	Hydrogen Peroxide: Its Role in Plant Biology and Crosstalk with Signalling Networks. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2812.	4.1	147

#	ARTICLE	IF	CITATIONS
568	Molecular and Cellular Response to Experimental <i>Anisakis pegreffii</i> (Nematoda, Anisakidae) Third-Stage Larval Infection in Rats. <i>Frontiers in Immunology</i> , 2018, 9, 2055.	4.8	19
569	OpenProt: a more comprehensive guide to explore eukaryotic coding potential and proteomes. <i>Nucleic Acids Research</i> , 2019, 47, D403-D410.	14.5	71
570	GDP- <sc>l</sc>-fucose synthase is a CD4 ⁺ T cell-specific autoantigen in DRB3*02:02 patients with multiple sclerosis. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	71
571	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. <i>Nature Communications</i> , 2018, 9, 4205.	12.8	74
572	Novel tacrine-pyridinium hybrid reactivators of organophosphorus-inhibited acetylcholinesterase: Synthesis, molecular docking, and in vitro reactivation study. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 3784-3786.	2.2	9
573	Network-Based Methods for Prediction of Drug-Target Interactions. <i>Frontiers in Pharmacology</i> , 2018, 9, 1134.	3.5	131
574	Mycobacterium tuberculosis serine/threonine protein kinases: structural information for the design of their specific ATP-competitive inhibitors. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 1315-1336.	2.9	18
575	Proteomic analysis of <i>Lactobacillus casei</i> GCRL163 cell-free extracts reveals a SecB homolog and other biomarkers of prolonged heat stress. <i>PLoS ONE</i> , 2018, 13, e0206317.	2.5	15
576	De Novo Hepatic Transcriptome Assembly and Systems Level Analysis of Three Species of Dietary Fish, <i>Sardinops sagax</i> , <i>Scomber japonicus</i> , and <i>Pleuronichthys verticalis</i> . <i>Genes</i> , 2018, 9, 521.	2.4	1
577	A combined computational and experimental approach reveals the structure of a C/EBP β -Spi1 interaction required for IL1B gene transcription. <i>Journal of Biological Chemistry</i> , 2018, 293, 19942-19956.	3.4	5
578	Elevated Autoantibodies in Subacute Human Spinal Cord Injury Are Naturally Occurring Antibodies. <i>Frontiers in Immunology</i> , 2018, 9, 2365.	4.8	33
579	Comparative Glycomics of Immunoglobulin A and G From Saliva and Plasma Reveals Biomarker Potential. <i>Frontiers in Immunology</i> , 2018, 9, 2436.	4.8	59
580	Probing the molecular basis for affinity/potency- and efficacy-based subtype-selectivity exhibited by benzodiazepine-site modulators at GABAA receptors. <i>Biochemical Pharmacology</i> , 2018, 158, 339-358.	4.4	6
581	Comparative proteomics identified immune response proteins involved in response to vaccination with heat-inactivated <i>Mycobacterium bovis</i> and mycobacterial challenge in cattle. <i>Veterinary Immunology and Immunopathology</i> , 2018, 206, 54-64.	1.2	8
582	Comparative analysis of the <i>Pocillopora damicornis</i> genome highlights role of immune system in coral evolution. <i>Scientific Reports</i> , 2018, 8, 16134.	3.3	112
583	Cell migration inhibition activity of a non-RGD disintegrin from <i>Crotalus durissus collilineatus</i> venom. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2018, 24, 28.	1.4	10
584	A Conditional Dependency on MELK for the Proliferation of Triple-Negative Breast Cancer Cells. <i>IScience</i> , 2018, 9, 149-160.	4.1	12
585	Prioritising candidate genes causing QTL using hierarchical orthologous groups. <i>Bioinformatics</i> , 2018, 34, i612-i619.	4.1	5

#	ARTICLE	IF	CITATIONS
586	In silico identification of lipid-binding α helices of uncoupling protein α . Biomedical Reports, 2018, 9, 313-317.	2.0	1
587	Defining the Mammalian Peroxisomal Proteome. Sub-Cellular Biochemistry, 2018, 89, 47-66.	2.4	26
588	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. Nature, 2018, 562, 589-594.	27.8	623
589	Minimal PAM specificity of a highly similar SpCas9 ortholog. Science Advances, 2018, 4, eaau0766.	10.3	183
590	Organic Particles: Heterogeneous Hubs for Microbial Interactions in Aquatic Ecosystems. Frontiers in Microbiology, 2018, 9, 2569.	3.5	51
591	The C-terminal D/E-rich domain of MBD3 is a putative Z-DNA mimic that competes for α DNA-binding activity. Nucleic Acids Research, 2018, 46, 11806-11821.	14.5	6
592	The proteome of perilymph in patients with vestibular schwannoma. A possibility to identify biomarkers for tumor associated hearing loss?. PLoS ONE, 2018, 13, e0198442.	2.5	29
593	Sequence-based analysis and prediction of lantibiotics: A machine learning approach. Computational Biology and Chemistry, 2018, 77, 199-206.	2.3	3
594	ClinVar at five years: Delivering on the promise. Human Mutation, 2018, 39, 1623-1630.	2.5	159
595	Circular Permutation Obscures Universality of a Ribosomal Protein. Journal of Molecular Evolution, 2018, 86, 581-592.	1.8	8
596	DNA methylation patterns in peripheral blood mononuclear cells from Holstein cattle with variable milk yield. BMC Genomics, 2018, 19, 744.	2.8	13
598	ProteinExplorer: A Repository-Scale Resource for Exploration of Protein Detection in Public Mass Spectrometry Data Sets. Journal of Proteome Research, 2018, 17, 4227-4234.	3.7	17
599	A recessive lethal chondrodysplasia in a miniature zebu family results from an insertion affecting the chondroitin sulfat domain of aggrecan. BMC Genetics, 2018, 19, 91.	2.7	5
600	Large-scale docking predicts that sORF-encoded peptides may function through protein-peptide interactions in Arabidopsis thaliana. PLoS ONE, 2018, 13, e0205179.	2.5	10
601	Two active site arginines are critical determinants of substrate binding and catalysis in MenD: a thiamine-dependent enzyme in menaquinone biosynthesis. Biochemical Journal, 2018, 475, 3651-3667.	3.7	11
602	Structural and Functional Insights Into Lysostaphin-Substrate Interaction. Frontiers in Molecular Biosciences, 2018, 5, 60.	3.5	32
603	Ontology-based validation and identification of regulatory phenotypes. Bioinformatics, 2018, 34, i857-i865.	4.1	5
604	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126

#	ARTICLE	IF	CITATIONS
605	Evidence of polygenic adaptation to high altitude from Tibetan and Sherpa genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 2919-2930.	2.5	39
606	In Vitro Assembly of Diverse Bacterial Microcompartment Shell Architectures. <i>Nano Letters</i> , 2018, 18, 7030-7037.	9.1	61
607	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , 2018, 14, e1006474.	3.2	33
608	Characterization of ML-005, a Novel Metaproteomics-Derived Esterase. <i>Frontiers in Microbiology</i> , 2018, 9, 1925.	3.5	6
609	Receptor pharmacophore ensemble (REPHARMBLE): a probabilistic pharmacophore modeling approach using multiple protein-ligand complexes. <i>Journal of Molecular Modeling</i> , 2018, 24, 282.	1.8	11
610	The genome of <i>Naegleria lovaniensis</i> , the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba <i>N. fowleri</i> . <i>BMC Genomics</i> , 2018, 19, 654.	2.8	23
611	Impact of nanoparticle surface functionalization on the protein corona and cellular adhesion, uptake and transport. <i>Journal of Nanobiotechnology</i> , 2018, 16, 70.	9.1	70
612	From Molecules to Mechanisms: Functional Proteomics and Its Application to Renal Tubule Physiology. <i>Physiological Reviews</i> , 2018, 98, 2571-2606.	28.8	27
613	PMLPR: A novel method for predicting subcellular localization based on recommender systems. <i>Scientific Reports</i> , 2018, 8, 12006.	3.3	12
614	What bacteria want. <i>Environmental Microbiology</i> , 2018, 20, 4221-4229.	3.8	73
615	Epigenome-Wide Analyses Identify Two Novel Associations With Recurrent Stroke in the Vitamin Intervention for Stroke Prevention Clinical Trial. <i>Frontiers in Genetics</i> , 2018, 9, 358.	2.3	12
616	Engineered Stochastic Adhesion Between Microbes as a Protection Mechanism Against Environmental Stress. <i>Cellular and Molecular Bioengineering</i> , 2018, 11, 367-382.	2.1	2
617	Maintaining Biological Cultures and Measuring Gene Expression in <i>Aphis nerii</i> : A Non-model System for Plant-insect Interactions. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	0
618	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. <i>Nature Plants</i> , 2018, 4, 792-801.	9.3	27
619	The Thaumarchaeon <i>N. gargensis</i> carries functional bioABD genes and has a promiscuous <i>E. coli</i> β -bioH-complementing esterase EstN1. <i>Scientific Reports</i> , 2018, 8, 13823.	3.3	11
620	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	5.5	117
621	Origin and phylogenetic relationships of [4Fe-4S]-containing O ₂ sensors of bacteria. <i>Environmental Microbiology</i> , 2018, 20, 4567-4586.	3.8	13
622	Systematic Identification and Classification of β -Lactamases Based on Sequence Similarity Criteria: β -Lactamase Annotation. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	1.2	15

#	ARTICLE	IF	CITATIONS
623	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. BMC Genomics, 2018, 19, 351.	2.8	49
624	A Comparative Study of Outer Membrane Proteome between Paired Colistin-Susceptible and Extremely Colistin-Resistant <i>Klebsiella pneumoniae</i> Strains. ACS Infectious Diseases, 2018, 4, 1692-1704.	3.8	15
625	A biochemical and genetic discovery pipeline identifies PLC β 4 as a nonreceptor activator of heterotrimeric G-proteins. Journal of Biological Chemistry, 2018, 293, 16964-16983.	3.4	20
626	Proteomic Approaches for the Discovery of Biofluid Biomarkers of Neurodegenerative Dementias. Proteomes, 2018, 6, 32.	3.5	52
627	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: Boiga). Journal of Molecular Evolution, 2018, 86, 531-545.	1.8	14
628	Adoption of an improved PSO to explore a compound multi-objective energy function in protein structure prediction. Applied Soft Computing Journal, 2018, 72, 539-551.	7.2	26
629	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. Journal of Proteome Research, 2018, 17, 3418-3430.	3.7	27
630	IRSOM, a reliable identifier of ncRNAs based on supervised self-organizing maps with rejection. Bioinformatics, 2018, 34, i620-i628.	4.1	9
631	<i>In vitro</i> versus <i>in vivo</i> compositional landscapes of histone sequence preferences in eucaryotic genomes. Bioinformatics, 2018, 34, 3454-3460.	4.1	8
632	The Amino Acid Composition of Quadruplex Binding Proteins Reveals a Shared Motif and Predicts New Potential Quadruplex Interactors. Molecules, 2018, 23, 2341.	3.8	51
633	Single-platform “multi-omic” profiling: unified mass spectrometry and computational workflows for integrative proteomics–metabolomics analysis. Molecular Omics, 2018, 14, 307-319.	2.8	41
634	Structural Basis of Pan-Ebolavirus Neutralization by a Human Antibody against a Conserved, yet Cryptic Epitope. MBio, 2018, 9, .	4.1	34
635	Role of phosphate sensing in bone and mineral metabolism. Nature Reviews Endocrinology, 2018, 14, 637-655.	9.6	121
636	Activity-Based Protein Profiling of Intraoperative Serine Hydrolase Activities during Cardiac Surgery. Journal of Proteome Research, 2018, 17, 3547-3556.	3.7	7
637	Taxonomic Landscape of the Dark Proteomes: Whole-Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. Proteomics, 2018, 18, 1800243.	2.2	27
638	New monoclonal antibodies specific for mammalian protamines P1 and P2. Systems Biology in Reproductive Medicine, 2018, 64, 424-447.	2.1	6
639	A Luminal Loop of Wilson Disease Protein Binds Copper and Is Required for Protein Activity. Biophysical Journal, 2018, 115, 1007-1018.	0.5	3
640	Disulfide bridge formation to increase thermostability of DFPase enzyme: A computational study. Computational Biology and Chemistry, 2018, 77, 272-278.	2.3	6

#	ARTICLE	IF	CITATIONS
641	Carcinogenic Pesticide Control via Hijacking Endosymbiosis; The Paradigm of DSB-A from <i>Wolbachia pipiensis</i> for the Management of <i>Otiorynchus singularis</i> . <i>In Vivo</i> , 2018, 32, 1051-1062.	1.3	2
642	Identification of the Bisabolol Synthase in the Endangered Candeia Tree (<i>Eremanthus erythropappus</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	3.6	13
643	The role of solute carrier (SLC) transporters in actinomycin D pharmacokinetics in paediatric cancer patients. <i>European Journal of Clinical Pharmacology</i> , 2018, 74, 1575-1584.	1.9	3
644	De novo transcriptome assembly of the lobster cockroach <i>Nauphoeta cinerea</i> (Blaberidae). <i>Genetics and Molecular Biology</i> , 2018, 41, 713-721.	1.3	8
645	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	21.4	55
646	Influenza virus infection causes global RNAPII termination defects. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 885-893.	8.2	48
647	Widespread evolutionary crosstalk among protein domains in the context of multi-domain proteins. <i>PLoS ONE</i> , 2018, 13, e0203085.	2.5	0
648	Computational Methods for Analysis of the DNA-Binding Preferences of Cys2His2 Zinc-Finger Proteins. <i>Methods in Molecular Biology</i> , 2018, 1867, 15-28.	0.9	6
649	PKC μ contributes to lipid-induced insulin resistance through cross talk with p70S6K and through previously unknown regulators of insulin signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8996-E9005.	7.1	51
650	The Protein Coded by a Short Open Reading Frame, Not by the Annotated Coding Sequence, Is the Main Gene Product of the Dual-Coding Gene MIEF1. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2402-2411.	3.8	44
651	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. <i>PLoS Computational Biology</i> , 2018, 14, e1006372.	3.2	8
652	Extracellular glucose level regulates dependence on <scp>GRP</scp>78 for cell surface localization of multipass transmembrane proteins in HeLa cells. <i>FEBS Letters</i> , 2018, 592, 3295-3304.	2.8	5
653	COSMIC-3D provides structural perspectives on cancer genetics for drug discovery. <i>Nature Genetics</i> , 2018, 50, 1200-1202.	21.4	31
654	How cyclophosphamide at environmentally relevant concentration influences <i>Daphnia magna</i> life history and its proteome. <i>PLoS ONE</i> , 2018, 13, e0195366.	2.5	15
655	Gene Regulatory Variation in <i>Drosophila melanogaster</i> Renal Tissue. <i>Genetics</i> , 2018, 210, 287-301.	2.9	11
656	Inhibition of hydrogen-yielding dark fermentation by ascomycetous yeasts. <i>International Journal of Hydrogen Energy</i> , 2018, 43, 10967-10979.	7.1	22
657	ECOdrug: a database connecting drugs and conservation of their targets across species. <i>Nucleic Acids Research</i> , 2018, 46, D930-D936.	14.5	56
658	MultitaskProtDB-II: an update of a database of multitasking/moonlighting proteins. <i>Nucleic Acids Research</i> , 2018, 46, D645-D648.	14.5	44

#	ARTICLE	IF	CITATIONS
659	PDBe: towards reusable data delivery infrastructure at protein data bank in Europe. Nucleic Acids Research, 2018, 46, D486-D492.	14.5	76
660	Minimotif Miner 4: a million peptide minimotifs and counting. Nucleic Acids Research, 2018, 46, D465-D470.	14.5	15
661	The Encyclopedia of Proteome Dynamics: a big data ecosystem for (prote)omics. Nucleic Acids Research, 2018, 46, D1202-D1209.	14.5	19
662	ActiveDriverDB: human disease mutations and genome variation in post-translational modification sites of proteins. Nucleic Acids Research, 2018, 46, D901-D910.	14.5	82
663	Computational functional genomics-based approaches in analgesic drug discovery and repurposing. Pharmacogenomics, 2018, 19, 783-797.	1.3	23
664	Gene3D: Extensive prediction of globular domains in proteins. Nucleic Acids Research, 2018, 46, D435-D439.	14.5	129
665	The MetaCyc database of metabolic pathways and enzymes. Nucleic Acids Research, 2018, 46, D633-D639.	14.5	658
666	FunCoup 4: new species, data, and visualization. Nucleic Acids Research, 2018, 46, D601-D607.	14.5	44
667	Leveraging Experimental Details for an Improved Understanding of Host-Pathogen Interactome. Current Protocols in Bioinformatics, 2018, 61, 8.26.1-8.26.12.	25.8	2
668	Lectin Microarray Combined with Mass Spectrometry Identifies Haptoglobin-Related Protein (HPR) as a Potential Serologic Biomarker for Separating Nonbacterial Pneumonia from Bacterial Pneumonia in Childhood. Proteomics - Clinical Applications, 2018, 12, e1800030.	1.6	15
669	The draft genome sequence of cork oak. Scientific Data, 2018, 5, 180069.	5.3	98
670	Carbonyl reduction of NNK by recombinant human lung enzymes: identification of HSD17 β 12 as the reductase important in (R)-NNAL formation in human lung. Carcinogenesis, 2018, 39, 1079-1088.	2.8	7
671	iPTMnet: an integrated resource for protein post-translational modification network discovery. Nucleic Acids Research, 2018, 46, D542-D550.	14.5	120
672	BAGEL4: a user-friendly web server to thoroughly mine RiPPs and bacteriocins. Nucleic Acids Research, 2018, 46, W278-W281.	14.5	593
673	HotSpot Wizard 3.0: web server for automated design of mutations and smart libraries based on sequence input information. Nucleic Acids Research, 2018, 46, W356-W362.	14.5	171
674	Curcumin exerts its antitumor effects in a context dependent fashion. Journal of Proteomics, 2018, 182, 65-72.	2.4	16
675	Molecular Mechanisms Preventing Senescence in Response to Prolonged Darkness in a Desiccation-Tolerant Plant. Plant Physiology, 2018, 177, 1319-1338.	4.8	26
676	The way is the goal: how SecA transports proteins across the cytoplasmic membrane in bacteria. FEMS Microbiology Letters, 2018, 365, .	1.8	64

#	ARTICLE	IF	CITATIONS
677	A functional glycoproteomics approach identifies CD13 as a novel E-selectin ligand in breast cancer. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2069-2080.	2.4	23
678	Comparative Genomics Reveals the Core Gene Toolbox for the Fungus-Insect Symbiosis. <i>MBio</i> , 2018, 9, .	4.1	17
679	Analysis of tail-anchored protein translocation pathway in plants. <i>Biochemistry and Biophysics Reports</i> , 2018, 14, 161-167.	1.3	2
680	Structure-based design and profiling of novel 17 β -HSD14 inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2018, 155, 61-76.	5.5	9
681	ProteomeTools: Systematic Characterization of 21 Post-translational Protein Modifications by Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) Using Synthetic Peptides. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1850-1863.	3.8	78
682	Bioinformatics-based tools in drug discovery: the cartography from single gene to integrative biological networks. <i>Drug Discovery Today</i> , 2018, 23, 1658-1665.	6.4	14
683	ADReCS-Target: target profiles for aiding drug safety research and application. <i>Nucleic Acids Research</i> , 2018, 46, D911-D917.	14.5	23
684	Removal of selenate from brine using anaerobic bacteria and zero valent iron. <i>Journal of Environmental Management</i> , 2018, 222, 348-358.	7.8	11
685	Draft genome sequence of <i>Trametes villosa</i> (Sw.) Kreisel CCMB561, a tropical white-rot Basidiomycota from the semiarid region of Brazil. <i>Data in Brief</i> , 2018, 18, 1581-1587.	1.0	6
686	Straightforward hit identification approach in fragment-based discovery of bromodomain-containing protein 4 (BRD4) inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 3399-3405.	3.0	16
687	De novo nonsense mutation in WHSC1 (NSD2) in patient with intellectual disability and dysmorphic features. <i>Journal of Human Genetics</i> , 2018, 63, 919-922.	2.3	29
688	Hydrogel-immobilized Supercharged Proteins. <i>Advanced Biology</i> , 2018, 2, 1700240.	3.0	14
689	Hymenoptera Genome Database: Using HymenopteraMine to Enhance Genomic Studies of Hymenopteran Insects. <i>Methods in Molecular Biology</i> , 2018, 1757, 513-556.	0.9	12
690	The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 115-139.	0.9	13
691	Thymoquinone increases the expression of neuroprotective proteins while decreasing the expression of pro-inflammatory cytokines and the gene expression NF κ B pathway signaling targets in LPS/IFN γ -activated BV-2 microglia cells. <i>Journal of Neuroimmunology</i> , 2018, 320, 87-97.	2.3	64
692	SWISS-MODEL: homology modelling of protein structures and complexes. <i>Nucleic Acids Research</i> , 2018, 46, W296-W303.	14.5	8,474
693	Chinook salmon (<i>Oncorhynchus tshawytscha</i>) genome and transcriptome. <i>PLoS ONE</i> , 2018, 13, e0195461.	2.5	85
694	Iron Inhibits the Secretion of Apolipoprotein E in Cultured Human Adipocytes. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 6, 215-217.e8.	4.5	10

#	ARTICLE	IF	CITATIONS
695	The Solution Structure of CCL28 Reveals Structural Lability that Does Not Constrain Antifungal Activity. <i>Journal of Molecular Biology</i> , 2018, 430, 3266-3282.	4.2	14
696	Cone Snail Glutamyl Cyclase Sequences from Transcriptomic Analysis and Mass Spectrometric Characterization of Two Pyroglutamyl Conotoxins. <i>Journal of Proteome Research</i> , 2018, 17, 2695-2703.	3.7	10
697	Fragment Based Molecular Dynamics for Drug Design. <i>Communications in Computer and Information Science</i> , 2018, , 49-58.	0.5	1
698	RecA a universal drug target in pathogenic bacteria. <i>Frontiers in Bioscience - Landmark</i> , 2018, 23, 36-42.	3.0	15
699	Fine-tuning of substrate preferences of the Src-family kinase Lck revealed through a high-throughput specificity screen. <i>ELife</i> , 2018, 7, .	6.0	51
700	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
701	The transcription factor Rfx7 limits metabolism of NK cells and promotes their maintenance and immunity. <i>Nature Immunology</i> , 2018, 19, 809-820.	14.5	42
702	PopViz: a webserver for visualizing minor allele frequencies and damage prediction scores of human genetic variations. <i>Bioinformatics</i> , 2018, 34, 4307-4309.	4.1	55
703	A Novel Heterozygous Missense Mutation in <i>GNAT1</i> Leads to Autosomal Dominant Riggs Type of Congenital Stationary Night Blindness. <i>BioMed Research International</i> , 2018, 2018, 1-10.	1.9	8
704	Candidate genes and molecular markers associated with brown planthopper (<i>Nilaparvata lugens</i> Stål) resistance in rice cultivar Rathu Heenati. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	7
705	Investigation of the interaction of allergens of Glycine max with IgE-antibody for designing of peptidomimetics based anti-allergen. <i>International Immunopharmacology</i> , 2018, 61, 394-404.	3.8	5
706	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	12.8	139
707	Accelerating molecular discovery through data and physical sciences: Applications to peptide-membrane interactions. <i>Journal of Chemical Physics</i> , 2018, 148, 241744.	3.0	10
708	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018, 50, 937-943.	21.4	55
709	Idiopathic Scoliosis Families Highlight Actin-Based and Microtubule-Based Cellular Projections and Extracellular Matrix in Disease Etiology. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2663-2672.	1.8	19
710	Theoretical and Applied Aspects of Systems Biology. <i>Computational Biology</i> , 2018, , .	0.2	3
711	Computational Modeling of Multidrug-Resistant Bacteria. <i>Computational Biology</i> , 2018, , 195-220.	0.2	4
713	Crystal structure of the flavin reductase of <i>Acinetobacter baumannii</i> p-hydroxyphenylacetate 3-hydroxylase (HPAH) and identification of amino acid residues underlying its regulation by aromatic ligands. <i>Archives of Biochemistry and Biophysics</i> , 2018, 653, 24-38.	3.0	6

#	ARTICLE	IF	CITATIONS
714	Environmental superbugs: The case study of <i>Pedobacter</i> spp.. <i>Environmental Pollution</i> , 2018, 241, 1048-1055.	7.5	54
715	The effect of high-energy environments on the structure of laccase-polymerized poly(catechol). <i>Ultrasonics Sonochemistry</i> , 2018, 48, 275-280.	8.2	23
716	Time- and polarity-dependent proteomic changes associated with homeostatic scaling at central synapses. <i>ELife</i> , 2018, 7, .	6.0	49
717	A variant in <i>LMX1A</i> causes autosomal recessive severe-to-profound hearing impairment. <i>Human Genetics</i> , 2018, 137, 471-478.	3.8	18
718	Novel application of normalized pointwise mutual information (NPMI) to mine biomedical literature for gene sets associated with disease: Use case in breast carcinogenesis. <i>Computational Toxicology</i> , 2018, 7, 46-57.	3.3	9
719	Discovering hidden knowledge through auditing clinical diagnostic knowledge bases. <i>Journal of Biomedical Informatics</i> , 2018, 84, 75-81.	4.3	5
720	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	6.0	149
721	Mutational analysis of the pro-peptide of a marine intracellular subtilisin protease supports its role in inhibition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 965-977.	2.6	5
722	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. <i>PLoS Computational Biology</i> , 2018, 14, e1006101.	3.2	17
723	PrimAlign: PageRank-inspired Markovian alignment for large biological networks. <i>Bioinformatics</i> , 2018, 34, i537-i546.	4.1	25
724	Predicting Interactions between Virus and Host Proteins Using Repeat Patterns and Composition of Amino Acids. <i>Journal of Healthcare Engineering</i> , 2018, 2018, 1-9.	1.9	35
725	Differential 3â€™ processing of specific transcripts expands regulatory and protein diversity across neuronal cell types. <i>ELife</i> , 2018, 7, .	6.0	30
726	Prediction of auxin response elements based on data fusion in <i>Arabidopsis thaliana</i> . <i>Molecular Biology Reports</i> , 2018, 45, 763-772.	2.3	6
727	Multimomics Data Triangulation for Asthma Candidate Biomarkers and Precision Medicine. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 392-409.	2.0	15
728	ezTag: tagging biomedical concepts via interactive learning. <i>Nucleic Acids Research</i> , 2018, 46, W523-W529.	14.5	27
729	Sequencing and Annotation of the Genome of <i>Mycobacterium tuberculosis</i> MYC004, a Strain Causing Meningitis in Mexico. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
730	StraPep: a structure database of bioactive peptides. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	41
732	The OB-fold proteins of the <i>Trypanosoma brucei</i> editosome execute RNA-chaperone activity. <i>Nucleic Acids Research</i> , 2018, 46, 10353-10367.	14.5	7

#	ARTICLE	IF	CITATIONS
733	Serum protein electrophoresis in healthy and injured southern white rhinoceros (<i>Ceratotherium</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	2.5	15
734	Automatic extraction of gene-disease associations from literature using joint ensemble learning. PLoS ONE, 2018, 13, e0200699.	2.5	50
735	Biological Databases. , 2018, , 13-34.		1
736	Biopolymers from a Bacterial Extracellular Matrix Affect the Morphology and Structure of Calcium Carbonate Crystals. Crystal Growth and Design, 2018, 18, 5582-5591.	3.0	32
737	The Bits Between Proteins. , 2018, , .		1
738	Differences between fast and slow muscles in scallops revealed through proteomics and transcriptomics. BMC Genomics, 2018, 19, 377.	2.8	22
739	Proteome-wide identification of epitope-based vaccine candidates against multi-drug resistant <i>Proteus mirabilis</i> . Biologicals, 2018, 55, 27-37.	1.4	12
740	TelNet - a database for human and yeast genes involved in telomere maintenance. BMC Genetics, 2018, 19, 32.	2.7	36
741	A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaii's Last Remaining Crow Species. Genes, 2018, 9, 393.	2.4	22
742	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. Methods in Enzymology, 2018, 606, 1-71.	1.0	99
743	Guarding the gateway to histidine biosynthesis in plants: <i>Medicago truncatula</i> ATP-phosphoribosyltransferase in relaxed and tense states. Biochemical Journal, 2018, 475, 2681-2697.	3.7	6
744	Plant Glycine-Rich Proteins in Stress Response: An Emerging, Still Prospective Story. Frontiers in Plant Science, 2018, 9, 302.	3.6	112
745	Soil Selenium (Se) Biofortification Changes the Physiological, Biochemical and Epigenetic Responses to Water Stress in <i>Zea mays</i> L. by Inducing a Higher Drought Tolerance. Frontiers in Plant Science, 2018, 9, 389.	3.6	67
746	The Hydrophobin-Like OmSSP1 May Be an Effector in the Ericoid Mycorrhizal Symbiosis. Frontiers in Plant Science, 2018, 9, 546.	3.6	20
747	Construction of ParÃ rubber tree genome and multi-transcriptome database accelerates rubber researches. BMC Genomics, 2018, 19, 922.	2.8	31
748	<i>Escherichia coli</i> B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. BMC Systems Biology, 2018, 12, 66.	3.0	39
749	Loose ends: almost one in five human genes still have unresolved coding status. Nucleic Acids Research, 2018, 46, 7070-7084.	14.5	62
750	High-throughput profiling of the circulating proteome suggests sexually dimorphic corticosteroid signaling following ischemic stroke. Physiological Genomics, 2018, 50, 876-883.	2.3	8

#	ARTICLE	IF	CITATIONS
751	GPCR-SAS: A web application for statistical analyses on G protein-coupled receptors sequences. PLoS ONE, 2018, 13, e0199843.	2.5	7
752	High Quality de Novo Transcriptome Assembly of Croton tiglium. Frontiers in Molecular Biosciences, 2018, 5, 62.	3.5	48
753	Evidence for a Unique DNA-Dependent RNA Polymerase in Cereal Crops. Molecular Biology and Evolution, 2018, 35, 2454-2462.	8.9	21
754	Characterization of FGD5 Expression in Primary Breast Cancers and Lymph Node Metastases. Journal of Histochemistry and Cytochemistry, 2018, 66, 787-799.	2.5	9
755	Predicting human protein function with multi-task deep neural networks. PLoS ONE, 2018, 13, e0198216.	2.5	58
756	Combined Ligand- and Receptor-Based Virtual Screening Methodology to Identify Structurally Diverse Protein Tyrosine Phosphatase 1B Inhibitors. ChemMedChem, 2018, 13, 1939-1948.	3.2	5
757	Transcriptome response of human skeletal muscle to divergent exercise stimuli. Journal of Applied Physiology, 2018, 124, 1529-1540.	2.5	61
758	Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma. Blood, 2018, 132, 1146-1158.	1.4	218
759	Quorum-Quenching Bacteria Isolated From Red Sea Sediments Reduce Biofilm Formation by Pseudomonas aeruginosa. Frontiers in Microbiology, 2018, 9, 1354.	3.5	77
760	Transcriptomics investigation of thyroid hormone disruption in the olfactory system of the Rana [Lithobates] catesbeiana tadpole. Aquatic Toxicology, 2018, 202, 46-56.	4.0	17
761	CASTp 3.0: computed atlas of surface topography of proteins. Nucleic Acids Research, 2018, 46, W363-W367.	14.5	1,341
762	Proteomic Analyses on an Ancient Egyptian Cheese and Biomolecular Evidence of Brucellosis. Analytical Chemistry, 2018, 90, 9673-9676.	6.5	38
763	Conotoxin Diversity in Chelyconus ermineus (Born, 1778) and the Convergent Origin of Piscivory in the Atlantic and Indo-Pacific Cones. Genome Biology and Evolution, 2018, 10, 2643-2662.	2.5	28
764	A conserved loop-wedge motif moderates reaction site search and recognition by FEN1. Nucleic Acids Research, 2018, 46, 7858-7872.	14.5	13
765	An overview of Phoneutria nigriventer spider venom using combined transcriptomic and proteomic approaches. PLoS ONE, 2018, 13, e0200628.	2.5	46
766	From in silico to in vitro: a trip to reveal flavonoid binding on the <i>Rattus norvegicus</i> Kir6.1 ATP-sensitive inward rectifier potassium channel. PeerJ, 2018, 6, e4680.	2.0	14
767	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. BMC Genomics, 2018, 19, 395.	2.8	42
768	Cutting an NKG2D Ligand Short: Cellular Processing of the Peculiar Human NKG2D Ligand ULBP4. Frontiers in Immunology, 2018, 9, 620.	4.8	19

#	ARTICLE	IF	CITATIONS
769	Meta-Analysis of Maternal and Fetal Transcriptomic Data Elucidates the Role of Adaptive and Innate Immunity in Preterm Birth. <i>Frontiers in Immunology</i> , 2018, 9, 993.	4.8	30
770	The Bacteroidetes Q-Rule: Pyroglutamate in Signal Peptidase I Substrates. <i>Frontiers in Microbiology</i> , 2018, 9, 230.	3.5	16
771	Genome Sequence, Assembly and Characterization of Two <i>Metschnikowia fructicola</i> Strains Used as Biocontrol Agents of Postharvest Diseases. <i>Frontiers in Microbiology</i> , 2018, 9, 593.	3.5	58
772	Comparative Genomics Reveals the Regulatory Complexity of Bifidobacterial Arabinose and Arabino-Oligosaccharide Utilization. <i>Frontiers in Microbiology</i> , 2018, 9, 776.	3.5	45
773	Distribution Patterns of Polyphosphate Metabolism Pathway and Its Relationships With Bacterial Durability and Virulence. <i>Frontiers in Microbiology</i> , 2018, 9, 782.	3.5	34
774	Whole-Cell MALDI-TOF MS Versus 16S rRNA Gene Analysis for Identification and Dereplication of Recurrent Bacterial Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 1294.	3.5	76
775	Comparative Metagenomics Provides Insight Into the Ecosystem Functioning of the Shark Bay Stromatolites, Western Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1359.	3.5	34
776	Protein engineering of enzymes involved in lipid modification. , 2018, , 11-43.		2
777	In silico approach in reveal traditional medicine plants pharmacological material basis. <i>Chinese Medicine</i> , 2018, 13, 33.	4.0	75
778	Biological Implications of Differential Expression of Mitochondrial-Shaping Proteins in Parkinson's Disease. <i>Antioxidants</i> , 2018, 7, 1.	5.1	99
779	High and Low Levels of an NTRK2-Driven Genetic Profile Affect Motor- and Cognition-Associated Frontal Gray Matter in Prodromal Huntington's Disease. <i>Brain Sciences</i> , 2018, 8, 116.	2.3	3
780	Pigment Production by the Edible Filamentous Fungus <i>Neurospora Intermedia</i> . <i>Fermentation</i> , 2018, 4, 11.	3.0	27
781	Network-Based Methods for Identifying Key Active Proteins in the Extracellular Electron Transfer Process in <i>Shewanella oneidensis</i> MR-1. <i>Genes</i> , 2018, 9, 41.	2.4	10
782	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	2.4	24
783	Multifunctional Activity-Based Protein Profiling of the Developing Lung. <i>Journal of Proteome Research</i> , 2018, 17, 2623-2634.	3.7	9
784	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
785	Comparative Secretome Profiling and Mutant Protein Identification in Metastatic Prostate Cancer Cells by Quantitative Mass Spectrometry-based Proteomics. <i>Cancer Genomics and Proteomics</i> , 2018, 15, 279-290.	2.0	19
786	In silico analysis of the α -amylase family GH57: eventual subfamilies reflecting enzyme specificities. <i>3 Biotech</i> , 2018, 8, 307.	2.2	21

#	ARTICLE	IF	CITATIONS
787	PON-tstab: Protein Variant Stability Predictor. Importance of Training Data Quality. International Journal of Molecular Sciences, 2018, 19, 1009.	4.1	48
788	CD9 and CD81 Interactions and Their Structural Modelling in Sperm Prior to Fertilization. International Journal of Molecular Sciences, 2018, 19, 1236.	4.1	26
789	Anti-Correlation between the Dynamics of the Active Site Loop and C-Terminal Tail in Relation to the Homodimer Asymmetry of the Mouse Erythroid 5-Aminolevulinate Synthase. International Journal of Molecular Sciences, 2018, 19, 1899.	4.1	7
790	Proteomic Analyses of the Unexplored Sea Anemone <i>Bunodactis verrucosa</i> . Marine Drugs, 2018, 16, 42.	4.6	23
791	In Silico Discovery of a Substituted 6-Methoxy-quinalidine with Leishmanicidal Activity in <i>Leishmania infantum</i> . Molecules, 2018, 23, 772.	3.8	20
792	Cytotoxic, Anti-Proliferative and Apoptosis Activity of l-Amino Acid Oxidase from Malaysian <i>Cryptelytrops purpureomaculatus</i> (CP-LAAO) Venom on Human Colon Cancer Cells. Molecules, 2018, 23, 1388.	3.8	18
793	True Lies: Using Proteomics to Assess the Accuracy of Transcriptome-Based Venomics in Centipedes Uncovers False Positives and Reveals Startling Intraspecific Variation in <i>Scolopendra subspinipes</i> . Toxins, 2018, 10, 96.	3.4	40
794	Fungal Cytochrome P450s and the P450 Complement (CYPome) of <i>Fusarium graminearum</i> . Toxins, 2018, 10, 112.	3.4	101
795	HFSP: high speed homology-driven function annotation of proteins. Bioinformatics, 2018, 34, i304-i312.	4.1	22
796	Differential lncRNA expression profiles reveal the potential roles of lncRNAs in antiviral immune response of <i>Crassostrea gigas</i> . Fish and Shellfish Immunology, 2018, 81, 233-241.	3.6	47
797	An Open Library of Human Kinase Domain Constructs for Automated Bacterial Expression. Biochemistry, 2018, 57, 4675-4689.	2.5	37
798	Negative selection in tumor genome evolution acts on essential cellular functions and the immunopeptidome. Genome Biology, 2018, 19, 67.	8.8	81
799	Deep mutational analysis reveals functional trade-offs in the sequences of EGFR autophosphorylation sites. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7303-E7312.	7.1	28
800	PRP-19, a conserved pre-mRNA processing factor and E3 ubiquitin ligase, inhibits the nuclear accumulation of GLP-1/Notch intracellular domain. Biology Open, 2018, 7, .	1.2	8
801	LMDIPred: A web-server for prediction of linear peptide sequences binding to SH3, WW and PDZ domains. PLoS ONE, 2018, 13, e0200430.	2.5	14
802	Identification and functional analysis of glycemic trait loci in the China Health and Nutrition Survey. PLoS Genetics, 2018, 14, e1007275.	3.5	30
803	Molecular phenotyping of laboratory mouse strains using 500 multiple reaction monitoring mass spectrometry plasma assays. Communications Biology, 2018, 1, 78.	4.4	22
804	Genome instability is a consequence of transcription deficiency in patients with bone marrow failure harboring biallelic <i>ERCC6L2</i> variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7777-7782.	7.1	37

#	ARTICLE	IF	CITATIONS
805	Enrichment of extracellular vesicles from human synovial fluid using size exclusion chromatography. <i>Journal of Extracellular Vesicles</i> , 2018, 7, 1490145.	12.2	78
806	Dual localized kinesinâ€12 <sc>POK</sc> 2 plays multiple roles during cell division and interacts with <sc>MAP</sc> 65â€3. <i>EMBO Reports</i> , 2018, 19, .	4.5	35
807	The leaf transcriptome of fennel (<i>Foeniculum vulgare</i> Mill.) enables characterization of the t-anethole pathway and the discovery of microsatellites and single-nucleotide variants. <i>Scientific Reports</i> , 2018, 8, 10459.	3.3	14
808	Engineering a Rugged Nanoscaffold To Enhance Plug-and-Display Vaccination. <i>ACS Nano</i> , 2018, 12, 8855-8866.	14.6	180
809	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by <i>Trachymyrmex septentrionalis</i> Ants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
810	Alzheimer disease pathology and the cerebrospinal fluid proteome. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 66.	6.2	67
811	Two New Secreted Proteases Generate a Casein-Derived Antimicrobial Peptide in <i>Bacillus cereus</i> Food Born Isolate Leading to Bacterial Competition in Milk. <i>Frontiers in Microbiology</i> , 2018, 9, 1148.	3.5	29
812	Structure Based Virtual Screening Studies to Identify Novel Potential Compounds for GPR142 and Their Relative Dynamic Analysis for Study of Type 2 Diabetes. <i>Frontiers in Chemistry</i> , 2018, 6, 23.	3.6	40
813	IMPACT web portal: oncology database integrating molecular profiles with actionable therapeutics. <i>BMC Medical Genomics</i> , 2018, 11, 26.	1.5	5
814	Cysteine peptidases of <i>Eudiplozoon nipponicum</i> : a broad repertoire of structurally assorted cathepsins L in contrast to the scarcity of cathepsins B in an invasive species of haematophagous monogenean of common carp. <i>Parasites and Vectors</i> , 2018, 11, 142.	2.5	30
815	A recombinant <i>Fasciola gigantica</i> 14-3-3 epsilon protein (rFg14-3-3e) modulates various functions of goat peripheral blood mononuclear cells. <i>Parasites and Vectors</i> , 2018, 11, 152.	2.5	26
816	Identification and structural characterization of a histidinol phosphate phosphatase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 10102-10118.	3.4	10
817	VARReporter: variant reporter for cancer research of massive parallel sequencing. <i>BMC Genomics</i> , 2018, 19, 86.	2.8	2
818	STAT3, stem cells, cancer stem cells and p63. <i>Cellular and Molecular Biology Letters</i> , 2018, 23, 12.	7.0	188
819	Early and late feathering in turkey and chicken: same gene but different mutations. <i>Genetics Selection Evolution</i> , 2018, 50, 7.	3.0	11
820	Sex differences in the late first trimester human placenta transcriptome. <i>Biology of Sex Differences</i> , 2018, 9, 4.	4.1	109
821	JAMI: a Java library for molecular interactions and data interoperability. <i>BMC Bioinformatics</i> , 2018, 19, 133.	2.6	6
822	PKRank: a novel learning-to-rank method for ligand-based virtual screening using pairwise kernel and RankSVM. <i>Artificial Life and Robotics</i> , 2018, 23, 205-212.	1.2	6

#	ARTICLE	IF	CITATIONS
823	Alternative splicing of ALCAM enables tunable regulation of cell-cell adhesion through differential proteolysis. <i>Scientific Reports</i> , 2018, 8, 3208.	3.3	13
824	SLALOM, a flexible method for the identification and statistical analysis of overlapping continuous sequence elements in sequence- and time-series data. <i>BMC Bioinformatics</i> , 2018, 19, 24.	2.6	2
825	LocText: relation extraction of protein localizations to assist database curation. <i>BMC Bioinformatics</i> , 2018, 19, 15.	2.6	120
826	Structural biology data archiving “where we are and what lies ahead. <i>FEBS Letters</i> , 2018, 592, 2153-2167.	2.8	11
827	ProteomeVis: a web app for exploration of protein properties from structure to sequence evolution across organisms’ proteomes. <i>Bioinformatics</i> , 2018, 34, 3557-3565.	4.1	7
828	iPath3.0: interactive pathways explorer v3. <i>Nucleic Acids Research</i> , 2018, 46, W510-W513.	14.5	210
829	An Escherichia coli Nitrogen Starvation Response Is Important for Mutualistic Coexistence with Rhodospseudomonas palustris. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	7
830	Metabolic Reprogramming of Vibrio cholerae Impaired in Respiratory NADH Oxidation Is Accompanied by Increased Copper Sensitivity. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	9
831	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 207-234.	6.5	108
832	Identification of residue pairing in interacting β^2 -strands from a predicted residue contact map. <i>BMC Bioinformatics</i> , 2018, 19, 146.	2.6	4
833	PPI network analyses of human WD40 protein family systematically reveal their tendency to assemble complexes and facilitate the complex predictions. <i>BMC Systems Biology</i> , 2018, 12, 41.	3.0	9
834	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. <i>Scientific Reports</i> , 2018, 8, 6518.	3.3	31
835	PedAM: a database for Pediatric Disease Annotation and Medicine. <i>Nucleic Acids Research</i> , 2018, 46, D977-D983.	14.5	27
836	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018, 9, 3268.	12.8	221
837	BED: a Biological Entity Dictionary based on a graph data model. <i>F1000Research</i> , 2018, 7, 195.	1.6	1
838	BALCONY: an R package for MSA and functional compartments of protein variability analysis. <i>BMC Bioinformatics</i> , 2018, 19, 300.	2.6	11
839	Efficient proximity labeling in living cells and organisms with TurboID. <i>Nature Biotechnology</i> , 2018, 36, 880-887.	17.5	1,103
840	Proteomics: Clinical and research applications in respiratory diseases. <i>Respirology</i> , 2018, 23, 993-1003.	2.3	15

#	ARTICLE	IF	CITATIONS
841	The Human Centrosomal Protein CCDC146 Binds Chlamydia trachomatis Inclusion Membrane Protein CT288 and Is Recruited to the Periphery of the Chlamydia-Containing Vacuole. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 254.	3.9	22
842	Positive and Negative Regulation of Angiogenesis by Soluble Vascular Endothelial Growth Factor Receptor-1. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1306.	4.1	67
843	High-throughput prediction of disordered moonlighting regions in protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1097-1110.	2.6	29
844	Recent advancements, challenges, and practical considerations in the mass spectrometry-based analytics of protein biotherapeutics: A viewpoint from the biosimilar industry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 161, 214-238.	2.8	44
845	Functional insights into the infective larval stage of <i>Anisakis simplex</i> s.s., <i>Anisakis pegreffii</i> and their hybrids based on gene expression patterns. <i>BMC Genomics</i> , 2018, 19, 592.	2.8	30
846	In silico identification of inhibitors against <i>Plasmodium falciparum</i> histone deacetylase 1 (PfHDAC-1). <i>Journal of Molecular Modeling</i> , 2018, 24, 232.	1.8	8
847	Monitoring changes in the Gene Ontology and their impact on genomic data analysis. <i>GigaScience</i> , 2018, 7, .	6.4	4
848	Functional diversity of TMPRSS6 isoforms and variants expressed in hepatocellular carcinoma cell lines. <i>Scientific Reports</i> , 2018, 8, 12562.	3.3	12
849	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	14.5	65
850	Membrane Active Peptides and Their Biophysical Characterization. <i>Biomolecules</i> , 2018, 8, 77.	4.0	126
851	Synthesis versus degradation: directions of amino acid metabolism during <i>Arabidopsis</i> abiotic stress response. <i>Plant Molecular Biology</i> , 2018, 98, 121-135.	3.9	243
852	Genetics of hearing loss in the Arab population of Northern Israel. <i>European Journal of Human Genetics</i> , 2018, 26, 1840-1847.	2.8	21
853	Identification and characterization of a new antifungal peptide in fermented milk product containing bioprotective <i>Lactobacillus</i> cultures. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	24
854	Further evidence for a differential interaction of brivaracetam and levetiracetam with the synaptic vesicle 2A protein. <i>Epilepsia</i> , 2018, 59, e147-e151.	5.1	22
855	Next-Generation Transcriptome Assembly: Strategies and Performance Analysis. , 0, , .		16
856	Development and characterization of a novel monoclonal antibody that recognizes an epitope in the central protein interaction domain of RapGEF1 (C3G). <i>Molecular Biology Reports</i> , 2018, 45, 1809-1819.	2.3	6
857	Dysregulation of the calcium handling protein, CCDC47, is associated with diabetic cardiomyopathy. <i>Cell and Bioscience</i> , 2018, 8, 45.	4.8	5
858	Deep genome annotation of the opportunistic human pathogen <i>Streptococcus pneumoniae</i> D39. <i>Nucleic Acids Research</i> , 2018, 46, 9971-9989.	14.5	93

#	ARTICLE	IF	CITATIONS
859	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.	3.2	33
860	Identification of Potential Nematicidal Compounds against the Pine Wood Nematode, Bursaphelenchus xylophilus through an In Silico Approach. Molecules, 2018, 23, 1828.	3.8	20
861	Flow cytometric detection of most proteins in the cell surface proteome is unaffected by trypsin treatment. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 803-810.	1.5	7
862	Efficiency of Stratification for Ensemble Docking Using Reduced Ensembles. Journal of Chemical Information and Modeling, 2018, 58, 1915-1925.	5.4	8
863	Intron retention is a source of neopeptides in cancer. Nature Biotechnology, 2018, 36, 1056-1058.	17.5	212
864	Draft genome of Glyptosternon maculatum, an endemic fish from Tibet Plateau. GigaScience, 2018, 7, .	6.4	18
865	Human proteins that interact with RNA/DNA hybrids. Genome Research, 2018, 28, 1405-1414.	5.5	130
866	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
867	Edema Induced by a Crotalus durissus terrificus Venom Serine Protease (Cdtsp 2) Involves the PAR Pathway and PKC and PLC Activation. International Journal of Molecular Sciences, 2018, 19, 2405.	4.1	11
868	Mutational analysis of CCL20 reveals flexibility of N-terminal amino acid composition and length. Journal of Leukocyte Biology, 2018, 104, 423-434.	3.3	6
869	Green coffee bean extract and 5-O-caffeoylquinic acid regulate fat metabolism in Caenorhabditis elegans. Journal of Functional Foods, 2018, 48, 586-593.	3.4	29
870	The Evolutionary Conserved Î³-Core Motif Influences the Anti-Candida Activity of the Penicillium chrysogenum Antifungal Protein PAF. Frontiers in Microbiology, 2018, 9, 1655.	3.5	29
871	The Genetics of a Behavioral Speciation Phenotype in an Island System. Genes, 2018, 9, 346.	2.4	16
872	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. Soil Biology and Biochemistry, 2018, 125, 290-299.	8.8	37
873	Structural Analysis of Hippocampal Kinase Signal Transduction. ACS Chemical Neuroscience, 2018, 9, 3072-3085.	3.5	6
874	Epigenetic Variability Confounds Transcriptome but Not Proteome Profiling for Coexpression-based Gene Function Prediction. Molecular and Cellular Proteomics, 2018, 17, 2082-2090.	3.8	9
875	Evaluating the Possibility of Detecting Variants in Shotgun Proteomics via LeTE-Fusion Analysis Pipeline. Journal of Proteome Research, 2018, 17, 2937-2952.	3.7	5
876	Worldwide Protein Data Bank validation information: usage and trends. Acta Crystallographica Section D: Structural Biology, 2018, 74, 237-244.	2.3	15

#	ARTICLE	IF	CITATIONS
877	A molecular model for LINC complex regulation: activation of SUN2 for KASH binding. <i>Molecular Biology of the Cell</i> , 2018, 29, 2012-2023.	2.1	20
878	Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. <i>Translational Psychiatry</i> , 2018, 8, 160.	4.8	68
879	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	14.5	18
880	p62-Dependent Phase Separation of Patient-Derived KEAP1 Mutations and NRF2. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	51
881	Ribonucleases as Drug Targets. <i>Trends in Pharmacological Sciences</i> , 2018, 39, 855-866.	8.7	11
882	Molecular Dynamics Simulations Reveal Structural Differences among Allelic Variants of Membrane-Anchored Cytochrome P450 2D6. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1962-1975.	5.4	21
883	The human iron-proteome. <i>Metallomics</i> , 2018, 10, 1223-1231.	2.4	106
884	Identification of errors in the IEDB using ontologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	4
885	The IUPHAR/BPS Guide to PHARMACOLOGY in 2018: updates and expansion to encompass the new guide to IMMUNOPHARMACOLOGY. <i>Nucleic Acids Research</i> , 2018, 46, D1091-D1106.	14.5	1,584
886	Searching for New Leads To Treat Epilepsy: Target-Based Virtual Screening for the Discovery of Anticonvulsant Agents. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1331-1342.	5.4	11
887	Ubiquitin Proteasome pathway proteins as potential drug targets in parasite <i>Trypanosoma cruzi</i> . <i>Scientific Reports</i> , 2018, 8, 8399.	3.3	28
888	SDS-PAGE fractionation to increase metaproteomic insight into the taxonomic and functional composition of microbial communities for biogas plant samples. <i>Engineering in Life Sciences</i> , 2018, 18, 498-509.	3.6	27
889	Data on a thermostable enzymatic one-pot reaction for the production of a high-value compound from L-arabinose. <i>Data in Brief</i> , 2018, 19, 1341-1354.	1.0	1
890	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	14.5	190
891	Alcohol-Related Alterations in Placental Imprinted Gene Expression in Humans Mediate Effects of Prenatal Alcohol Exposure on Postnatal Growth. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 1431-1443.	2.4	20
892	Expanding the horizons of microRNA bioinformatics. <i>Rna</i> , 2018, 24, 1005-1017.	3.5	27
893	A High Quality Genome for <i>Mus spicilegus</i> , a Close Relative of House Mice with Unique Social and Ecological Adaptations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2145-2152.	1.8	8
894	The gonadal transcriptome of the unisexual Amazon molly <i>Poecilia formosa</i> in comparison to its sexual ancestors, <i>Poecilia mexicana</i> and <i>Poecilia latipinna</i> . <i>BMC Genomics</i> , 2018, 19, 12.	2.8	14

#	ARTICLE	IF	CITATIONS
895	Introduction of novel thermostable α -amylases from genus <i>Anoxybacillus</i> and proposing to group the Bacillaceae related α -amylases under five individual GH13 subfamilies. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 95.	3.6	8
896	Detection of single alpha-helices in large protein sequence sets using hardware acceleration. <i>Journal of Structural Biology</i> , 2018, 204, 109-116.	2.8	6
897	Structural Insights on Fragment Binding Mode Conservation. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 5963-5973.	6.4	21
898	GFPT1 deficiency in muscle leads to myasthenia and myopathy in mice. <i>Human Molecular Genetics</i> , 2018, 27, 3218-3232.	2.9	18
899	HMMER Cut-off Threshold Tool (HMMERCTTER): Supervised classification of superfamily protein sequences with a reliable cut-off threshold. <i>PLoS ONE</i> , 2018, 13, e0193757.	2.5	16
900	From phylogeny to protein dynamics: A computational hierarchical quest for potent drug identification against an emerging enteropathogen <i>Yersinia enterocolitica</i> . <i>Journal of Molecular Liquids</i> , 2018, 265, 372-389.	4.9	10
901	Bacterial denitrifying nitric oxide reductases and aerobic respiratory terminal oxidases use similar delivery pathways for their molecular substrates. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 712-724.	1.0	10
902	Nitric oxide synthase: What is its potential role in the physiology of staphylococci in meat products?. <i>International Journal of Food Microbiology</i> , 2018, 282, 28-34.	4.7	20
903	Deciphering the multicomponent synergy mechanism from a systems pharmacology perspective: Application to Gualou Xiebai Decoction for coronary heart disease. <i>Journal of Functional Foods</i> , 2018, 47, 143-155.	3.4	21
904	Targeting phosphorylated p53 to elicit tumor-reactive T helper responses against head and neck squamous cell carcinoma. <i>Oncolmmunology</i> , 2018, 7, e1466771.	4.6	14
905	Design, Synthesis, and Biological Evaluation of Tetrahydro- β -carboline Derivatives as Selective Sub-nanomolar Gelatinase Inhibitors. <i>ChemMedChem</i> , 2018, 13, 1343-1352.	3.2	4
906	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018, 9, 2320.	12.8	23
907	Biological Databases. <i>Translational Bioinformatics</i> , 2018, , 303-337.	0.0	0
908	Developments in toxicogenomics: understanding and predicting compound-induced toxicity from gene expression data. <i>Molecular Omics</i> , 2018, 14, 218-236.	2.8	90
909	Laminins in Metastatic Cancer. <i>Molecular Biology</i> , 2018, 52, 350-371.	1.3	36
910	Direct Cellulase Gene Amplification From Hot Spring Using the Guidance of 16S rRNA Amplicon Metagenomics. , 2018, , 309-325.		1
911	BASiNET—Biological Sequences NETwork: a case study on coding and non-coding RNAs identification. <i>Nucleic Acids Research</i> , 2018, 46, e96-e96.	14.5	38
912	Protein Structure Databases. , 2019, , 460-471.		0

#	ARTICLE	IF	CITATIONS
913	3DPatch: fast 3D structure visualization with residue conservation. Bioinformatics, 2019, 35, 332-334.	4.1	2
914	Actin from the apicomplexan <i>Neospora caninum</i> (NcACT) has different isoforms in 2D electrophoresis. Parasitology, 2019, 146, 33-41.	1.5	2
915	Modification of Crocodile Spermatozoa Refutes the Tenet That Post-testicular Sperm Maturation Is Restricted To Mammals*. Molecular and Cellular Proteomics, 2019, 18, S58-S76.	3.8	30
916	Evolutionary and structure-function analysis elucidates diversification of prokaryotic and eukaryotic trehalases. Journal of Biomolecular Structure and Dynamics, 2019, 37, 2926-2937.	3.5	5
917	Lung Cancer Classification Models Using Discriminant Information of Mutated Genes in Protein Amino Acids Sequences. Arabian Journal for Science and Engineering, 2019, 44, 3197-3211.	3.0	5
918	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. Briefings in Bioinformatics, 2019, 20, 1878-1912.	6.5	310
919	Root bacterial endophytes confer drought resistance and enhance expression and activity of a vacuolar H ⁺ -pumping pyrophosphatase in pepper plants. Environmental Microbiology, 2019, 21, 3212-3228.	3.8	60
920	Use of omics analytical methods in the study of genetically modified maize varieties tested in 90 days feeding trials. Food Chemistry, 2019, 292, 359-371.	8.2	13
921	Protein Structural Bioinformatics: An Overview. , 2019, , 445-459.		23
922	Integrative Bioinformatics. , 2019, , 1092-1098.		0
923	Selection-based design of in silico dengue epitope ensemble vaccines. Chemical Biology and Drug Design, 2019, 93, 21-28.	3.2	9
924	The Evolution of Protein Family Databases. , 2019, , 34-45.		1
925	Transmembrane Domain Prediction. , 2019, , 46-52.		0
926	Proteomics Data Representation and Databases. , 2019, , 76-83.		0
927	Protein Post-Translational Modification Prediction. , 2019, , 15-27.		1
928	Biological Database Searching. , 2019, , 29-38.		0
929	Bioinformatics Data Models, Representation and Storage. , 2019, , 110-116.		4
930	Genome Analysis – Identification of Genes Involved in Host-Pathogen Protein-Protein Interaction Networks. , 2019, , 410-424.		0

#	ARTICLE	IF	CITATIONS
931	Genome Annotation. , 2019, , 195-209.		3
933	Review and comparative assessment of similarity-based methods for prediction of drugâ€“protein interactions in the druggable human proteome. Briefings in Bioinformatics, 2019, 20, 2066-2087.	6.5	19
934	Proteinâ€“Protein Interaction Databases. , 2019, , 988-996.		3
935	Sequence Similarity Searching. Current Protocols in Protein Science, 2019, 95, e71.	2.8	50
936	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 336-349.	3.0	4
937	Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. Nucleic Acids Research, 2019, 47, 7809-7824.	14.5	47
938	Genetic variability of hypoxiaâ€“inducible factor alpha (<i>HIFA</i>) genes in familial erythrocytosis: Analysis of the literature and genome databases. European Journal of Haematology, 2019, 103, 287-299.	2.2	12
939	<i>In Silico</i>Phylogenetic and Structural Analyses of Plant Endogenous Danger Signaling Molecules upon Stress. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-14.	4.0	8
940	Discovery of novel <i>Schistosoma mansoni</i> PDE4A inhibitors as potential agents against schistosomiasis. Future Medicinal Chemistry, 2019, 11, 1703-1720.	2.3	8
941	PaleAle 5.0: prediction of protein relative solvent accessibility by deep learning. Amino Acids, 2019, 51, 1289-1296.	2.7	25
942	Characterization of novel small RNAs (sRNAs) contributing to the desiccation response of <i>Salmonella enterica</i> serovar Typhimurium. RNA Biology, 2019, 16, 1643-1657.	3.1	9
943	Familial Intracranial Aneurysm in Newfoundland: Clinical and Genetic Analysis. Canadian Journal of Neurological Sciences, 2019, 46, 518-526.	0.5	2
944	Parallel Evolution of Complex Centipede Venoms Revealed by Comparative Proteotranscriptomic Analyses. Molecular Biology and Evolution, 2019, 36, 2748-2763.	8.9	24
945	A consensus <i>S. cerevisiae</i> metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. Nature Communications, 2019, 10, 3586.	12.8	217
946	Transcriptome annotation and characterization of novel toxins in six scorpion species. BMC Genomics, 2019, 20, 645.	2.8	9
947	Claudin-low-like mouse mammary tumors show distinct transcriptomic patterns uncoupled from genomic drivers. Breast Cancer Research, 2019, 21, 85.	5.0	18
948	Ageing-Time Dependent Changes of Angiotensin I-Converting Enzyme-Inhibiting Activity of Protein Hydrolysates Obtained from Dry-Cured Pork Loins Inoculated with Probiotic Lactic Acid Bacteria. International Journal of Peptide Research and Therapeutics, 2019, 25, 1173-1185.	1.9	6
949	De novo mutations in mitochondrial DNA of iPSCs produce immunogenic neoepitopes in mice and humans. Nature Biotechnology, 2019, 37, 1137-1144.	17.5	74

#	ARTICLE	IF	CITATIONS
950	Predicting Protein-Protein Interactions based on Biological Information using Extreme Gradient Boosting. , 2019, , .		10
951	ALG9 Mutation Carriers Develop Kidney and Liver Cysts. Journal of the American Society of Nephrology: JASN, 2019, 30, 2091-2102.	6.1	91
952	Origins of peptidases. Biochimie, 2019, 166, 4-18.	2.6	30
953	Emerging concepts in pseudoenzyme classification, evolution, and signaling. Science Signaling, 2019, 12, .	3.6	80
954	Anti-Myelin Proteolipid Protein Peptide Monoclonal Antibodies Recognize Cell Surface Proteins on Developing Neurons and Inhibit Their Differentiation. Journal of Neuropathology and Experimental Neurology, 2019, 78, 819-843.	1.7	3
955	Secretome profiling of PC3/nKR cells, a novel highly migrating prostate cancer subline derived from PC3 cells. PLoS ONE, 2019, 14, e0220807.	2.5	3
956	Structural and functional characterization of SiiA, an auxiliary protein from the SPI4a-encoded type 1 secretion system from <i>Salmonella enterica</i> . Molecular Microbiology, 2019, 112, 1403-1422.	2.5	9
957	Biosynthetic homeostasis and resilience of the complement system in health and infectious disease. EBioMedicine, 2019, 45, 303-313.	6.1	20
958	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. Nature Biotechnology, 2019, 37, 953-961.	17.5	353
959	Discovering protein drug targets using knowledge graph embeddings. Bioinformatics, 2020, 36, 603-610.	4.1	143
960	<scp>SALM</scp> 1 controls synapse development by promoting F-actin/PIP2-dependent Neurexin clustering. EMBO Journal, 2019, 38, e101289.	7.8	17
961	Epistatic Analysis of the Contribution of Rabs and Kifs to CATCHR Family Dependent Golgi Organization. Frontiers in Cell and Developmental Biology, 2019, 7, 126.	3.7	4
962	Differential gene expression analysis of symbiotic and aposymbiotic Exaiptasia anemones under immune challenge with <i>Vibrio coralliilyticus</i> . Ecology and Evolution, 2019, 9, 8279-8293.	1.9	10
963	Nascent Polypeptide Domain Topology and Elongation Rate Direct the Cotranslational Hierarchy of Hsp70 and TRiC/CCT. Molecular Cell, 2019, 75, 1117-1130.e5.	9.7	93
964	Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. PLoS ONE, 2019, 14, e0217889.	2.5	84
965	Differentially Expressed MiRNAs and tRNA Genes Affect Host Homeostasis During Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus Infections in Young Pigs. Frontiers in Genetics, 2019, 10, 691.	2.3	15
966	Transcriptomic Analysis of Marine Gastropod <i>Hemifusus tuba</i> Provides Novel Insights into Conotoxin Genes. Marine Drugs, 2019, 17, 466.	4.6	6
967	Inferring novel genes related to colorectal cancer via random walk with restart algorithm. Gene Therapy, 2019, 26, 373-385.	4.5	3

#	ARTICLE	IF	CITATIONS
968	Global transcriptome and gene co-expression network analyses on the development of distyly in <i>Primula oreodoxa</i> . <i>Heredity</i> , 2019, 123, 784-794.	2.6	15
969	Membrane protein-regulated networks across human cancers. <i>Nature Communications</i> , 2019, 10, 3131.	12.8	67
970	Proteogenomic Analysis of Protein Sequence Alterations in Breast Cancer Cells. <i>Scientific Reports</i> , 2019, 9, 10381.	3.3	19
971	PhenPath: a tool for characterizing biological functions underlying different phenotypes. <i>BMC Genomics</i> , 2019, 20, 548.	2.8	8
972	Genome-wide screen identifies novel genes required for <i>Borrelia burgdorferi</i> survival in its Ixodes tick vector. <i>PLoS Pathogens</i> , 2019, 15, e1007644.	4.7	25
973	Dependency Between Protein-Protein Interactions and Protein Variability and Evolutionary Rates in Vertebrates: Observed Relationships and Stochastic Modeling. <i>Journal of Molecular Evolution</i> , 2019, 87, 184-198.	1.8	3
974	De Novo Missense Variants in WDR37 Cause a Severe Multisystemic Syndrome. <i>American Journal of Human Genetics</i> , 2019, 105, 425-433.	6.2	24
975	From genomic variation to protein aberration: Mutational analysis of single nucleotide polymorphism present in ULBP6 gene and implication in immune response. <i>Computers in Biology and Medicine</i> , 2019, 111, 103354.	7.0	7
976	In silico site-directed mutagenesis of the <i>Daphnia magna</i> ecdysone receptor identifies critical amino acids for species-specific and inter-species differences in agonist binding. <i>Computational Toxicology</i> , 2019, 12, 100091.	3.3	3
977	Identification of a new family of pyrazolo[3,4-d]pyrimidine derivatives as multitarget Fyn-Blk-Lyn inhibitors active on B- and T-lymphoma cell lines. <i>European Journal of Medicinal Chemistry</i> , 2019, 181, 111545.	5.5	13
978	Structure solution and analyses of the first true lipase obtained from metagenomics indicate potential for increased thermostability. <i>New Biotechnology</i> , 2019, 53, 65-72.	4.4	10
979	Differential Interactome and Innate Immune Response Activation of Two Structurally Distinct Misfolded Protein Oligomers. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3464-3478.	3.5	7
980	A 4-cyano-3-methylisoquinoline inhibitor of <i>Plasmodium falciparum</i> growth targets the sodium efflux pump PfATP4. <i>Scientific Reports</i> , 2019, 9, 10292.	3.3	20
981	Statistical compression of protein sequences and inference of marginal probability landscapes over competing alignments using finite state models and Dirichlet priors. <i>Bioinformatics</i> , 2019, 35, i360-i369.	4.1	6
982	PRRDB 2.0: a comprehensive database of pattern-recognition receptors and their ligands. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	27
983	Evolution of Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2019, 1910, 469-504.	0.9	30
984	Decoding the PTM-switchboard of Notch. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 118507.	4.1	25
985	A non-synonymous SNP in exon 3 of the <i>KIT</i> gene is responsible for the classic grey phenotype in alpacas (<i>Vicugna pacos</i>). <i>Animal Genetics</i> , 2019, 50, 493-500.	1.7	18

#	ARTICLE	IF	CITATIONS
986	Environmental conditions shape the nature of a minimal bacterial genome. <i>Nature Communications</i> , 2019, 10, 3100.	12.8	43
987	Wheat bran thermal treatment in a hot air oven does not affect the fermentation and colonisation process by human faecal microbiota. <i>Journal of Functional Foods</i> , 2019, 60, 103440.	3.4	3
988	Acetaminophen Overdose as a Potential Risk Factor for Parkinson's Disease. <i>Clinical and Translational Science</i> , 2019, 12, 609-616.	3.1	6
989	Mapping non-host resistance to the stem rust pathogen in an interspecific barberry hybrid. <i>BMC Plant Biology</i> , 2019, 19, 319.	3.6	5
990	SeqScrub: a web tool for automatic cleaning and annotation of FASTA file headers for bioinformatic applications. <i>BioTechniques</i> , 2019, 67, 50-54.	1.8	6
991	Global Analysis of Intercellular Homeodomain Protein Transfer. <i>Cell Reports</i> , 2019, 28, 712-722.e3.	6.4	28
992	Recent Advances in the Machine Learning-Based Drug-Target Interaction Prediction. <i>Current Drug Metabolism</i> , 2019, 20, 194-202.	1.2	48
993	Overview of a High-Throughput Pipeline for Streamlining the Production of Recombinant Proteins. <i>Methods in Molecular Biology</i> , 2019, 2025, 33-49.	0.9	9
994	Making the Most of Trait-Based Approaches for Microbial Ecology. <i>Trends in Microbiology</i> , 2019, 27, 814-823.	7.7	49
995	Automated feature engineering improves prediction of protein-protein interactions. <i>Amino Acids</i> , 2019, 51, 1187-1200.	2.7	18
996	ANKRD26-RET - A novel gene fusion involving RET in papillary thyroid carcinoma. <i>Cancer Genetics</i> , 2019, 238, 10-17.	0.4	11
997	Sirius: A Resource for Analyzing Drug-Disease Relationships for Drug Repositioning. <i>Lecture Notes in Electrical Engineering</i> , 2019, , 235-244.	0.4	0
998	Activity and Phylogenetics of the Broadly Occurring Family of Microbial Nep1-Like Proteins. <i>Annual Review of Phytopathology</i> , 2019, 57, 367-386.	7.8	70
999	Extracellular Vesicles and Their Potential Use in Monitoring Cancer Progression and Therapy: The Contribution of Proteomics. <i>Journal of Oncology</i> , 2019, 2019, 1-19.	1.3	64
1000	Reference genome and comparative genome analysis for the WHO reference strain for <i>Mycobacterium bovis</i> BCG Danish, the present tuberculosis vaccine. <i>BMC Genomics</i> , 2019, 20, 561.	2.8	16
1001	High-throughput mass spectrometry and bioinformatics analysis of breast cancer proteomic data. <i>Data in Brief</i> , 2019, 25, 104125.	1.0	5
1002	Machine-learning-guided directed evolution for protein engineering. <i>Nature Methods</i> , 2019, 16, 687-694.	19.0	580
1003	Combined alignments of sequences and domains characterize unknown proteins with remotely related protein search PSIsearch2D. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, ,	3.0	1

#	ARTICLE	IF	CITATIONS
1004	Chromatin-dependent regulation of secondary metabolite biosynthesis in fungi: is the picture complete?. FEMS Microbiology Reviews, 2019, 43, 591-607.	8.6	56
1005	Tâ€type calcium channels drive the proliferation of androgenâ€receptor negative prostate cancer cells. Prostate, 2019, 79, 1580-1586.	2.3	14
1006	MicroScopeâ€an integrated resource for community expertise of gene functions and comparative analysis of microbial genomic and metabolic data. Briefings in Bioinformatics, 2019, 20, 1071-1084.	6.5	71
1007	The human 18S rRNA m6A methyltransferase METTL5 is stabilized by TRMT112. Nucleic Acids Research, 2019, 47, 7719-7733.	14.5	312
1008	Liver Cancer Cell Lines Treated with Doxorubicin under Normoxia and Hypoxia: Cell Viability and Oncologic Protein Profile. Cancers, 2019, 11, 1024.	3.7	41
1009	Natural and non-toxic products from Fabaceae Brazilian plants as a replacement for traditional antifouling biocides: an inhibition potential against initial biofouling. Environmental Science and Pollution Research, 2019, 26, 27112-27127.	5.3	16
1010	Targeted next generation sequencing screening of Lynch syndrome in Tunisian population. Familial Cancer, 2019, 18, 343-348.	1.9	4
1011	PlantMP: a database for moonlighting plant proteins. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	19
1012	Systems biology-based investigation of cooperating microRNAs as monotherapy or adjuvant therapy in cancer. Nucleic Acids Research, 2019, 47, 7753-7766.	14.5	126
1013	Benchmark and integration of resources for the estimation of human transcription factor activities. Genome Research, 2019, 29, 1363-1375.	5.5	552
1014	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. PLoS ONE, 2019, 14, e0209958.	2.5	11
1015	Binding affinities of human IgG1 and chimerized pig and rabbit derivatives to human, pig and rabbit Fc gamma receptor IIIA. PLoS ONE, 2019, 14, e0219999.	2.5	3
1016	Rare, functional, somatic variants in gene families linked to cancer genes: GPCR signaling as a paradigm. Oncogene, 2019, 38, 6491-6506.	5.9	20
1017	Large-scale Discovery of Substrates of the Human Kinome. Scientific Reports, 2019, 9, 10503.	3.3	79
1018	A computer-assisted discovery of novel potential anti-obesity compounds as selective carbonic anhydrase VA inhibitors. European Journal of Medicinal Chemistry, 2019, 181, 111565.	5.5	23
1019	Tryptophan Oxidation in the UQCRC1 Subunit of Mitochondrial Complex III (Ubiquinol-Cytochrome C) Tj ETQq1 1 0.784314 rgBT /Overl Molecular Dynamics Simulation Study. Scientific Reports, 2019, 9, 10694.	3.3	14
1020	Diversity of tryptophan halogenases in sponges of the genus Aplysina. FEMS Microbiology Ecology, 2019, 95, .	2.7	11
1021	Systematic analysis of the intersection of disease mutations with protein modifications. BMC Medical Genomics, 2019, 12, 109.	1.5	16

#	ARTICLE	IF	CITATIONS
1022	Viruses as key reservoirs of antibiotic resistance genes in the environment. ISME Journal, 2019, 13, 2856-2867.	9.8	88
1023	Demographic model for inheritable cardiac disease. Archives of Biochemistry and Biophysics, 2019, 672, 108056.	3.0	4
1024	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. GigaScience, 2019, 8, .	6.4	4
1025	Transcriptome characterization and differentially expressed genes under flooding and drought stress in the biomass grasses <i>Phalaris arundinacea</i> and <i>Dactylis glomerata</i> . Annals of Botany, 2019, 124, 717-730.	2.9	7
1026	Cell Wall Enzymes in <i>Zygnema circumcarinatum</i> UTEX 1559 Respond to Osmotic Stress in a Plant-Like Fashion. Frontiers in Plant Science, 2019, 10, 732.	3.6	13
1027	Comparative Genomics of Wild Bee and Flower Isolated <i>Lactobacillus</i> Reveals Potential Adaptation to the Bee Host. Genome Biology and Evolution, 2019, 11, 2151-2161.	2.5	38
1029	TYR Gene in Llamas: Polymorphisms and Expression Study in Different Color Phenotypes. Frontiers in Genetics, 2019, 10, 568.	2.3	13
1030	Molecular composition of the paralyzing venom of three solitary wasps (Hymenoptera: Pompilidae) collected in southeast Mexico. Toxicon, 2019, 168, 98-102.	1.6	5
1031	SeQuery: an interactive graph database for visualizing the GPCR superfamily. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	6
1032	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGlâ€5. Human Mutation, 2019, 40, 1474-1485.	2.5	8
1033	Computational Systems Pharmacology-Target Mapping for Fentanyl-Laced Cocaine Overdose. ACS Chemical Neuroscience, 2019, 10, 3486-3499.	3.5	19
1034	PhyreRisk: A Dynamic Web Application to Bridge Genomics, Proteomics and 3D Structural Data to Guide Interpretation of Human Genetic Variants. Journal of Molecular Biology, 2019, 431, 2460-2466.	4.2	21
1035	Genome-wide identification and comparative analysis of drought-related microRNAs in two maize inbred lines with contrasting drought tolerance by deep sequencing. PLoS ONE, 2019, 14, e0219176.	2.5	40
1036	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. Current Drug Metabolism, 2019, 20, 224-228.	1.2	75
1037	Immune and environmentalâ€driven gene expression during invasion: An ecoâ€immunological application of RNAâ€Seq. Ecology and Evolution, 2019, 9, 6708-6721.	1.9	16
1038	Selective Proteolysis of Î±â€Lactalbumin by Endogenous Enzymes of Human Milk at Acidic pH. Molecular Nutrition and Food Research, 2019, 63, 1900259.	3.3	2
1039	High-Throughput Site-Directed Mutagenesis. Methods in Molecular Biology, 2019, 2025, 281-296.	0.9	2
1040	Mineral-Chitin Composites in Molluscs. Biologically-inspired Systems, 2019, , 57-93.	0.2	3

#	ARTICLE	IF	CITATIONS
1041	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018–2019 Additions to neXtProt and the CAFA3 Challenge. <i>Journal of Proteome Research</i> , 2019, 18, 4154-4166.	3.7	20
1042	CFAP70 mutations lead to male infertility due to severe astheno-teratozoospermia. A case report. <i>Human Reproduction</i> , 2019, 34, 2071-2079.	0.9	43
1043	Classification of human Herpesviridae proteins using Domain-architecture Aware Inference of Orthologs (DAIO). <i>Virology</i> , 2019, 529, 29-42.	2.4	12
1044	ModelBricks—modules for reproducible modeling improving model annotation and provenance. <i>Npj Systems Biology and Applications</i> , 2019, 5, 37.	3.0	13
1045	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019, 36, 2086-2103.	8.9	10
1046	Comparative Genomic Characterization of the Multimammate Mouse <i>Mastomys coucha</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2805-2812.	8.9	6
1047	PhaSePro: the database of proteins driving liquid–liquid phase separation. <i>Nucleic Acids Research</i> , 2020, 48, D360-D367.	14.5	100
1048	Continuous salt stress-induced long non-coding RNAs and DNA methylation patterns in soybean roots. <i>BMC Genomics</i> , 2019, 20, 730.	2.8	56
1049	Estradiol and genistein effects on the sea bass (<i>Dicentrarchus labrax</i>) scales: Transcriptome dataset. <i>Data in Brief</i> , 2019, 27, 104587.	1.0	4
1050	Constructing a Tandem Mass Spectral Library for Forensic Ricin Identification. <i>Journal of Proteome Research</i> , 2019, 18, 3926-3935.	3.7	5
1051	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. <i>Frontiers in Physiology</i> , 2019, 10, 1216.	2.8	8
1052	NMDA Receptor Opening and Closing—Transitions of a Molecular Machine Revealed by Molecular Dynamics. <i>Biomolecules</i> , 2019, 9, 546.	4.0	15
1053	Conotoxin Diversity in the Venom Gland Transcriptome of the Magician™s Cone, <i>Pionoconus magus</i> . <i>Marine Drugs</i> , 2019, 17, 553.	4.6	22
1054	Structure and functional implications of WYL domain-containing bacterial DNA damage response regulator PafBC. <i>Nature Communications</i> , 2019, 10, 4653.	12.8	23
1055	Complete Genome Sequence of the Biocontrol Agent <i>Bacillus velezensis</i> UFLA258 and Its Comparison with Related Species: Diversity within the Commons. <i>Genome Biology and Evolution</i> , 2019, 11, 2818-2823.	2.5	10
1056	Salivary proteome characterization of alcohol and tobacco dependents. <i>Drug and Alcohol Dependence</i> , 2019, 204, 107510.	3.2	17
1057	Genistein and estradiol have common and specific impacts on the sea bass (<i>Dicentrarchus labrax</i>) skin-scale barrier. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 195, 105448.	2.5	7
1058	Unraveling the structural landscape of intra-chain domain interfaces: Implication in the evolution of domain-domain interactions. <i>PLoS ONE</i> , 2019, 14, e0220336.	2.5	5

#	ARTICLE	IF	CITATIONS
1059	A Genocentric Approach to Discovery of Mendelian Disorders. American Journal of Human Genetics, 2019, 105, 974-986.	6.2	30
1060	Genomic Basis of Convergent Island Phenotypes in Boa Constrictors. Genome Biology and Evolution, 2019, 11, 3123-3143.	2.5	14
1061	The sequence and de novo assembly of hog deer genome. Scientific Data, 2019, 6, 180305.	5.3	10
1062	Learning by Doing: A Laboratory Based Training Course on Dispatching Communication System. Journal of Physics: Conference Series, 2019, 1237, 022191.	0.4	0
1063	Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. Nature Genetics, 2019, 51, 1616-1623.	21.4	226
1064	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. Genome Biology, 2019, 20, 224.	8.8	469
1065	Differential proteomics analysis reveals that Azospirillum brasilense (Sp7) promotes virus tolerance in maize and tomato seedlings. European Journal of Plant Pathology, 2019, 155, 1241-1263.	1.7	10
1066	Aerodynamic design and optimization of a high-loaded axial fan stage using a curvature control method. Journal of Mechanical Science and Technology, 2019, 33, 3871-3883.	1.5	4
1067	Mechanism of Action of Non-Synonymous Single Nucleotide Variations Associated with H^+ -Carbonic Anhydrase II Deficiency. Molecules, 2019, 24, 3987.	3.8	18
1068	The Rhododendron Genome and Chromosomal Organization Provide Insight into Shared Whole-Genome Duplications across the Heath Family (Ericaceae). Genome Biology and Evolution, 2019, 11, 3353-3371.	2.5	47
1069	The mutational landscape of quinolone resistance in Escherichia coli. PLoS ONE, 2019, 14, e0224650.	2.5	25
1070	NFE2L3 Controls Colon Cancer Cell Growth through Regulation of DUX4, a CDK1 Inhibitor. Cell Reports, 2019, 29, 1469-1481.e9.	6.4	62
1071	4-(3-Aminoazetidin-1-yl)pyrimidin-2-amines as High-Affinity Non-imidazole Histamine H3Receptor Agonists with in Vivo Central Nervous System Activity. Journal of Medicinal Chemistry, 2019, 62, 10848-10866.	6.4	6
1072	MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. Genome Biology, 2019, 20, 223.	8.8	130
1073	The Empusa code generator and its application to GBOL, an extendable ontology for genome annotation. Scientific Data, 2019, 6, 254.	5.3	13
1074	Engineered Chymotrypsin for Mass Spectrometry-Based Detection of Protein Glycosylation. ACS Chemical Biology, 2019, 14, 2616-2628.	3.4	10
1075	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	4
1076	Amino Acid and Sugar Catabolism in the Marine Bacterium Phaeobacter inhibens DSM 17395 from an Energetic Viewpoint. Applied and Environmental Microbiology, 2019, 85, .	3.1	8

#	ARTICLE	IF	CITATIONS
1077	Sequencing of the black rockfish chromosomal genome provides insight into sperm storage in the female ovary. <i>DNA Research</i> , 2019, 26, 453-464.	3.4	19
1078	Genetic and metabolic signatures of <i>Salmonella enterica</i> subsp. <i>enterica</i> associated with animal sources at the pangenomic scale. <i>BMC Genomics</i> , 2019, 20, 814.	2.8	29
1079	Genetic Support for Longevity-Enhancing Drug Targets: Issues, Preliminary Data, and Future Directions. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, S61-S71.	3.6	4
1080	MitoRibo-Tag Mice Provide a Tool for In Vivo Studies of Mitochondrial Composition. <i>Cell Reports</i> , 2019, 29, 1728-1738.e9.	6.4	24
1081	Mabellini: a genome-wide database for understanding the structural proteome and evaluating prospective antimicrobial targets of the emerging pathogen <i>Mycobacterium abscessus</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	12
1082	The evolution of contact prediction: evidence that contact selection in statistical contact prediction is changing. <i>Bioinformatics</i> , 2020, 36, 1750-1756.	4.1	5
1083	Predicting Drug-Target Interactions With Multi-Label Classification and Label Partitioning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1596-1607.	3.0	34
1084	Structures of a dimodular nonribosomal peptide synthetase reveal conformational flexibility. <i>Science</i> , 2019, 366, .	12.6	99
1085	Understanding allergic multimorbidity within the non-eosinophilic interactome. <i>PLoS ONE</i> , 2019, 14, e0224448.	2.5	12
1086	The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , 2020, 48, D328-D334.	14.5	121
1087	Structural and functional aspects of mannuronic acid-specific PL6 alginate lyase from the human gut microbe <i>Bacteroides cellulosilyticus</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 17915-17930.	3.4	40
1088	Strong Enrichment of Aromatic and Sulfur-Containing Residues in Ligand-Protein Binding Sites. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4921-4928.	5.4	0
1089	Machine learning-based chemical binding similarity using evolutionary relationships of target genes. <i>Nucleic Acids Research</i> , 2019, 47, e128-e128.	14.5	13
1090	The <i>Bacillus subtilis</i> endospore crust: protein interaction network, architecture and glycosylation state of a potential glycoprotein layer. <i>Molecular Microbiology</i> , 2019, 112, 1576-1592.	2.5	19
1091	<p></p>CSF levels of apolipoprotein C1 and autotaxin found to associate with neuropathic pain and fibromyalgia</p>. <i>Journal of Pain Research</i> , 2019, Volume 12, 2875-2889.	2.0	8
1092	Computational and experimental analysis of the glycosylphosphatidylinositol-anchored proteome of the human parasitic nematode <i>Brugia malayi</i> . <i>PLoS ONE</i> , 2019, 14, e0216849.	2.5	4
1093	Protein Engineering of Multi-Modular Transcription Factor Alcohol Dehydrogenase Repressor 1 (Adr1p), a Tool for Dissecting In Vitro Transcription Activation. <i>Biomolecules</i> , 2019, 9, 497.	4.0	0
1094	High-throughput DNA sequencing technologies for water and wastewater analysis. <i>Science Progress</i> , 2019, 102, 351-376.	1.9	16

#	ARTICLE	IF	CITATIONS
1095	Molecular Evolution of Extensively Drug-Resistant (XDR) <i>Pseudomonas aeruginosa</i> Strains From Patients and Hospital Environment in a Prolonged Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 1742.	3.5	10
1096	HERCing: Structural and Functional Relevance of the Large HERC Ubiquitin Ligases. <i>Frontiers in Physiology</i> , 2019, 10, 1014.	2.8	27
1097	Hybrid genome assembly and annotation of <i>Danionella translucida</i> . <i>Scientific Data</i> , 2019, 6, 156.	5.3	21
1098	Construction of complete <i>Tupaia belangeri</i> transcriptome database by whole-genome and comprehensive RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 12372.	3.3	16
1099	Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. <i>Molecular Biology and Evolution</i> , 2019, 36, 2842-2853.	8.9	30
1100	Inhibition of digestive trypsin by plant Kunitz proteins reduces the viability of <i>Spodoptera cosmioides</i> larvae. <i>Annals of Applied Biology</i> , 2019, 175, 336-349.	2.5	11
1101	SAR by Space: Enriching Hit Sets from the Chemical Space. <i>Molecules</i> , 2019, 24, 3096.	3.8	24
1102	Deeper Profiles and Cascaded Recurrent and Convolutional Neural Networks for state-of-the-art Protein Secondary Structure Prediction. <i>Scientific Reports</i> , 2019, 9, 12374.	3.3	62
1103	Raptor genomes reveal evolutionary signatures of predatory and nocturnal lifestyles. <i>Genome Biology</i> , 2019, 20, 181.	8.8	11
1104	Clinical implications of convergent procoagulant toxicity and differential antivenom efficacy in Australian elapid snake venoms. <i>Toxicology Letters</i> , 2019, 316, 171-182.	0.8	20
1105	Assessing the utility of seed coat-specific promoters to engineer cell wall polysaccharide composition of mucilage. <i>Plant Molecular Biology</i> , 2019, 101, 373-387.	3.9	9
1106	ComplexBrowser: A Tool for Identification and Quantification of Protein Complexes in Large-scale Proteomics Datasets. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2324-2334.	3.8	14
1107	Size and structure of the sequence space of repeat proteins. <i>PLoS Computational Biology</i> , 2019, 15, e1007282.	3.2	14
1108	Structure-function guided modeling of chemokine-GPCR specificity for the chemokine XCL1 and its receptor XCR1. <i>Science Signaling</i> , 2019, 12, .	3.6	16
1109	Response mechanism of mine-isolated fungus <i>Aspergillus niger</i> IOC 4687 to copper stress determined by proteomics. <i>Metallomics</i> , 2019, 11, 1558-1566.	2.4	9
1110	Anticancer agents found in environment affect <i>Daphnia</i> at population, individual and molecular levels. <i>Aquatic Toxicology</i> , 2019, 215, 105288.	4.0	12
1111	Diversity of astacin-like metalloproteases identified by transcriptomic analysis in Peruvian <i>Loxosceles laeta</i> spider venom and in vitro activity characterization. <i>Biochimie</i> , 2019, 167, 81-92.	2.6	12
1112	Amyloid-like Assembly Activates a Phosphatase in the Developing <i>Drosophila</i> Embryo. <i>Cell</i> , 2019, 178, 1403-1420.e21.	28.9	9

#	ARTICLE	IF	CITATIONS
1113	Network-guided analysis of hippocampal proteome identifies novel proteins that colocalize with A β in a mice model of early-stage Alzheimer's disease. <i>Neurobiology of Disease</i> , 2019, 132, 104603.	4.4	13
1114	SamPler – a novel method for selecting parameters for gene functional annotation routines. <i>BMC Bioinformatics</i> , 2019, 20, 454.	2.6	5
1115	In Silico Genetics Revealing 5 Mutations in <i>CEBPA</i> Gene Associated With Acute Myeloid Leukemia. <i>Cancer Informatics</i> , 2019, 18, 117693511987081.	1.9	4
1116	Experimental data from flesh quality assessment and shelf life monitoring of high pressure processed European sea bass (<i>Dicentrarchus labrax</i>) fillets. <i>Data in Brief</i> , 2019, 26, 104451.	1.0	7
1117	Determining the pathogenicity of CFTR missense variants: Multiple comparisons of in silico predictors and variant annotation databases. <i>Genetics and Molecular Biology</i> , 2019, 42, 560-570.	1.3	6
1118	GLUT1 and TUBB4 in Glioblastoma Could be Efficacious Targets. <i>Cancers</i> , 2019, 11, 1308.	3.7	25
1119	Dataset of de novo assembly and functional annotation of the transcriptome of blueberry (<i>Vaccinium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	6
1120	Metaproteomics analysis of microbial diversity of human saliva and tongue dorsum in young healthy individuals. <i>Journal of Oral Microbiology</i> , 2019, 11, 1654786.	2.7	27
1121	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
1122	Navigating in vitro bioactivity data by investigating available resources using model compounds. <i>Scientific Data</i> , 2019, 6, 45.	5.3	1
1123	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019, 14, e0206484.	2.5	133
1124	A Convolutional Neural Network System to Discriminate Drug-Target Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1315-1324.	3.0	17
1125	OPA1: 516 unique variants and 831 patients registered in an updated centralized Variome database. <i>Orphanet Journal of Rare Diseases</i> , 2019, 14, 214.	2.7	39
1126	Transcriptomic Signatures of Experimental Alkaloid Consumption in a Poison Frog. <i>Genes</i> , 2019, 10, 733.	2.4	12
1127	Hibernation induces widespread transcriptional remodeling in metabolic tissues of the grizzly bear. <i>Communications Biology</i> , 2019, 2, 336.	4.4	61
1128	Targeted enzyme gene re-positioning: A computational approach for discovering alternative bacterial enzymes for the synthesis of plant-specific secondary metabolites. <i>Metabolic Engineering Communications</i> , 2019, 9, e00102.	3.6	3
1129	Large-Scale Molecular Evolutionary Analysis Uncovers a Variety of Polynucleotide Kinase Clp1 Family Proteins in the Three Domains of Life. <i>Genome Biology and Evolution</i> , 2019, 11, 2713-2726.	2.5	6
1130	Fail-safe genetic codes designed to intrinsically contain engineered organisms. <i>Nucleic Acids Research</i> , 2019, 47, 10439-10451.	14.5	22

#	ARTICLE	IF	CITATIONS
1131	The Evolution of Reverse Gyrase Suggests a Nonhyperthermophilic Last Universal Common Ancestor. <i>Molecular Biology and Evolution</i> , 2019, 36, 2737-2747.	8.9	29
1132	Pathogenic APC Variants in Latvian Familial Adenomatous Polyposis Patients. <i>Medicina (Lithuania)</i> , 2019, 55, 612.	2.0	1
1133	A combined molecular biology and network pharmacology approach to investigate the multi-target mechanisms of Chaihu Shugan San on Alzheimer's disease. <i>Biomedicine and Pharmacotherapy</i> , 2019, 120, 109370.	5.6	57
1134	Temporal changes in transcriptome profile provide insights of White Spot Syndrome Virus infection in <i>Litopenaeus vannamei</i> . <i>Scientific Reports</i> , 2019, 9, 13509.	3.3	32
1135	Novel three-finger toxins from <i>Micrurus dumerilii</i> and <i>Micrurus mipartitus</i> coral snake venoms: Phylogenetic relationships and characterization of Clarkitoxin-I-Mdum. <i>Toxicon</i> , 2019, 170, 85-93.	1.6	9
1136	Functional Metagenomics to Mine Soil Microbiome for Novel Cadmium Resistance Genetic Determinants. <i>Pedosphere</i> , 2019, 29, 298-310.	4.0	19
1137	Arabidopsis immunity regulator EDS1 in a PAD4/SAG101-unbound form is a monomer with an inherently inactive conformation. <i>Journal of Structural Biology</i> , 2019, 208, 107390.	2.8	19
1138	Proteomics and proteoforms: Bottom-up or top-down, how to use high-resolution mass spectrometry to reach the Grail. , 2019, , 529-567.		1
1139	Quantitative Subcellular Proteomics of the Orbitofrontal Cortex of Schizophrenia Patients. <i>Journal of Proteome Research</i> , 2019, 18, 4240-4253.	3.7	21
1140	Evaluation of bottom-up and top-down mass spectrum identifications with different customized protein sequences databases. <i>Bioinformatics</i> , 2020, 36, 1030-1036.	4.1	4
1141	funtpr: identifying protein positions for variation driven functional tuning. <i>Nucleic Acids Research</i> , 2019, 47, e142-e142.	14.5	29
1142	LPI-BLS: Predicting lncRNA-protein interactions with a broad learning system-based stacked ensemble classifier. <i>Neurocomputing</i> , 2019, 370, 88-93.	5.9	48
1143	Proteomic approach underlying the hippocampal neurodegeneration caused by low doses of methylmercury after long-term exposure in adult rats. <i>Metallomics</i> , 2019, 11, 390-403.	2.4	49
1144	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	2.4	8
1145	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	12.8	193
1146	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	12.8	146
1147	Structural insights into the tyrosine phosphorylation-mediated inhibition of SH3 domain-ligand interactions. <i>Journal of Biological Chemistry</i> , 2019, 294, 4608-4620.	3.4	12
1148	P-Mart: Interactive Analysis of Ion Abundance Global Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 1426-1432.	3.7	3

#	ARTICLE	IF	CITATIONS
1149	Investigating <i>Lactococcus lactis</i> MG1363 Response to Phage p2 Infection at the Proteome Level. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 704-714.	3.8	12
1150	Tobramycin reduces key virulence determinants in the proteome of <i>Pseudomonas aeruginosa</i> outer membrane vesicles. <i>PLoS ONE</i> , 2019, 14, e0211290.	2.5	24
1151	Structure and Evolution of Glycogen Branching Enzyme N-Termini From Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 3354.	3.5	23
1152	Mitogenic Signals Stimulate the CREB Coactivator CRTC3 through PP2A Recruitment. <i>IScience</i> , 2019, 11, 134-145.	4.1	16
1153	Identification and Characterization of Canine Ligament Progenitor Cells and Their Extracellular Matrix Niche. <i>Journal of Proteome Research</i> , 2019, 18, 1328-1339.	3.7	7
1154	Study of the whole genome, methylome and transcriptome of <i>Cordyceps militaris</i> . <i>Scientific Reports</i> , 2019, 9, 898.	3.3	17
1155	Towards comprehensive annotation of <i>Drosophila melanogaster</i> enzymes in FlyBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	8
1156	Light Modulates the Physiology of Nonphototrophic Actinobacteria. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	22
1157	Identification, Functional Characterization, and Regulon Prediction of the Zinc Uptake Regulator (zur) of <i>Bacillus anthracis</i> – An Insight Into the Zinc Homeostasis of the Pathogen. <i>Frontiers in Microbiology</i> , 2018, 9, 3314.	3.5	20
1158	Alzheimer's Disease Is Responsible for Progressive Age-Dependent Differential Expression of Various Protein Cascades in Retina of Mice. <i>ACS Chemical Neuroscience</i> , 2019, 10, 2418-2433.	3.5	8
1159	Could advances in representation learning in Artificial Intelligence provide the new paradigm for data integration in drug discovery?. <i>Expert Opinion on Drug Discovery</i> , 2019, 14, 191-194.	5.0	1
1160	Comprehensive catalog of dendritically localized mRNA isoforms from sub-cellular sequencing of single mouse neurons. <i>BMC Biology</i> , 2019, 17, 5.	3.8	50
1161	Proteomes of Paired Human Cerebrospinal Fluid and Plasma: Relation to Blood–Brain Barrier Permeability in Older Adults. <i>Journal of Proteome Research</i> , 2019, 18, 1162-1174.	3.7	40
1162	N-glycoproteins exhibit a positive expression level–evolutionary rate correlation. <i>Journal of Evolutionary Biology</i> , 2019, 32, 390-394.	1.7	4
1163	A neutral evolution test derived from a theoretical amino acid substitution model. <i>Journal of Theoretical Biology</i> , 2019, 467, 31-38.	1.7	5
1164	Re-analysis of the coral <i>Acropora digitifera</i> transcriptome reveals a complex lncRNAs-mRNAs interaction network implicated in Symbiodinium infection. <i>BMC Genomics</i> , 2019, 20, 48.	2.8	13
1165	Cysteine-Rich Receptor-Like Kinase Gene Family Identification in the <i>Phaseolus</i> Genome and Comparative Analysis of Their Expression Profiles Specific to Mycorrhizal and Rhizobial Symbiosis. <i>Genes</i> , 2019, 10, 59.	2.4	30
1166	Phloem Companion Cell-Specific Transcriptomic and Epigenomic Analyses Identify MRF1, a Regulator of Flowering. <i>Plant Cell</i> , 2019, 31, 325-345.	6.6	30

#	ARTICLE	IF	CITATIONS
1167	Architectural Dynamics of CaMKII-Actin Networks. <i>Biophysical Journal</i> , 2019, 116, 104-119.	0.5	23
1168	Promiscuous Ligands from Experimentally Determined Structures, Binding Conformations, and Protein Family-Dependent Interaction Hotspots. <i>ACS Omega</i> , 2019, 4, 1729-1737.	3.5	18
1169	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	4.7	49
1170	Ask1 and Akt act synergistically to promote ROS-dependent regeneration in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007926.	3.5	37
1171	Novel interactions of Selenium Binding Protein family with the PICOT containing proteins AtGRXS14 and AtGRXS16 in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2019, 281, 102-112.	3.6	8
1172	Distinct mechanisms of substrate selectivity in the DRE-TIM metallolyase superfamily: A role for the LeuA dimer regulatory domain. <i>Archives of Biochemistry and Biophysics</i> , 2019, 664, 1-8.	3.0	2
1173	Bi-allelic Mutations in ARMC2 Lead to Severe Astheno-Teratozoospermia Due to Sperm Flagellum Malformations in Humans and Mice. <i>American Journal of Human Genetics</i> , 2019, 104, 331-340.	6.2	113
1174	Identification of human endogenous retrovirus transcripts in Hodgkin Lymphoma cells. <i>Molecular Biology Reports</i> , 2019, 46, 1885-1893.	2.3	13
1175	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 45-56.	3.6	10
1176	Lignocellulolytic characterization and comparative secretome analysis of a <i>Trichoderma erinaceum</i> strain isolated from decaying sugarcane straw. <i>Fungal Biology</i> , 2019, 123, 330-340.	2.5	7
1177	Substrate-assisted mechanism of catalytic hydrolysis of misaminoacylated tRNA required for protein synthesis fidelity. <i>Biochemical Journal</i> , 2019, 476, 719-732.	3.7	3
1178	The (R)-enantiomer of the 6-chromanol derivate SUL-121 improves renal graft perfusion via antagonism of the β_1 -adrenoceptor. <i>Scientific Reports</i> , 2019, 9, 13.	3.3	28
1179	PomBase 2018: user-driven reimplementations of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019, 47, D821-D827.	14.5	157
1180	Molecular mechanisms of temperature acclimation and adaptation in marine diatoms. <i>ISME Journal</i> , 2019, 13, 2415-2425.	9.8	48
1181	Spark-IDPP: high-throughput and scalable prediction of intrinsically disordered protein regions with Spark clusters on the Cloud. <i>Cluster Computing</i> , 2019, 22, 487-508.	5.0	21
1182	Genome-wide identification of MST, SUT and SWEET family sugar transporters in root parasitic angiosperms and analysis of their expression during host parasitism. <i>BMC Plant Biology</i> , 2019, 19, 196.	3.6	26
1183	Parallel Molecular Evolution in Pathways, Genes, and Sites in High-Elevation Hummingbirds Revealed by Comparative Transcriptomics. <i>Genome Biology and Evolution</i> , 2019, 11, 1573-1585.	2.5	49
1184	Identification of Breast Cancer Stem Cell Related Genes Using Functional Cellular Assays Combined With Single-Cell RNA Sequencing in MDA-MB-231 Cells. <i>Frontiers in Genetics</i> , 2019, 10, 500.	2.3	26

#	ARTICLE	IF	CITATIONS
1185	Exploring the systematic effect of N-ε-substituted PxxP motifs on peptoid affinity to ARHGEF5/TIM SH3 domain and its relationship with ARHGEF5/TIM activation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 979-991.	2.6	4
1186	Altered Levels of Proteins and Phosphoproteins, in the Absence of Early Causative Transcriptional Changes, Shape the Molecular Pathogenesis in the Brain of Young Presymptomatic Ki91 SCA3/MJD Mouse. <i>Molecular Neurobiology</i> , 2019, 56, 8168-8202.	4.0	15
1187	Network analysis of hyphae forming proteins in <i>Candida albicans</i> identifies important proteins responsible for pathovirulence in the organism. <i>Heliyon</i> , 2019, 5, e01916.	3.2	11
1188	Phage tail fibre assembly proteins employ a modular structure to drive the correct folding of diverse fibres. <i>Nature Microbiology</i> , 2019, 4, 1645-1653.	13.3	45
1189	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	3.8	14
1190	Characterization of the pleiotropic LysR-type transcription regulator LeuO of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2019, 47, 7363-7379.	14.5	13
1191	Sea Anemone Toxins: A Structural Overview. <i>Marine Drugs</i> , 2019, 17, 325.	4.6	54
1192	Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. <i>Molecular Biology and Evolution</i> , 2019, 36, 2631-2655.	8.9	48
1193	Metagenomic screening of microbiomes identifies pathogen-enriched environments. <i>Environmental Sciences Europe</i> , 2019, 31, .	5.5	6
1194	Protein interactions and consensus clustering analysis uncover insights into herpesvirus virion structure and function relationships. <i>PLoS Biology</i> , 2019, 17, e3000316.	5.6	18
1195	Conformational coupling by trans-phosphorylation in calcium calmodulin dependent kinase II. <i>PLoS Computational Biology</i> , 2019, 15, e1006796.	3.2	5
1196	Consequences of Y chromosome microdeletions beyond male infertility. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 1329-1337.	2.5	29
1197	Locally advanced rectal cancer transcriptomic-based secretome analysis reveals novel biomarkers useful to identify patients according to neoadjuvant chemoradiotherapy response. <i>Scientific Reports</i> , 2019, 9, 8702.	3.3	14
1198	In silico analysis of PFN1 related to amyotrophic lateral sclerosis. <i>PLoS ONE</i> , 2019, 14, e0215723.	2.5	10
1199	Embryonic development of a parthenogenetic vertebrate, the mourning gecko (<i>Lepidodactylus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.8	19
1200	A genome-wide scan for genes under balancing selection in the plant pathogen <i>Ralstonia solanacearum</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 123.	3.2	24
1201	Computational design of a chimeric epitope-based vaccine to protect against <i>Staphylococcus aureus</i> infections. <i>Molecular and Cellular Probes</i> , 2019, 46, 101414.	2.1	28
1202	De Novo Assembly and Annotation of the Larval Transcriptome of Two Spadefoot Toads Widely Divergent in Developmental Rate. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2647-2655.	1.8	5

#	ARTICLE	IF	CITATIONS
1203	Deciphering the intrinsic properties of fungal proteases in optimizing phytopathogenic interaction. <i>Gene</i> , 2019, 711, 143934.	2.2	5
1204	Genetic variant pathogenicity prediction trained using disease-specific clinical sequencing data sets. <i>Genome Research</i> , 2019, 29, 1144-1151.	5.5	19
1205	Conditional Deletion of Eaf1 Induces Murine Prostatic Intraepithelial Neoplasia in Mice. <i>Neoplasia</i> , 2019, 21, 752-764.	5.3	6
1206	Developmental dynamics of lncRNAs across mammalian organs and species. <i>Nature</i> , 2019, 571, 510-514.	27.8	219
1207	The CYPome of the model xenobiotic-biotransforming fungus <i>Cunninghamella elegans</i> . <i>Scientific Reports</i> , 2019, 9, 9240.	3.3	28
1208	The Transcriptome Landscape of Walnut Interspecies Hybrid (<i>Juglans hindsii</i> × <i>Juglans regia</i>) and Regulation of Cambial Activity in Relation to Grafting. <i>Frontiers in Genetics</i> , 2019, 10, 577.	2.3	9
1209	Nrf2 Activation Promotes Lung Cancer Metastasis by Inhibiting the Degradation of Bach1. <i>Cell</i> , 2019, 178, 316-329.e18.	28.9	385
1210	ProSNEx: a web-based application for exploration and analysis of protein structures using network formalism. <i>Nucleic Acids Research</i> , 2019, 47, W471-W476.	14.5	15
1211	Differential analysis of combinatorial protein complexes with ComplexXChange. <i>BMC Bioinformatics</i> , 2019, 20, 300.	2.6	4
1212	In Silico Identification of Potential Inhibitor Against a Fungal Histone Deacetylase, RPD3 from <i>Magnaporthe oryzae</i> . <i>Molecules</i> , 2019, 24, 2075.	3.8	4
1213	A case of Coffinâ€“Siris syndrome with severe congenital heart disease and a novel <i>SMARCA4</i> variant. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003962.	1.2	10
1214	Phosphorylation mapping of laminin Î±1-chain: Kinases in association with active sites. <i>Computational Biology and Chemistry</i> , 2019, 80, 480-497.	2.3	0
1215	Total RNA Analysis of Bacterial Community Structural and Functional Shifts Throughout Vertebrate Decomposition. <i>Journal of Forensic Sciences</i> , 2019, 64, 1707-1719.	1.6	12
1216	Combining nextâ€“generation sequencing and progeny testing for rapid identification of induced recessive and dominant mutations in maize M 2 individuals. <i>Plant Journal</i> , 2019, 100, 851-862.	5.7	7
1217	<i>Salmonella enterica</i> subsp. <i>enterica</i> Seroovar Heidelberg Food Isolates Associated with a Salmonellosis Outbreak Have Enhanced Stress Tolerance Capabilities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	23
1218	What determines host specificity in hyperspecialized plant parasitic nematodes?. <i>BMC Genomics</i> , 2019, 20, 457.	2.8	11
1219	After the Taxonomic Identification Phase: Addressing the Functions of Symbiotic Communities Within Marine Invertebrates. , 2019, , 105-144.		2
1220	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , 2019, 27, 3097-3106.e5.	6.4	47

#	ARTICLE	IF	CITATIONS
1221	A Multidimensional Characterization of E3-Ubiquitin Ligase and Substrate Interaction Network. <i>IScience</i> , 2019, 16, 177-191.	4.1	23
1223	Efficient Approaches for Solving the Large-Scale k-Medoids Problem: Towards Structured Data. <i>Studies in Computational Intelligence</i> , 2019, , 199-219.	0.9	13
1224	Global Proteome and Ubiquitinome Changes in the Soluble and Insoluble Fractions of Q175 Huntington Mice Brains. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1705-1720.	3.8	26
1225	Transcriptome analysis of the model grass <i>Lolium temulentum</i> exposed to green leaf volatiles. <i>BMC Plant Biology</i> , 2019, 19, 222.	3.6	15
1226	Leveraging genetic interactions for adverse drug-drug interaction prediction. <i>PLoS Computational Biology</i> , 2019, 15, e1007068.	3.2	18
1227	Molecular mechanisms involved in drug-induced liver injury caused by urate-lowering Chinese herbs: A network pharmacology study and biology experiments. <i>PLoS ONE</i> , 2019, 14, e0216948.	2.5	20
1228	Five-Membered α -Heterocyclic Scaffolds as Novel Amino Bioisosteres at β -Aminobutyric Acid (GABA) Type A Receptors and GABA Transporters. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 5797-5809.	6.4	20
1229	Genomic Locus of a <i>Penicillium crustosum</i> Pigment as an Integration Site for Secondary Metabolite Gene Expression. <i>ACS Chemical Biology</i> , 2019, 14, 1227-1234.	3.4	13
1230	MHCSeqNet: a deep neural network model for universal MHC binding prediction. <i>BMC Bioinformatics</i> , 2019, 20, 270.	2.6	56
1231	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	2.5	27
1232	Exploiting orthology and de novo transcriptome assembly to refine target sequence information. <i>BMC Medical Genomics</i> , 2019, 12, 69.	1.5	2
1233	Diverse spinal commissural neuron populations revealed by fate mapping and molecular profiling using a novel Robo3 Cre mouse. <i>Journal of Comparative Neurology</i> , 2019, 527, 2948-2972.	1.6	12
1234	Modeling post-translational modifications and cancer-associated mutations that impact the heterochromatin protein 1-importin heterodimers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 904-916.	2.6	5
1235	Type IV collagen. , 2019, , 37-49.		16
1236	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	8.1	518
1237	Kalium 2.0, a comprehensive database of polypeptide ligands of potassium channels. <i>Scientific Data</i> , 2019, 6, 73.	5.3	28
1238	Plasmodium pseudo-Tyrosine Kinase-like binds PP1 and SERA5 and is exported to host erythrocytes. <i>Scientific Reports</i> , 2019, 9, 8120.	3.3	9
1239	Circulating Levels of Interferon Regulatory Factor-5 Associates With Subgroups of Systemic Lupus Erythematosus Patients. <i>Frontiers in Immunology</i> , 2019, 10, 1029.	4.8	11

#	ARTICLE	IF	CITATIONS
1240	Development of Allosteric BRAF Peptide Inhibitors Targeting the Dimer Interface of BRAF. <i>ACS Chemical Biology</i> , 2019, 14, 1471-1480.	3.4	34
1241	Systematic Analysis of Metabolic Pathway Distributions of Bacterial Energy Reserves. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2489-2496.	1.8	9
1242	HNCDB: An Integrated Gene and Drug Database for Head and Neck Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 371.	2.8	7
1243	Kinase Atlas: Druggability Analysis of Potential Allosteric Sites in Kinases. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 6512-6524.	6.4	52
1244	WDSPdb: an updated resource for WD40 proteins. <i>Bioinformatics</i> , 2019, 35, 4824-4826.	4.1	18
1245	Analysis of hereditary cancer syndromes by using a panel of genes: novel and multiple pathogenic mutations. <i>BMC Cancer</i> , 2019, 19, 535.	2.6	77
1246	Exploring the overlapping binding sites of ifenprodil and EVT 101 in GluN2B-containing NMDA receptors using novel chicken embryo forebrain cultures and molecular modeling. <i>Pharmacology Research and Perspectives</i> , 2019, 7, e00480.	2.4	9
1247	Flavin secretion of <i>Clostridium acetobutylicum</i> in a bioelectrochemical system - Is an iron limitation involved?. <i>Bioelectrochemistry</i> , 2019, 129, 242-250.	4.6	13
1248	A missense mutation (p.Tyr452Cys) in the CAD gene compromises reproductive success in French Normande cattle. <i>Journal of Dairy Science</i> , 2019, 102, 6340-6356.	3.4	21
1249	Dynamic expression of tRNA-derived small RNAs define cellular states. <i>EMBO Reports</i> , 2019, 20, e47789.	4.5	100
1250	Overproduction of single cell oil from xylose rich sugarcane bagasse hydrolysate by an engineered oleaginous yeast <i>Rhodotorula mucilaginosa</i> ILPL32. <i>Fuel</i> , 2019, 254, 115653.	6.4	17
1251	Decoding the human serum interactome of snake-derived antimicrobial peptide Ctn[15-34]: Toward an explanation for unusually long half-life. <i>Journal of Proteomics</i> , 2019, 204, 103372.	2.4	10
1252	Alteration of Proteomes in First-Generation Cultures of <i>Bacillus pumilus</i> Spores Exposed to Outer Space. <i>MSystems</i> , 2019, 4, .	3.8	8
1253	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	13.3	170
1254	A novel derivative of artemisinin inhibits cell proliferation and metastasis via down-regulation of cathepsin K in breast cancer. <i>European Journal of Pharmacology</i> , 2019, 858, 172382.	3.5	23
1255	Mutational landscape of Zika virus strains worldwide and its structural impact on proteins. <i>Gene</i> , 2019, 708, 57-62.	2.2	6
1256	Halogens in Protein-Ligand Binding Mechanism: A Structural Perspective. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9341-9356.	6.4	106
1257	Network Integrative Genomic and Transcriptomic Analysis of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains Identifies Genes for Antibiotic Resistance and Virulence. <i>MSystems</i> , 2019, 4, .	3.8	15

#	ARTICLE	IF	CITATIONS
1258	DP-BINDER: machine learning model for prediction of DNA-binding proteins by fusing evolutionary and physicochemical information. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 645-658.	2.9	50
1259	Molecular modelling studies on the interactions of 7-methoxytacrine-4-pyridinealdoxime with VX-inhibited human acetylcholinesterase. A near attack approach to assess different spacer-lengths. <i>Chemico-Biological Interactions</i> , 2019, 307, 195-205.	4.0	5
1260	Simple ClinVar: an interactive web server to explore and retrieve gene and disease variants aggregated in ClinVar database. <i>Nucleic Acids Research</i> , 2019, 47, W99-W105.	14.5	51
1261	HOT or not: examining the basis of high-occupancy target regions. <i>Nucleic Acids Research</i> , 2019, 47, 5735-5745.	14.5	41
1262	The Impact of Pyroglutamate:Sulfolobus acidocaldarius Has a Growth Advantage over Saccharolobus solfataricus in Glutamate-Containing Media. <i>Archaea</i> , 2019, 2019, 1-9.	2.3	3
1263	Genomic Characterization of Arcobacter butzleri Isolated From Shellfish: Novel Insight Into Antibiotic Resistance and Virulence Determinants. <i>Frontiers in Microbiology</i> , 2019, 10, 670.	3.5	44
1264	Predicting protein sub-Golgi locations by combining functional domain enrichment scores with pseudo-amino acid compositions. <i>Journal of Theoretical Biology</i> , 2019, 473, 38-43.	1.7	17
1265	Biosynthesis of Long Chain Alkyl Diols and Long Chain Alkenols in <i>Nannochloropsis</i> spp. (Eustigmatophyceae). <i>Plant and Cell Physiology</i> , 2019, 60, 1666-1682.	3.1	9
1266	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	5.5	111
1267	Identification of a potential allosteric site of Golgi α -mannosidase II using computer-aided drug design. <i>PLoS ONE</i> , 2019, 14, e0216132.	2.5	5
1268	Estudio proteómico 2DE-DIGE en plasma sanguíneo de pacientes en etapa infantil con leucemia linfoblástica aguda. <i>Revista Colombiana De Química</i> , 2019, 48, 5-15.	0.4	1
1269	A Functional Agonist of Insect Olfactory Receptors: Behavior, Physiology and Structure. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 134.	3.7	15
1271	Introducing a New Model of Sweet Taste Receptor, a Class C G-protein Coupled Receptor (C GPCR). <i>Cell Biochemistry and Biophysics</i> , 2019, 77, 227-243.	1.8	11
1272	Effects of temperature changes in the transcriptional profile of the emerging fish pathogen <i>Francisella noatunensis</i> subsp. <i>orientalis</i> . <i>Microbial Pathogenesis</i> , 2019, 133, 103548.	2.9	4
1273	Charging the code " tRNA modification complexes. <i>Current Opinion in Structural Biology</i> , 2019, 55, 138-146.	5.7	45
1274	The thermophilic biomass-degrading bacterium <i>Caldicellulosiruptor bescii</i> utilizes two enzymes to oxidize glyceraldehyde 3-phosphate during glycolysis. <i>Journal of Biological Chemistry</i> , 2019, 294, 9995-10005.	3.4	18
1275	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. <i>Environmental Microbiology</i> , 2019, 21, 3627-3637.	3.8	69
1276	BRCA1 and BRCA2 specific in silico tools for variant interpretation in the CAGI 5 ENIGMA challenge. <i>Human Mutation</i> , 2019, 40, 1593-1611.	2.5	11

#	ARTICLE	IF	CITATIONS
1277	Systematic profiling of SH3-mediated Tauâ€“Partner interaction network in Alzheimer's disease by integrating in silico analysis and in vitro assay. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 90, 265-272.	2.4	6
1278	Optimized Cross-Linking Mass Spectrometry for in Situ Interaction Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 2545-2558.	3.7	32
1279	Local and regional scale habitat heterogeneity contribute to genetic adaptation in a commercially important marine mollusc (<i>Haliotis rubra</i>) from southeastern Australia. <i>Molecular Ecology</i> , 2019, 28, 3053-3072.	3.9	32
1280	CEâ€“MS-based urinary biomarkers to distinguish non-significant from significant prostate cancer. <i>British Journal of Cancer</i> , 2019, 120, 1120-1128.	6.4	25
1281	INGA 2.0: improving protein function prediction for the dark proteome. <i>Nucleic Acids Research</i> , 2019, 47, W373-W378.	14.5	24
1282	Variation in pigmentation gene expression is associated with distinct aposematic color morphs in the poison frog <i>Dendrobates auratus</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 85.	3.2	25
1283	Detection of Tumor NTRK Gene Fusions to Identify Patients Who May Benefit from Tyrosine Kinase (TRK) Inhibitor Therapy. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 553-571.	2.8	161
1284	Accurate peptide fragmentation predictions allow data driven approaches to replace and improve upon proteomics search engine scoring functions. <i>Bioinformatics</i> , 2019, 35, 5243-5248.	4.1	52
1285	Bacterial Community Succession, Transmigration, and Differential Gene Transcription in a Controlled Vertebrate Decomposition Model. <i>Frontiers in Microbiology</i> , 2019, 10, 745.	3.5	25
1286	Deep learning of the back-splicing code for circular RNA formation. <i>Bioinformatics</i> , 2019, 35, 5235-5242.	4.1	37
1287	CaverDock: a molecular docking-based tool to analyse ligand transport through protein tunnels and channels. <i>Bioinformatics</i> , 2019, 35, 4986-4993.	4.1	51
1288	Genome Sequence of â€œ <i>Candidatus</i> Serratia symbioticaâ€“Strain IS, a Facultative Bacterial Symbiont of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	9
1289	Formylated N-terminal methionine is absent from the <i>Mycoplasma hyopneumoniae</i> proteome: Implications for translation initiation. <i>International Journal of Medical Microbiology</i> , 2019, 309, 288-298.	3.6	2
1290	GROWTH POLE RING protein forms a 200-nm-diameter ring structure essential for polar growth and rod shape in <i>Agrobacterium tumefaciens</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10962-10967.	7.1	25
1291	Molecular modeling studies on the interactions of 7-methoxytacrine-4-pyridinealdoxime, 4-PA, 2-PAM, and obidoxime with VX-inhibited human acetylcholinesterase: a near attack conformation approach. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2019, 34, 1018-1029.	5.2	18
1292	Cell Cycle Kinase Polo Is Controlled by a Widespread 3â€² Untranslated Region Regulatory Sequence in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	6
1293	Biomolecular Data Resources: Bioinformatics Infrastructure for Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 199-222.	6.5	8
1294	Automated assessment of biological database assertions using the scientific literature. <i>BMC Bioinformatics</i> , 2019, 20, 216.	2.6	3

#	ARTICLE	IF	CITATIONS
1295	CRISPR/Cas9-mediated mutagenesis of phytoene desaturase in diploid and octoploid strawberry. <i>Plant Methods</i> , 2019, 15, 45.	4.3	92
1296	Impacts of cellulase deactivation at the moving air-liquid interface on cellulose conversions at low enzyme loadings. <i>Biotechnology for Biofuels</i> , 2019, 12, 96.	6.2	28
1297	Intrinsically Disordered Linkers Impart Processivity on Enzymes by Spatial Confinement of Binding Domains. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2119.	4.1	15
1298	Mechanism and impact of catecholamine conversion by <i>Vibrio cholerae</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 478-487.	1.0	8
1299	Engineering enzyme access tunnels. <i>Biotechnology Advances</i> , 2019, 37, 107386.	11.7	128
1300	Can Predicted Protein 3D Structures Provide Reliable Insights into whether Missense Variants Are Disease Associated?. <i>Journal of Molecular Biology</i> , 2019, 431, 2197-2212.	4.2	344
1301	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. <i>Nature Communications</i> , 2019, 10, 1847.	12.8	55
1302	Structural basis of ligand recognition at the human MT1 melatonin receptor. <i>Nature</i> , 2019, 569, 284-288.	27.8	140
1303	<i>MFSD8</i> gene mutations; evidence for phenotypic heterogeneity. <i>Ophthalmic Genetics</i> , 2019, 40, 141-145.	1.2	14
1304	Graph-based data integration from bioactive peptide databases of pharmaceutical interest: toward an organized collection enabling visual network analysis. <i>Bioinformatics</i> , 2019, 35, 4739-4747.	4.1	39
1305	<i>Ureaplasma diversum</i> protein interaction networks: evidence of horizontal gene transfer and evolution of reduced genomes among <i>Mollicutes</i> . <i>Canadian Journal of Microbiology</i> , 2019, 65, 596-612.	1.7	3
1306	Genetic Etiologies, Diagnosis, and Treatment of Tuberous Sclerosis Complex. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 217-240.	6.2	108
1307	Novel Tetrahydroquinazolinamines as Selective Histamine 3 Receptor Antagonists for the Treatment of Obesity. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 4638-4655.	6.4	12
1308	Investigation of the estuarine stonefish (<i>Synanceia horrida</i>) venom composition. <i>Journal of Proteomics</i> , 2019, 201, 12-26.	2.4	14
1309	tRNA Fragments Show Intertwining with mRNAs of Specific Repeat Content and Have Links to Disparities. <i>Cancer Research</i> , 2019, 79, 3034-3049.	0.9	72
1310	In silico analysis of the V66M variant of human BDNF in psychiatric disorders: An approach to precision medicine. <i>PLoS ONE</i> , 2019, 14, e0215508.	2.5	24
1311	Computational Biology Approach in Management of Big Data of Healthcare Sector. , 2019, , 247-267.		4
1312	Retrosynthetic design of metabolic pathways to chemicals not found in nature. <i>Current Opinion in Systems Biology</i> , 2019, 14, 82-107.	2.6	84

#	ARTICLE	IF	CITATIONS
1313	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	3.0	86
1314	Engineering of vitamin prototrophy in <i>Clostridium ljungdahlii</i> and <i>Clostridium autoethanogenum</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4633-4648.	3.6	25
1315	Deciphering the three-domain architecture in schlafens and the structures and roles of human schlafen12 and serpinB12 in transcriptional regulation. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 90, 59-76.	2.4	9
1316	The Plant <sc>PTM</sc> Viewer, a central resource for exploring plant protein modifications. <i>Plant Journal</i> , 2019, 99, 752-762.	5.7	97
1317	Phosphorylation mapping of Laminin Î²1-chain: Kinases in association with active sites. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	1
1318	PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S126-S140.	3.8	43
1319	Combination of gallium(<sc>iii</sc>) with acetate for combating antibiotic resistant <i>Pseudomonas aeruginosa</i>. <i>Chemical Science</i> , 2019, 10, 6099-6106.	7.4	52
1320	Hydrophobic and Bulk Polymerizable Protein-Based Elastomers Compatibilized with Surfactants. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 9103-9111.	6.7	6
1321	Bioinformatic and mutational studies of related toxin-antitoxin pairs in <i>Mycobacterium tuberculosis</i> predict and identify key functional residues. <i>Journal of Biological Chemistry</i> , 2019, 294, 9048-9063.	3.4	27
1322	Mass Spectrometry-Based Proteomics Analyses Using the OpenProt Database to Unveil Novel Proteins Translated from Non-Canonical Open Reading Frames. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	8
1323	Comparative Analysis of the Transcriptome and Proteome during Mouse Placental Development. <i>Journal of Proteome Research</i> , 2019, 18, 2088-2099.	3.7	21
1324	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	2.2	16
1325	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. <i>Future Generation Computer Systems</i> , 2019, 99, 73-85.	7.5	80
1326	Genes associated with Parkinson's disease respond to increasing polychlorinated biphenyl levels in the blood of healthy females. <i>Environmental Pollution</i> , 2019, 250, 107-117.	7.5	3
1327	Comprehensive Review of Human <i>Plasmodium falciparum</i> -Specific CD8+ T Cell Epitopes. <i>Frontiers in Immunology</i> , 2019, 10, 397.	4.8	19
1328	Clinical and Genetic Investigation of Premature Ovarian Insufficiency Cases from Turkey. <i>Journal of Gynecology Obstetrics and Human Reproduction</i> , 2019, 48, 817-823.	1.3	6
1329	Extended Multitarget Pharmacology of Anticancer Drugs. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3006-3017.	5.4	17
1330	Network reconstruction from infection cascades. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20180844.	3.4	22

#	ARTICLE	IF	CITATIONS
1331	The bumble bee microbiome increases survival of bees exposed to selenate toxicity. <i>Environmental Microbiology</i> , 2019, 21, 3417-3429.	3.8	47
1332	AnABlast: Re-searching for Protein-Coding Sequences in Genomic Regions. <i>Methods in Molecular Biology</i> , 2019, 1962, 207-214.	0.9	4
1333	Choosing the Best Gene Predictions with GeneValidator. <i>Methods in Molecular Biology</i> , 2019, 1962, 257-267.	0.9	0
1334	Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. <i>Methods in Molecular Biology</i> , 2019, 1962, 29-51.	0.9	66
1335	Shared Signature Dynamics Tempered by Local Fluctuations Enables Fold Adaptability and Specificity. <i>Molecular Biology and Evolution</i> , 2019, 36, 2053-2068.	8.9	45
1336	A comprehensive in silico analysis of sortase superfamily. <i>Journal of Microbiology</i> , 2019, 57, 431-443.	2.8	18
1337	Chicken Organic Anion-Transporting Polypeptide 1A2, a Novel Avian Hepatitis E Virus (HEV) ORF2-Interacting Protein, Is Involved in Avian HEV Infection. <i>Journal of Virology</i> , 2019, 93, .	3.4	5
1338	The Patchy Distribution of Restrictionâ€“Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. <i>Genes</i> , 2019, 10, 233.	2.4	27
1339	In Silico Analysis of Homologous Heterodimers of Cruzipain-Chagasin from Structural Models Built by Homology. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1320.	4.1	1
1340	Structural investigation of Rett-inducing MeCP2 mutations. <i>Genes and Diseases</i> , 2019, 6, 31-34.	3.4	5
1341	Nanotopography-based engineering of retroviral DNA integration patterns. <i>Nanoscale</i> , 2019, 11, 5693-5704.	5.6	3
1342	Lysosomal targeting of the ABC transporter TAPL is determined by membrane-localized charged residues. <i>Journal of Biological Chemistry</i> , 2019, 294, 7308-7323.	3.4	15
1343	RIBOi: a database for ribosome-interacting proteins. <i>Acta Biochimica Et Biophysica Sinica</i> , 2019, 51, 441-443.	2.0	1
1344	Characterizing emulsion properties of microalgal and cyanobacterial protein isolates. <i>Algal Research</i> , 2019, 39, 101471.	4.6	33
1345	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019, 431, 1650-1670.	4.2	41
1346	<i>CYP21A2</i> Gene Pathogenic Variants: A Multicenter Study on Genotypeâ€“Phenotype Correlation from a Portuguese Pediatric Cohort. <i>Hormone Research in Paediatrics</i> , 2019, 91, 33-45.	1.8	11
1347	Dissecting FOXP2 Oligomerization and DNA Binding. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 7662-7667.	13.8	26
1348	Cysteineâ€“Rich Antifungal Proteins from Filamentous Fungi are Promising Bioactive Natural Compounds in Antiâ€“<i>Candida</i> Therapy. <i>Israel Journal of Chemistry</i> , 2019, 59, 360-370.	2.3	19

#	ARTICLE	IF	CITATIONS
1349	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. <i>Journal of Molecular Biology</i> , 2019, 431, 2477-2484.	4.2	32
1350	Residue co-evolution helps predict interaction sites in α -helical membrane proteins. <i>Journal of Structural Biology</i> , 2019, 206, 156-169.	2.8	17
1351	Significantly different effects of tetrahydroberberrubine enantiomers on dopamine D1/D2 receptors revealed by experimental study and integrated in silico simulation. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 447-459.	2.9	6
1352	A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome. <i>Cell Reports</i> , 2019, 26, 2622-2635.e5.	6.4	57
1353	Automated exploration of gene ontology term and pathway networks with ClueGO-REST. <i>Bioinformatics</i> , 2019, 35, 3864-3866.	4.1	48
1354	Functional protein representations from biological networks enable diverse cross-species inference. <i>Nucleic Acids Research</i> , 2019, 47, e51-e51.	14.5	23
1355	One-step bioconversion of hemicellulose polymers to rhamnolipids with <i>Cellvibrio japonicus</i> : A proof-of-concept for a potential host strain in future bioeconomy. <i>GCB Bioenergy</i> , 2019, 11, 260-268.	5.6	17
1356	A Comparative Study of Cluster Detection Algorithms in Protein-Protein Interaction for Drug Target Discovery and Drug Repurposing. <i>Frontiers in Pharmacology</i> , 2019, 10, 109.	3.5	26
1357	In Silico Modeling of FDA-Approved Drugs for Discovery of Anticandida Agents: A Drug-Repurposing Approach. , 2019, , 463-526.		8
1358	In Silico Databases and Tools for Drug Repurposing. , 2019, , 703-742.		7
1359	Target discovery of chlorogenic acid derivatives from the flower buds of <i>Lonicera macranthoides</i> and their MAO B inhibitory mechanism. <i>FÄ-toterapÄ-t</i> , 2019, 134, 297-304.	2.2	19
1360	Positive-unlabelled learning of glycosylation sites in the human proteome. <i>BMC Bioinformatics</i> , 2019, 20, 112.	2.6	60
1361	Genetic variants of <i>VWF</i> gene in type 2 von Willebrand disease. <i>Haemophilia</i> , 2019, 25, e78-e85.	2.1	7
1362	Identification of the OXA-48 Carbapenemase Family by Use of Tryptic Peptides and Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	15
1363	Integrative analysis of Paneth cell proteomic and transcriptomic data from intestinal organoids reveals functional processes dependent on autophagy. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	2.4	20
1364	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. <i>Scientific Reports</i> , 2019, 9, 2249.	3.3	14
1365	Ant behaviour and brain gene expression of defending hosts depend on the ecological success of the intruding social parasite. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180192.	4.0	15
1366	Free Accessible Databases as a Source of Information about Food Components and Other Compounds with Anticancer Activity—Brief Review. <i>Molecules</i> , 2019, 24, 789.	3.8	6

#	ARTICLE	IF	CITATIONS
1367	AAV9-TAZ Gene Replacement Ameliorates Cardiac TMT Proteomic Profiles in a Mouse Model of Barth Syndrome. <i>Molecular Therapy - Methods and Clinical Development</i> , 2019, 13, 167-179.	4.1	17
1368	Ontology based text mining of gene-phenotype associations: application to candidate gene prediction. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	10
1369	Gene expression patterns indicate that a high-fatâ€“high-carbohydrate diet causes mitochondrial dysfunction in fish. <i>Genome</i> , 2019, 62, 53-67.	2.0	5
1370	Dissecting FOXP2 Oligomerization and DNA Binding. <i>Angewandte Chemie</i> , 2019, 131, 7744-7749.	2.0	6
1371	A TonB-dependent transporter is required for secretion of protease PopC across the bacterial outer membrane. <i>Nature Communications</i> , 2019, 10, 1360.	12.8	43
1372	Targeted interplay between bacterial pathogens and host autophagy. <i>Autophagy</i> , 2019, 15, 1620-1633.	9.1	38
1373	Proteomic and Bioinformatic Analyses for the Identification of Proteins With Low Allergenic Potential for Hazard Assessment. <i>Toxicological Sciences</i> , 2019, 170, 210-222.	3.1	17
1374	Asymmetric distribution of glucose transporter mRNA provides a growth advantage in yeast. <i>EMBO Journal</i> , 2019, 38, .	7.8	9
1375	A Molecular Modeling Approach to Identify Novel Inhibitors of the Major Facilitator Superfamily of Efflux Pump Transporters. <i>Antibiotics</i> , 2019, 8, 25.	3.7	32
1376	Electrostatics of Tau Protein by Molecular Dynamics. <i>Biomolecules</i> , 2019, 9, 116.	4.0	23
1377	The Light and Dark Sides of Virtual Screening: What Is There to Know?. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1375.	4.1	160
1378	Identification of genes involved in shea butter biosynthesis from <i>Vitellaria paradoxa</i> fruits through transcriptomics and functional heterologous expression. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3727-3736.	3.6	19
1379	Deciphering Within-Host Microevolution of <i>Mycobacterium tuberculosis</i> through Whole-Genome Sequencing: the Phenotypic Impact and Way Forward. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	6.6	43
1380	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2019, 36, 1172-1186.	8.9	13
1381	Mammary Gland Transcriptome and Proteome Modifications by Nutrient Restriction in Early Lactation Holstein Cows Challenged with Intra-Mammary Lipopolysaccharide. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1156.	4.1	13
1382	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	1.0	3
1383	Insights into Substrate and Inhibitor Selectivity among Human GLUT Transporters through Comparative Modeling and Molecular Docking. <i>ACS Omega</i> , 2019, 4, 4748-4760.	3.5	7
1384	Cell Shape and Population Migration Are Distinct Steps of <i>Proteus mirabilis</i> Swarming That Are Decoupled on High-Percentage Agar. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	22

#	ARTICLE	IF	CITATIONS
1385	Comprehensive Virulence Gene Profiling of Bovine Non- <i>aureus</i> Staphylococci Based on Whole-Genome Sequencing Data. <i>MSystems</i> , 2019, 4, .	3.8	32
1386	Investigation on salt-response mechanisms in <i>Arabidopsis thaliana</i> from UniProt protein knowledgebase. <i>Journal of Plant Interactions</i> , 2019, 14, 21-29.	2.1	17
1387	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	27.8	901
1388	Cu Transport by the Extended Family of CcoA-like Transporters (CalT) in Proteobacteria. <i>Scientific Reports</i> , 2019, 9, 1208.	3.3	10
1389	MorCVD: A Unified Database for Host-Pathogen Protein-Protein Interactions of Cardiovascular Diseases Related to Microbes. <i>Scientific Reports</i> , 2019, 9, 4039.	3.3	10
1390	PIRSitePredict for protein functional site prediction using position-specific rules. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	5
1391	Validation and Stabilization of a Prophage Lysin of <i>Clostridium perfringens</i> by Using Yeast Surface Display and Coevolutionary Models. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	16
1392	Differential Expression of mRNAs in the Brain Tissues of Patients with Alzheimer's Disease Based on GEO Expression Profile and Its Clinical Significance. <i>BioMed Research International</i> , 2019, 2019, 1-9.	1.9	31
1393	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. <i>PLoS Computational Biology</i> , 2019, 15, e1006848.	3.2	46
1394	Secreted frizzled related protein is a target of PaxB and plays a role in aquiferous system development in the freshwater sponge, <i>Ephydatia muelleri</i> . <i>PLoS ONE</i> , 2019, 14, e0212005.	2.5	8
1395	Probabilistic variable-length segmentation of protein sequences for discriminative motif discovery (DiMotif) and sequence embedding (ProtVecX). <i>Scientific Reports</i> , 2019, 9, 3577.	3.3	52
1396	Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. <i>Scientific Reports</i> , 2019, 9, 4192.	3.3	27
1397	PTMselect: optimization of protein modifications discovery by mass spectrometry. <i>Scientific Reports</i> , 2019, 9, 4181.	3.3	14
1398	A bacterial display system for effective selection of protein-biotin ligase BirA variants with novel peptide specificity. <i>Scientific Reports</i> , 2019, 9, 4118.	3.3	6
1399	SuCComBase: a manually curated repository of plant sulfur-containing compounds. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	10
1400	Cancer testis antigens in canine histiocytic sarcoma and other malignancies. <i>Veterinary and Comparative Oncology</i> , 2019, 17, 317-328.	1.8	4
1401	How good are pathogenicity predictors in detecting benign variants?. <i>PLoS Computational Biology</i> , 2019, 15, e1006481.	3.2	79
1402	Functional Segments on Intrinsically Disordered Regions in Disease-Related Proteins. <i>Biomolecules</i> , 2019, 9, 88.	4.0	16

#	ARTICLE	IF	CITATIONS
1403	ProtParCon: A Framework for Processing Molecular Data and Identifying Parallel and Convergent Amino Acid Replacements. <i>Genes</i> , 2019, 10, 181.	2.4	4
1404	Snails In Silico: A Review of Computational Studies on the Conopeptides. <i>Marine Drugs</i> , 2019, 17, 145.	4.6	21
1405	Identification and analysis of genes associated with papillary thyroid carcinoma by bioinformatics methods. <i>Bioscience Reports</i> , 2019, 39, .	2.4	14
1406	TogoGenome/TogoStanza: modularized Semantic Web genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	6
1407	DAKB-GPCRs: An Integrated Computational Platform for Drug Abuse Related GPCRs. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1283-1289.	5.4	23
1408	Fragment Hits: What do They Look Like and How do They Bind?. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 3381-3394.	6.4	53
1409	Shotgun Proteomics of Human Dentin with Different Prefractionation Methods. <i>Scientific Reports</i> , 2019, 9, 4457.	3.3	34
1410	Parallelism of Chemicostructural Properties between Filgrastim Originator and Three of Its Biosimilar Drugs. <i>Journal of Chemistry</i> , 2019, 2019, 1-15.	1.9	2
1411	CANTATAdb 2.0: Expanding the Collection of Plant Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2019, 1933, 415-429.	0.9	71
1412	Ca ²⁺ -dependent regulation of sodium channels NaV1.4 and NaV1.5 is controlled by the post-IQ motif. <i>Nature Communications</i> , 2019, 10, 1514.	12.8	30
1413	Genomic signatures of G-protein-coupled receptor expansions reveal functional transitions in the evolution of cephalopod signal transduction. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182929.	2.6	9
1414	Curated BLAST for Genomes. <i>MSystems</i> , 2019, 4, .	3.8	13
1415	Chemical synthesis, microbial transformation and biological evaluation of tetrahydroprotoberberines as dopamine D1/D2 receptor ligands. <i>Bioorganic and Medicinal Chemistry</i> , 2019, 27, 2100-2111.	3.0	10
1416	Large-scale proteomic analysis of human brain identifies proteins associated with cognitive trajectory in advanced age. <i>Nature Communications</i> , 2019, 10, 1619.	12.8	144
1417	CBSSD: community-based semantic subgroup discovery. <i>Journal of Intelligent Information Systems</i> , 2019, 53, 265-304.	3.9	11
1418	Conservation analysis showing high variability in the rate of evolution of regeneration-related genes. <i>AIP Conference Proceedings</i> , 2019, , .	0.4	0
1419	Machine learning-assisted directed protein evolution with combinatorial libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8852-8858.	7.1	375
1420	The First Transcriptome Assembly of Yenyuan Stream Salamander (<i>Batrachuperus yenyuanensis</i>) Provides Novel Insights into Its Molecular Evolution. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1529.	4.1	7

#	ARTICLE	IF	CITATIONS
1421	Mapping the diversity of microbial lignin catabolism: experiences from the eLignin database. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3979-4002.	3.6	85
1422	A Tail-Based Mechanism Drives Nucleosome Demethylation by the LSD2/NPAC Multimeric Complex. <i>Cell Reports</i> , 2019, 27, 387-399.e7.	6.4	31
1423	Pathogenic Germ Line Variants in a Patient With Severe Toxicity From Breast Radiotherapy. <i>Clinical Breast Cancer</i> , 2019, 19, e400-e405.	2.4	1
1424	Increased versatility despite reduced molecular complexity: evolution, structure and function of metazoan splicing factor PRPF39. <i>Nucleic Acids Research</i> , 2019, 47, 5867-5879.	14.5	7
1425	A global map of the protein shape universe. <i>PLoS Computational Biology</i> , 2019, 15, e1006969.	3.2	24
1426	Comparative analysis of homologous aminopeptidase PepN from pathogenic and non-pathogenic mycobacteria reveals divergent traits. <i>PLoS ONE</i> , 2019, 14, e0215123.	2.5	5
1427	Gi/o-Protein Coupled Receptors in the Aging Brain. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 89.	3.4	60
1428	The Effect of Molecular Weight on Passage of Proteins Through the Blood-Aqueous Barrier. , 2019, 60, 1461.		9
1429	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. <i>Nature Neuroscience</i> , 2019, 22, 691-699.	14.8	118
1430	Defining the <scp>RNA</scp> interactome by total <scp>RNA</scp> associated protein purification. <i>Molecular Systems Biology</i> , 2019, 15, e8689.	7.2	114
1431	Continuing occurrence of vancomycin resistance determinants in Danish pig farms 20 years after removing exposure to avoparcin. <i>Veterinary Microbiology</i> , 2019, 232, 84-88.	1.9	11
1432	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. <i>Nucleic Acids Research</i> , 2019, 47, 5293-5306.	14.5	49
1433	Trimeric autotransporter adhesins in <i>Acinetobacter baumannii</i> , coincidental evolution at work. <i>Infection, Genetics and Evolution</i> , 2019, 71, 116-127.	2.3	24
1434	Relationship between conformation shift and disease related variation sites in ATP-binding cassette transporter proteins. <i>Biophysics and Physicobiology</i> , 2019, 16, 68-79.	1.0	4
1435	Homotypic and heterotypic trans-assembly of human Rab-family small GTPases in reconstituted membrane tethering. <i>Journal of Biological Chemistry</i> , 2019, 294, 7722-7739.	3.4	16
1436	Structural and Computational Characterization of Disease-Related Mutations Involved in Protein-Protein Interfaces. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1583.	4.1	17
1437	Protein Structure Annotations. , 2019, , 201-234.		5
1438	Sweet and Sour Ehrlichia: Glycoproteomics and Phosphoproteomics Reveal New Players in Ehrlichia ruminantium Physiology and Pathogenesis. <i>Frontiers in Microbiology</i> , 2019, 10, 450.	3.5	8

#	ARTICLE	IF	CITATIONS
1439	Adaptations of <i>Alteromonas</i> sp. 76-1 to Polysaccharide Degradation: A CAZyme Plasmid for Ulvan Degradation and Two Alginolytic Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 504.	3.5	30
1440	Genetic and physical interactions between the organellar mechanosensitive ion channel homologs <scp>MSL</scp>1, <scp>MSL</scp>2, and <scp>MSL</scp>3 reveal a role for interâ€œorganellar communication in plant development. <i>Plant Direct</i> , 2019, 3, e00124.	1.9	18
1441	Plasma-sensitive <i>Escherichia coli</i> mutants reveal plasma resistance mechanisms. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20180846.	3.4	15
1442	An Acid Up-Regulated Surface Protein of <i>Lactobacillus paracasei</i> Strain GCRL 46 is Phylogenetically Related to the Secreted Glucan- (GpbB) and Immunoglobulin-Binding (SibA) Protein of Pathogenic <i>Streptococci</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1610.	4.1	8
1443	Methods for Systematic Identification of Membrane Proteins for Specific Capture of Cancer-Derived Extracellular Vesicles. <i>Cell Reports</i> , 2019, 27, 255-268.e6.	6.4	38
1444	High-Quality Draft Genome Sequence of the Microcolonial Black Fungus <i>Aeminium ludgeri</i> DSM 106916. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
1445	Genome Sequencing and Transcriptome Analysis of the Hop Downy Mildew Pathogen<i>Pseudoperonospora humuli</i>Reveal Species-Specific Genes for Molecular Detection. <i>Phytopathology</i> , 2019, 109, 1354-1366.	2.2	43
1446	Immunoscreening of the <i>M. tuberculosis</i> F15/LAM4/KZN secretome library against TB patientsâ€™ sera identifies unique active- and latent-TB specific biomarkers. <i>Tuberculosis</i> , 2019, 115, 161-170.	1.9	9
1447	Changes in protein expression in mussels <i>Mytilus galloprovincialis</i> dietarily exposed to PVP/PEI coated silver nanoparticles at different seasons. <i>Aquatic Toxicology</i> , 2019, 210, 56-68.	4.0	26
1448	A galling insect activates plant reproductive programs during gall development. <i>Scientific Reports</i> , 2019, 9, 1833.	3.3	54
1449	Immunomics Datasets and Tools: To Identify Potential Epitope Segments for Designing Chimeric Vaccine Candidate to Cervix Papilloma. <i>Data</i> , 2019, 4, 31.	2.3	4
1450	The structural features of <i>Acetobacterium</i> Âwoodii Fâ€•ATP synthase reveal the importance of the unique subunit Î³â€™loop in Na + translocation and ATP synthesis. <i>FEBS Journal</i> , 2019, 286, 1894-1907.	4.7	4
1451	Insights into Body Size Evolution: A Comparative Transcriptome Study on Three Species of Asian Sisoridae Catfish. <i>International Journal of Molecular Sciences</i> , 2019, 20, 944.	4.1	4
1452	Origins and clinical relevance of proteoforms in pediatric malignancies. <i>Expert Review of Proteomics</i> , 2019, 16, 185-200.	3.0	12
1453	Establishing synthesis pathwayâ€™host compatibility via enzyme solubility. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1405-1416.	3.3	6
1454	Caspase-4 disaggregates lipopolysaccharide micelles via LPS-CARD interaction. <i>Scientific Reports</i> , 2019, 9, 826.	3.3	24
1455	Ulcerative colitis: functional analysis of the in-depth proteome. <i>Clinical Proteomics</i> , 2019, 16, 4.	2.1	25
1456	Recent Progress in Structure-Based Evaluation of Compound Promiscuity. <i>ACS Omega</i> , 2019, 4, 2758-2765.	3.5	17

#	ARTICLE	IF	CITATIONS
1457	Inferring pathogen-host interactions between <i>Leptospira interrogans</i> and <i>Homo sapiens</i> using network theory. <i>Scientific Reports</i> , 2019, 9, 1434.	3.3	20
1458	Grammar of protein domain architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3636-3645.	7.1	46
1459	Misprediction of Structural Disorder in Halophiles. <i>Molecules</i> , 2019, 24, 479.	3.8	5
1460	Characterization and expression analysis of <i>KIT</i> and <i>MITF</i> genes in llamas and their relation to white coat color. <i>Animal Genetics</i> , 2019, 50, 143-149.	1.7	19
1461	De Novo Transcriptome Assembly of Agave H11648 by Illumina Sequencing and Identification of Cellulose Synthase Genes in Agave Species. <i>Genes</i> , 2019, 10, 103.	2.4	22
1462	Network Pharmacology Deciphering Mechanisms of Volatiles of <i>Wendan</i> Granule for the Treatment of Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-12.	1.2	12
1463	W protein expression by Newcastle disease virus. <i>Virus Research</i> , 2019, 263, 207-216.	2.2	25
1464	Multimodel inference for biomarker development: an application to schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 83.	4.8	17
1465	Conodipine-P1-3, the First Phospholipases A2 Characterized from Injected Cone Snail Venom*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 876a-891.	3.8	7
1466	Follicular fluid exosomes act on the bovine oocyte to improve oocyte competence to support development and survival to heat shock. <i>Reproduction, Fertility and Development</i> , 2019, 31, 888.	0.4	68
1467	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019, 10, .	4.1	35
1468	Evaluating Graph Database Systems for Biological Data. <i>Communications in Computer and Information Science</i> , 2019, , 27-42.	0.5	0
1469	Assessment of Flexible Shape Complementarity: New Opportunities to Explain and Induce Selectivity in Ligands of Protein Tyrosine Phosphatase 1B. <i>Molecular Informatics</i> , 2019, 38, e1800141.	2.5	1
1470	Solution structure and novel insights into phylogeny and mode of action of the Neosartorya (<i>Aspergillus</i>) <i>fischeri</i> antifungal protein (NFAP). <i>International Journal of Biological Macromolecules</i> , 2019, 129, 511-522.	7.5	16
1471	Structure of the complex I-like molecule NDH of <i>oxygenic</i> photosynthesis. <i>Nature</i> , 2019, 566, 411-414.	27.8	123
1472	Comparative analyses of phytochelatin synthase (<i>PCS</i>) genes in higher plants. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 178-194.	1.3	36
1473	The genome of the soybean cyst nematode (<i>Heterodera glycines</i>) reveals complex patterns of duplications involved in the evolution of parasitism genes. <i>BMC Genomics</i> , 2019, 20, 119.	2.8	55
1474	Genus-Wide Comparative Genomics Analysis of <i>Neisseria</i> to Identify New Genes Associated with Pathogenicity and Niche Adaptation of <i>Neisseria</i> Pathogens. <i>International Journal of Genomics</i> , 2019, 2019, 1-19.	1.6	17

#	ARTICLE	IF	CITATIONS
1475	Functional homogeneity and specificity of topological modules in human proteome. BMC Bioinformatics, 2019, 19, 553.	2.6	2
1476	Insights into the evolution of extracellular leucine-rich repeats in metazoans with special reference to Toll-like receptor 4. Journal of Biosciences, 2019, 44, 1.	1.1	6
1477	Sequential Windowed Acquisition of Reporter Masses for Quantitation-First Proteomics. Journal of Proteome Research, 2019, 18, 1893-1901.	3.7	0
1478	BioVR: a platform for virtual reality assisted biological data integration and visualization. BMC Bioinformatics, 2019, 20, 78.	2.6	33
1479	Interactions between RAMP2 and CRF receptors: The effect of receptor subtypes, splice variants and cell context. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 997-1003.	2.6	16
1480	Quantitative label-free mass spectrometry using contralateral and adjacent breast tissues reveal differentially expressed proteins and their predicted impacts on pathways and cellular functions in breast cancer. Journal of Proteomics, 2019, 199, 1-14.	2.4	11
1481	Discovery of Amantamide, a Selective CXCR7 Agonist from Marine Cyanobacteria. Organic Letters, 2019, 21, 1622-1626.	4.6	13
1482	Molecular modeling of LDLR aids interpretation of genomic variants. Journal of Molecular Medicine, 2019, 97, 533-540.	3.9	10
1483	Two subgroups in systemic lupus erythematosus with features of antiphospholipid or Sjögren's syndrome differ in molecular signatures and treatment perspectives. Arthritis Research and Therapy, 2019, 21, 62.	3.5	24
1484	Protein dynamics analysis reveals that missense mutations in cancer-related genes appear frequently on hinge-neighbor residues. Proteins: Structure, Function and Bioinformatics, 2019, 87, 512-519.	2.6	11
1485	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. Cell Reports, 2019, 26, 2078-2087.e3.	6.4	36
1486	Metabolic, Anti-apoptotic and Immune Evasion Strategies of Primary Human Myeloma Cells Indicate Adaptations to Hypoxia*. Molecular and Cellular Proteomics, 2019, 18, 936-953.	3.8	30
1487	Exploring the Papillomaviral Proteome to Identify Potential Candidates for a Chimeric Vaccine against Cervix Papilloma Using Immunomics and Computational Structural Vaccinology. Viruses, 2019, 11, 63.	3.3	30
1488	NRF2 Activation in Cancer: From DNA to Protein. Cancer Research, 2019, 79, 889-898.	0.9	140
1489	Blocking the catalytic mechanism of MurC ligase enzyme from Acinetobacter baumannii: An in Silico guided study towards the discovery of natural antibiotics. Journal of Molecular Liquids, 2019, 281, 117-133.	4.9	5
1490	Database on spermatozoa transcriptogram of catagorised Frieswal crossbred (Holstein Friesian X) Tj ETQq1 1 0.784314 rgBT/Overlook	2.1	15
1491	Chia Seed (<i>Salvia hispanica</i> L.) as a Source of Proteins and Bioactive Peptides with Health Benefits: A Review. Comprehensive Reviews in Food Science and Food Safety, 2019, 18, 480-499.	11.7	128
1492	The Role of SurA PPlase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. Journal of Molecular Biology, 2019, 431, 1267-1283.	4.2	22

#	ARTICLE	IF	CITATIONS
1493	Phototactic tails: Evolution and molecular basis of a novel sensory trait in sea snakes. <i>Molecular Ecology</i> , 2019, 28, 2013-2028.	3.9	15
1494	Conserved Central Intraviral Protein Interactome of the <i>Herpesviridae</i> Family. <i>MSystems</i> , 2019, 4, .	3.8	4
1495	A computational model based on long short-term memory for predicting organellar genes in plastid genomes. , 2019, , .		0
1496	OutCyte: a novel tool for predicting unconventional protein secretion. <i>Scientific Reports</i> , 2019, 9, 19448.	3.3	49
1497	The Cytoscape BioGateway App: explorative network building from an RDF store. <i>Bioinformatics</i> , 2020, 36, 1966-1967.	4.1	14
1498	Studying the Role of Protein Kinases CK1 in Organization of Cortical Microtubules in <i>Arabidopsis thaliana</i> Root Cells. <i>Cytology and Genetics</i> , 2019, 53, 441-450.	0.5	3
1499	De Novo Sequence-Based Method for ncRPI Prediction using Structural Information. , 2019, , .		0
1500	Characterization and Comparative Analysis of the <i>Staphylococcus aureus</i> Genomic Island <i>Sal2</i> : an <i>In Silico</i> Approach. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	17
1501	Domain-specific Quantification of Prion Protein in Cerebrospinal Fluid by Targeted Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2388-2400.	3.8	22
1502	Increased Adaptive Variation Despite Reduced Overall Genetic Diversity in a Rapidly Adapting Invader. <i>Frontiers in Genetics</i> , 2019, 10, 1221.	2.3	41
1503	BSite-pro: A Novel Approach for Binding Site Prediction in Protein Sequences. , 2019, , .		0
1504	Updated Genome Assembly and Annotation for <i>Metrosideros polymorpha</i> , an Emerging Model Tree Species of Ecological Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3513-3520.	1.8	4
1505	“One DB to rule them all” the RING: a Regulatory Interaction Graph combining TFs, genes/proteins, SNPs, diseases and drugs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	5
1506	Host-Microbe Interactions in the Chemosynthetic <i>Riftia pachyptila</i> Symbiosis. <i>MBio</i> , 2019, 10, .	4.1	38
1507	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
1508	Genome-Wide Analysis of Known and Potential Tetraspanins in <i>Entamoeba histolytica</i> . <i>Genes</i> , 2019, 10, 885.	2.4	8
1509	Exploring a New Natural Treating Agent for Primary Hypertension: Recent Findings and Forthcoming Perspectives. <i>Journal of Clinical Medicine</i> , 2019, 8, 2003.	2.4	6
1510	Identification of candidate cancer drivers by integrative Epi-DNA and Gene Expression (iEDGE) data analysis. <i>Scientific Reports</i> , 2019, 9, 16904.	3.3	4

#	ARTICLE	IF	CITATIONS
1511	Automatic annotation of protein residues in published papers. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 665-672.	0.8	2
1512	Transcriptome analysis identifies genes related to the waxy coating on blueberry fruit in two northern-adapted rabbiteye breeding populations. BMC Plant Biology, 2019, 19, 460.	3.6	22
1513	mPies: a novel metaproteomics tool for the creation of relevant protein databases and automatized protein annotation. Biology Direct, 2019, 14, 21.	4.6	13
1514	Backbone dihedral angles prediction servers for protein early-stage structure prediction. Bio-Algorithms and Med-Systems, 2019, 15, .	2.4	0
1515	Improved linking of motifs to their TFs using domain information. Bioinformatics, 2019, 36, 1655-1662.	4.1	1
1516	Global Vectors Representation of Protein Sequences and Its Application for Predicting Self-Interacting Proteins with Multi-Grained Cascade Forest Model. Genes, 2019, 10, 924.	2.4	10
1517	Cell-Specific DNA Methylation Signatures in Asthma. Genes, 2019, 10, 932.	2.4	30
1518	Structural insights into heme binding to IL-36 β proinflammatory cytokine. Scientific Reports, 2019, 9, 16893.	3.3	29
1519	Heat-induced hyperthermia impacts the follicular fluid proteome of the periovulatory follicle in lactating dairy cows. PLoS ONE, 2019, 14, e0227095.	2.5	15
1520	In-silico definition of the Drosophila melanogaster matrisome. Matrix Biology Plus, 2019, 4, 100015.	3.5	32
1521	Machine learning can be used to distinguish protein families and generate new proteins belonging to those families. Journal of Chemical Physics, 2019, 151, 175102.	3.0	2
1522	Conjoint Analysis of SMRT- and Illumina-Based RNA-Sequencing Data of Fenneropenaeus chinensis Provides Insight Into Sex-Biased Expression Genes Involved in Sexual Dimorphism. Frontiers in Genetics, 2019, 10, 1175.	2.3	5
1523	Transcriptional changes during hepatic ischemia-reperfusion in the rat. PLoS ONE, 2019, 14, e0227038.	2.5	13
1524	Drug Repositioning Predictions by Non-Negative Matrix Tri-Factorization of Integrated Association Data. , 2019, , .		6
1525	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. Frontiers in Genetics, 2019, 10, 1075.	2.3	14
1526	De novo Assembly and Characterization of Patagonian Toothfish Transcriptome and Develop of EST-SSR Markers for Population Genetics. Frontiers in Marine Science, 2019, 6, .	2.5	8
1527	Hybrid de novo transcriptome assembly of poinsettia (Euphorbia pulcherrima Willd. Ex Klotsch) bracts. BMC Genomics, 2019, 20, 900.	2.8	14
1528	Bacterial DNA induces the formation of heat-resistant disease-associated proteins in human plasma. Scientific Reports, 2019, 9, 17995.	3.3	10

#	ARTICLE	IF	CITATIONS
1529	<i>Chlamydia psittaci</i> -Infected Dendritic Cells Communicate with NK Cells via Exosomes To Activate Antibacterial Immunity. <i>Infection and Immunity</i> , 2019, 88, .	2.2	19
1530	A3 adenosine receptor activation mechanisms: molecular dynamics analysis of inactive, active, and fully active states. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 983-996.	2.9	10
1531	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in the human proteome based on multi-stage ensemble-learning models. <i>BMC Bioinformatics</i> , 2019, 20, 602.	2.6	10
1532	Adrenocortical Carcinoma Xenograft in Zebrafish Embryos as a Model To Study the In Vivo Cytotoxicity of Abiraterone Acetate. <i>Endocrinology</i> , 2019, 160, 2620-2629.	2.8	11
1533	Characterization of antibiotic resistance genes in the species of the rumen microbiota. <i>Nature Communications</i> , 2019, 10, 5252.	12.8	68
1534	(Hyper)Graph Embedding and Classification via Simplicial Complexes. <i>Algorithms</i> , 2019, 12, 223.	2.1	21
1535	Amino acid substitution scoring matrices specific to intrinsically disordered regions in proteins. <i>Scientific Reports</i> , 2019, 9, 16380.	3.3	19
1536	Full-Length Transcriptome Survey and Expression Analysis of Parasitoid Wasp <i>Chouioia cunea</i> upon Exposure to 1-Dodecene. <i>Scientific Reports</i> , 2019, 9, 18167.	3.3	4
1537	Coevolutionary Analysis of Protein Subfamilies by Sequence Reweighting. <i>Entropy</i> , 2019, 21, 1127.	2.2	13
1538	Limitations of Deuterium-Labelled Substrates for Quantifying NADPH Metabolism in Heterotrophic <i>Arabidopsis</i> Cell Cultures. <i>Metabolites</i> , 2019, 9, 205.	2.9	6
1539	Network inference with ensembles of bi-clustering trees. <i>BMC Bioinformatics</i> , 2019, 20, 525.	2.6	12
1540	ProTstab “ predictor for cellular protein stability. <i>BMC Genomics</i> , 2019, 20, 804.	2.8	17
1541	Identifying genetic variants underlying medication-induced osteonecrosis of the jaw in cancer and osteoporosis: a case control study. <i>Journal of Translational Medicine</i> , 2019, 17, 381.	4.4	24
1542	Identification and Analysis of Long Repeats of Proteins at the Domain Level. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 250.	4.1	6
1543	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 311.	4.1	10
1545	An exome-wide rare variant analysis of Korean men identifies three novel genes predisposing to prostate cancer. <i>Scientific Reports</i> , 2019, 9, 17173.	3.3	6
1546	Transcriptomic and microstructural analyses in <i>Liriodendron tulipifera</i> Linn. reveal candidate genes involved in nectary development and nectar secretion. <i>BMC Plant Biology</i> , 2019, 19, 531.	3.6	13
1547	Skeletal muscle alterations in tachycardia-induced heart failure are linked to deficient natriuretic peptide signalling and are attenuated by RAS-/NEP-inhibition. <i>PLoS ONE</i> , 2019, 14, e0225937.	2.5	3

#	ARTICLE	IF	CITATIONS
1548	Modern Approaches in the Identification and Quantification of Immunogenic Peptides in Cereals by LC-MS/MS. <i>Frontiers in Plant Science</i> , 2019, 10, 1470.	3.6	32
1549	The KLDpT activation loop motif is critical for MARK kinase activity. <i>PLoS ONE</i> , 2019, 14, e0225727.	2.5	3
1550	Expression Quantitative Trait Loci in Equine Skeletal Muscle Reveals Heritable Variation in Metabolism and the Training Responsive Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 1215.	2.3	11
1551	A Glyphosate Pulse to Brackish Long-Term Microcosms Has a Greater Impact on the Microbial Diversity and Abundance of Planktonic Than of Biofilm Assemblages. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	8
1552	Detection of ALDH3B2 in Human Placenta. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6292.	4.1	2
1553	Identification of highly conserved, serotype-specific dengue virus sequences: implications for vaccine design. <i>BMC Genomics</i> , 2019, 20, 921.	2.8	18
1554	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. <i>Genome Biology</i> , 2019, 20, 299.	8.8	58
1555	Investigation of the host transcriptional response to intracellular bacterial infection using <i>Dictyostelium discoideum</i> as a host model. <i>BMC Genomics</i> , 2019, 20, 961.	2.8	17
1556	The distributions of protein coding genes within chromatin domains in relation to human disease. <i>Epigenetics and Chromatin</i> , 2019, 12, 72.	3.9	7
1557	Systematic exploration of predicted destabilizing nonsynonymous single nucleotide polymorphisms (nsSNPs) of human aldehyde oxidase: A Bioinformatics study. <i>Pharmacology Research and Perspectives</i> , 2019, 7, e00538.	2.4	9
1558	Manually curated genome-scale reconstruction of the metabolic network of <i>Bacillus megaterium</i> DSM319. <i>Scientific Reports</i> , 2019, 9, 18762.	3.3	21
1559	Proteomics: a powerful tool to study plant responses to biotic stress. <i>Plant Methods</i> , 2019, 15, 135.	4.3	92
1560	A novel framework for horizontal and vertical data integration in cancer studies with application to survival time prediction models. <i>Biology Direct</i> , 2019, 14, 22.	4.6	34
1561	The X chromosome of the German cockroach, <i>Blattella germanica</i> , is homologous to a fly X chromosome despite 400 million years divergence. <i>BMC Biology</i> , 2019, 17, 100.	3.8	19
1562	Computational Modeling Explains the Multi Sterol Ligand Specificity of the N-Terminal Domain of Niemann-Pick C1-Like 1 Protein. <i>ACS Omega</i> , 2019, 4, 20894-20904.	3.5	6
1563	Evaluation of New Benzimidazole Derivatives as Cysticidal Agents: <i>In Vitro</i> , <i>In Vivo</i> and Docking Studies. <i>Chemical and Pharmaceutical Bulletin</i> , 2019, 67, 1293-1300.	1.3	1
1564	Comprehensive Identification and Characterization of Human Secretome Based on Integrative Proteomic and Transcriptomic Data. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 299.	3.7	25
1565	Draft Genome Assembly of a Fouling Barnacle, <i>Amphibalanus amphitrite</i> (Darwin, 1854): The First Reference Genome for Thecostraca. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	24

#	ARTICLE	IF	CITATIONS
1566	A Network Pharmacology Approach to Reveal the Underlying Mechanisms of <i>Paeonia lactiflora</i> Pall. On the Treatment of Alzheimer's Disease. Evidence-based Complementary and Alternative Medicine, 2019, 2019, 1-12.	1.2	23
1567	Charting the Complexity of the Marine Microbiome through Single-Cell Genomics. Cell, 2019, 179, 1623-1635.e11.	28.9	158
1568	Co-regulation map of the human proteome enables identification of protein functions. Nature Biotechnology, 2019, 37, 1361-1371.	17.5	106
1569	Novel redox-active enzymes for ligninolytic applications revealed from multiomics analyses of <i>Peniophora</i> sp. CBMAI 1063, a laccase hyper-producer strain. Scientific Reports, 2019, 9, 17564.	3.3	24
1570	A comprehensive review of bioactive peptides obtained from animal byproducts and their applications. Food and Function, 2019, 10, 6244-6266.	4.6	90
1571	Vitellogenesis in Blue Gourami is Accompanied by Brain Transcriptome Changes. Fishes, 2019, 4, 54.	1.7	2
1572	Early-life stress impairs developmental programming in Cadherin 13 (CDH13)-deficient mice. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 89, 158-168.	4.8	12
1573	A New Online Resource to Monitor New or Emerging Plant Pests: MEDISYS Media Monitoring and the Case of <i>Xylella fastidiosa</i> . Phytopathology, 2019, 109, 216-218.	2.2	6
1574	Berberine inhibits hepatitis C virus entry by targeting the viral E2 glycoprotein. Phytomedicine, 2019, 53, 62-69.	5.3	47
1575	Genetic landscape of isolated pediatric cataracts: extreme heterogeneity and variable inheritance patterns within genes. Human Genetics, 2019, 138, 847-863.	3.8	33
1576	Alchemical Grid Dock (AIGDock) calculations in the D3R Grand Challenge 3. Journal of Computer-Aided Molecular Design, 2019, 33, 61-69.	2.9	5
1577	<i>Dicer</i> regulates <i>Nosema ceranae</i> proliferation in honeybees. Insect Molecular Biology, 2019, 28, 74-85.	2.0	14
1578	Rapidly Display Glycan Symbols in 3D Structures: 3D-SNFG in LiteMol. Journal of Proteome Research, 2019, 18, 770-774.	3.7	20
1579	In silico analysis and molecular dynamics simulation of human superoxide dismutase 3 (SOD3) genetic variants. Journal of Cellular Biochemistry, 2019, 120, 3583-3598.	2.6	43
1580	Matrix effect on food allergen detection – A case study of fish parvalbumin. Food Chemistry, 2019, 274, 526-534.	8.2	20
1581	Changes in the urinary extracellular vesicle proteome are associated with nephronophthisis-related ciliopathies. Journal of Proteomics, 2019, 192, 27-36.	2.4	22
1582	Cross-ID: Analysis and Visualization of Complex XL-MS-Driven Protein Interaction Networks. Journal of Proteome Research, 2019, 18, 642-651.	3.7	13
1583	Structural Insights into Characterizing Binding Sites in Epidermal Growth Factor Receptor Kinase Mutants. Journal of Chemical Information and Modeling, 2019, 59, 453-462.	5.4	30

#	ARTICLE	IF	CITATIONS
1584	Identifying Driver Interfaces Enriched for Somatic Missense Mutations in Tumors. <i>Methods in Molecular Biology</i> , 2019, 1907, 51-72.	0.9	4
1585	A Centipede Toxin Family Defines an Ancient Class of CS β Defensins. <i>Structure</i> , 2019, 27, 315-326.e7.	3.3	17
1586	Repurposing Drugs Based on Evolutionary Relationships Between Targets of Approved Drugs and Proteins of Interest. <i>Methods in Molecular Biology</i> , 2019, 1903, 45-59.	0.9	4
1587	ABCF ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. <i>Journal of Molecular Biology</i> , 2019, 431, 3568-3590.	4.2	90
1588	Molecular Dynamics Simulations of Substrate Release from <i>Trypanosoma cruzi</i> UDP-Galactopyranose Mutase. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 809-817.	5.4	4
1589	Structural characterization and molecular dynamics simulations of the caprine and bovine solute carrier family 11 A1 (SLC11A1). <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 265-285.	2.9	5
1590	Identifying Potential Ageing-Modulating Drugs In Silico. <i>Trends in Endocrinology and Metabolism</i> , 2019, 30, 118-131.	7.1	15
1591	Structural adaptations of photosynthetic complex I enable ferredoxin-dependent electron transfer. <i>Science</i> , 2019, 363, 257-260.	12.6	162
1593	UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , 2019, 47, D506-D515.	14.5	6,185
1594	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	14.5	6,449
1595	MitoMiner v4.0: an updated database of mitochondrial localization evidence, phenotypes and diseases. <i>Nucleic Acids Research</i> , 2019, 47, D1225-D1228.	14.5	97
1596	Analysis of Brassica napus dehydrins and their Co-Expression regulatory networks in relation to cold stress. <i>Gene Expression Patterns</i> , 2019, 31, 7-17.	0.8	19
1597	The BioGRID interaction database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D529-D541.	14.5	1,096
1598	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613.	14.5	12,237
1599	<i>In Vivo</i> Applicability of Neosartorya fischeri Antifungal Protein 2 (NFAP2) in Treatment of Vulvovaginal Candidiasis. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	24
1600	The cAMP/PKA Pathway Inhibits Beta-amyloid Peptide Release from Human Platelets. <i>Neuroscience</i> , 2019, 397, 159-171.	2.3	13
1601	<i>In silico</i> hit optimization toward AKT inhibition: fragment-based approach, molecular docking and molecular dynamics study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 4301-4311.	3.5	10
1602	IID 2018 update: context-specific physical protein-protein interactions in human, model organisms and domesticated species. <i>Nucleic Acids Research</i> , 2019, 47, D581-D589.	14.5	164

#	ARTICLE	IF	CITATIONS
1603	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. <i>Nucleic Acids Research</i> , 2019, 47, D1090-D1101.	14.5	45
1604	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432.	14.5	3,937
1605	A proteomics approach for the identification of species-specific immunogenic proteins in the <i>Mycobacterium abscessus</i> complex. <i>Microbes and Infection</i> , 2019, 21, 154-162.	1.9	11
1606	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632.	3.7	1,228
1607	RNAct: Protein-RNA interaction predictions for model organisms with supporting experimental data. <i>Nucleic Acids Research</i> , 2019, 47, D601-D606.	14.5	80
1608	VarSome: the human genomic variant search engine. <i>Bioinformatics</i> , 2019, 35, 1978-1980.	4.1	1,143
1609	Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. <i>Nucleic Acids Research</i> , 2019, 47, D564-D572.	14.5	27
1610	Auxin Function in the Brown Alga <i>Dictyota dichotoma</i> . <i>Plant Physiology</i> , 2019, 179, 280-299.	4.8	24
1611	Inhibition of Protein Secretion in <i>Escherichia coli</i> and Sub-MIC Effects of Arylomycin Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	15
1612	Vacuolar hydrolysis and efflux: current knowledge and unanswered questions. <i>Autophagy</i> , 2019, 15, 212-227.	9.1	26
1613	Algorithms for learning parsimonious context trees. <i>Machine Learning</i> , 2019, 108, 879-911.	5.4	0
1614	A Text Mining Pipeline Using Active and Deep Learning Aimed at Curating Information in Computational Neuroscience. <i>Neuroinformatics</i> , 2019, 17, 391-406.	2.8	17
1615	Predicting combinative drug pairs via multiple classifier system with positive samples only. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 168, 1-10.	4.7	13
1616	Energy-Coupling Factor Transporters as Novel Antimicrobial Targets. <i>Advanced Therapeutics</i> , 2019, 2, 1800066.	3.2	18
1617	Novel rearrangements involving the RET gene in papillary thyroid carcinoma. <i>Cancer Genetics</i> , 2019, 230, 13-20.	0.4	20
1618	Genome sequence of the opportunistic human pathogen <i>Magnusiomyces capitatus</i> . <i>Current Genetics</i> , 2019, 65, 539-560.	1.7	14
1619	The SUPERFAMILY 2.0 database: a significant proteome update and a new webserver. <i>Nucleic Acids Research</i> , 2019, 47, D490-D494.	14.5	126
1620	Predicting the ligand-binding properties of <i>Borrelia burgdorferi</i> s.s. Bmp proteins in light of the conserved features of related <i>Borrelia</i> proteins. <i>Journal of Theoretical Biology</i> , 2019, 462, 97-108.	1.7	5

#	ARTICLE	IF	CITATIONS
1621	Unipept 4.0: Functional Analysis of Metaproteome Data. <i>Journal of Proteome Research</i> , 2019, 18, 606-615.	3.7	112
1622	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	14.5	1,291
1623	Searching for serum protein markers of equine squamous gastric disease using gel electrophoresis and mass spectrometry. <i>Equine Veterinary Journal</i> , 2019, 51, 581-586.	1.7	7
1624	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	11.1	150
1625	Systems Biology Approaches Toward Understanding Primary Mitochondrial Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 19.	2.3	12
1626	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	28.9	1,087
1627	Structural Modeling and in Silico Screening of Potential Small-Molecule Allosteric Agonists of a Glucagon-like Peptide 1 Receptor. <i>ACS Omega</i> , 2019, 4, 961-970.	3.5	16
1628	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 796-805.	3.8	27
1629	A web application and service for imputing and visualizing missense variant effect maps. <i>Bioinformatics</i> , 2019, 35, 3191-3193.	4.1	13
1630	An Annotated Genome for <i>Haliotis rufescens</i> (Red Abalone) and Resequenced Green, Pink, Pinto, Black, and White Abalone Species. <i>Genome Biology and Evolution</i> , 2019, 11, 431-438.	2.5	41
1631	The HIV gp41 Fusion Protein Inhibits T-Cell Activation through the Lentiviral Lytic Peptide 2 Motif. <i>Biochemistry</i> , 2019, 58, 818-832.	2.5	1
1632	Comprehensive Prediction of Target RNA Editing Sites for PLS-Class PPR Proteins in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 862-874.	3.1	28
1633	Folding and Misfolding of Human Membrane Proteins in Health and Disease: From Single Molecules to Cellular Proteostasis. <i>Chemical Reviews</i> , 2019, 119, 5537-5606.	47.7	184
1634	Tamoxifen mechanically reprograms the tumor microenvironment via $\text{HIF-1}\alpha$ and reduces cancer cell survival. <i>EMBO Reports</i> , 2019, 20, .	4.5	58
1635	Drug Design Inspired by Nature: Crystallographic Detection of an Auto-Tailored Protease Inhibitor Template. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 4051-4055.	13.8	13
1636	Cone snail prolyl-4-hydroxylase β -subunit sequences derived from transcriptomic data and mass spectrometric analysis of variable proline hydroxylation in <i>C. amadis</i> venom. <i>Journal of Proteomics</i> , 2019, 194, 37-48.	2.4	3
1637	Varying dietary protein and fat elicits differential transcriptomic expression within stress response pathways in preweaned Holstein heifers. <i>Journal of Dairy Science</i> , 2019, 102, 1630-1641.	3.4	2
1638	Biophysical characterization and ligand-binding properties of the elongation factor Tu from <i>Mycobacterium tuberculosis</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2019, 51, 139-149.	2.0	1

#	ARTICLE	IF	CITATIONS
1639	Organic cation transporter 3 (Oct3) is a distinct catecholamines clearance route in adipocytes mediating the beiging of white adipose tissue. <i>PLoS Biology</i> , 2019, 17, e2006571.	5.6	41
1640	Genome-wide association study of an unusual dolphin mortality event reveals candidate genes for susceptibility and resistance to cetacean morbillivirus. <i>Evolutionary Applications</i> , 2019, 12, 718-732.	3.1	13
1641	Effect of Acceptor Chain Length and Hydrophobicity on Polymerization Kinetics of the <i>Neisseria meningitidis</i> Group C Polysialyltransferase. <i>Biochemistry</i> , 2019, 58, 679-686.	2.5	4
1642	<i>Plasmodium</i> palmitoylation machinery engineered in <i>E. coli</i> for high-throughput screening of palmitoyl acyltransferase inhibitors. <i>FEBS Open Bio</i> , 2019, 9, 248-264.	2.3	14
1643	Von der Natur inspiriertes Wirkstoffdesign: kristallographische Detektion eines selbstgenerierten Inhibitor-Grundgerüsts. <i>Angewandte Chemie</i> , 2019, 131, 4091-4096.	2.0	3
1644	Coordinated downregulation of the photosynthetic apparatus as a protective mechanism against UV exposure in the diatom <i>Corethron hystrix</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1837-1850.	3.6	5
1645	Pros and cons of virtual screening based on public "Big Data": In silico mining for new bromodomain inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2019, 165, 258-272.	5.5	12
1646	Leishmanicidal therapy targeted to parasite proteases. <i>Life Sciences</i> , 2019, 219, 163-181.	4.3	24
1647	Genome-wide DNA methylation and transcriptomic profiles in the lifestyle strategies and asexual development of the forest fungal pathogen <i>Heterobasidion parviporum</i> . <i>Epigenetics</i> , 2019, 14, 16-40.	2.7	11
1648	Statistical force-field for structural modeling using chemical cross-linking/mass spectrometry distance constraints. <i>Bioinformatics</i> , 2019, 35, 3005-3012.	4.1	13
1650	BioTransformer: a comprehensive computational tool for small molecule metabolism prediction and metabolite identification. <i>Journal of Cheminformatics</i> , 2019, 11, 2.	6.1	269
1651	Bioinformatic analysis of long-lasting transcriptional and translational changes in the basolateral amygdala following acute stress. <i>PLoS ONE</i> , 2019, 14, e0209846.	2.5	18
1652	Activation of the Bile Acid Pathway and No Observed Antimicrobial Peptide Sequences in the Skin of a Poison Frog. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 581-589.	1.8	1
1653	Using a Chemical Genetic Screen to Enhance Our Understanding of the Antimicrobial Properties of Gallium against <i>Escherichia coli</i> . <i>Genes</i> , 2019, 10, 34.	2.4	16
1654	Proteomic profiling of the white shrimp <i>Litopenaeus vannamei</i> (Boone, 1931) hemocytes infected with white spot syndrome virus reveals the induction of allergy-related proteins. <i>Developmental and Comparative Immunology</i> , 2019, 91, 37-49.	2.3	27
1655	Targeting metabolic pathways proteins of <i>Orientia tsutsugamushi</i> using combined hierarchical approach to combat scrub typhus. <i>Journal of Molecular Recognition</i> , 2019, 32, e2766.	2.1	13
1656	Polysaccharides for tissue engineering: Current landscape and future prospects. <i>Carbohydrate Polymers</i> , 2019, 205, 601-625.	10.2	104
1657	Comparative Genomics of <i>Lactobacillus brevis</i> Reveals a Significant Plasmidome Overlap of Brewery and Insect Isolates. <i>Current Microbiology</i> , 2019, 76, 37-47.	2.2	13

#	ARTICLE	IF	CITATIONS
1658	Quality assessment for the putative intrinsic disorder in proteins. <i>Bioinformatics</i> , 2019, 35, 1692-1700.	4.1	20
1659	PopHumanScan: the online catalog of human genome adaptation. <i>Nucleic Acids Research</i> , 2019, 47, D1080-D1089.	14.5	22
1660	CMAUP: a database of collective molecular activities of useful plants. <i>Nucleic Acids Research</i> , 2019, 47, D1118-D1127.	14.5	68
1661	BitterDB: taste ligands and receptors database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D1179-D1185.	14.5	133
1662	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
1663	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. <i>Nucleic Acids Research</i> , 2019, 47, D550-D558.	14.5	85
1664	iEKP2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	14.5	22
1665	OrthoInspector 3.0: open portal for comparative genomics. <i>Nucleic Acids Research</i> , 2019, 47, D411-D418.	14.5	46
1666	Cross-Reactivity between Major IgE Epitopes of Family 5 Allergens from <i>Dermatophagoides pteronyssinus</i> and <i>Blomia tropicalis</i> . <i>International Archives of Allergy and Immunology</i> , 2019, 178, 10-18.	2.1	7
1667	4-HNE carbonylation induces local conformational changes on bovine serum albumin and thioredoxin. A molecular dynamics study. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 86, 298-307.	2.4	17
1668	COSMIC: the Catalogue Of Somatic Mutations In Cancer. <i>Nucleic Acids Research</i> , 2019, 47, D941-D947.	14.5	3,196
1669	PubChem 2019 update: improved access to chemical data. <i>Nucleic Acids Research</i> , 2019, 47, D1102-D1109.	14.5	2,217
1670	iDog: an integrated resource for domestic dogs and wild canids. <i>Nucleic Acids Research</i> , 2019, 47, D793-D800.	14.5	33
1671	Translocatome: a novel resource for the analysis of protein translocation between cellular organelles. <i>Nucleic Acids Research</i> , 2019, 47, D495-D505.	14.5	17
1672	Genenames.org: the HGNC and VGNC resources in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D786-D792.	14.5	292
1673	RetroRules: a database of reaction rules for engineering biology. <i>Nucleic Acids Research</i> , 2019, 47, D1229-D1235.	14.5	74
1674	Disrupted Synthesis of a Di-N-acetylated Sugar Perturbs Mature Glycoform Structure and Microheterogeneity in the O-Linked Protein Glycosylation System of <i>Neisseria elongata</i> subsp. <i>glycolytica</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	4
1675	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	13.3	1,094

#	ARTICLE	IF	CITATIONS
1676	Riluzole Attenuates L-DOPA-Induced Abnormal Involuntary Movements Through Decreasing CREB1 Activity: Insights from a Rat Model. <i>Molecular Neurobiology</i> , 2019, 56, 5111-5121.	4.0	3
1677	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751.	14.5	879
1678	Molecular phylogenetics supports a clade of red algal parasites retaining native plastids: taxonomy and terminology revised. <i>Journal of Phycology</i> , 2019, 55, 279-288.	2.3	8
1679	Scop3D: Online Visualization of Mutation Rates on Protein Structure. <i>Journal of Proteome Research</i> , 2019, 18, 765-769.	3.7	2
1680	Plasma Concentrations of Myeloid-Derived Growth Factor in Healthy Individuals and Patients with Acute Myocardial Infarction as Assessed by Multiple Reaction Monitoring-Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 1302-1308.	6.5	13
1681	Genetic variations in human papillomavirus and cervical cancer outcomes. <i>International Journal of Cancer</i> , 2019, 144, 2206-2214.	5.1	21
1682	ARGDIT: a validation and integration toolkit for Antimicrobial Resistance Gene Databases. <i>Bioinformatics</i> , 2019, 35, 2466-2474.	4.1	12
1683	The comparative biochemistry of viruses and humans: an evolutionary path towards autoimmunity. <i>Biological Chemistry</i> , 2019, 400, 629-638.	2.5	17
1684	Giant tortoise genomes provide insights into longevity and age-related disease. <i>Nature Ecology and Evolution</i> , 2019, 3, 87-95.	7.8	79
1685	SIFTS: updated Structure Integration with Function, Taxonomy and Sequences resource allows 40-fold increase in coverage of structure-based annotations for proteins. <i>Nucleic Acids Research</i> , 2019, 47, D482-D489.	14.5	165
1686	SCOPe: classification of large macromolecular structures in the structural classification of proteinsâ€™ extended database. <i>Nucleic Acids Research</i> , 2019, 47, D475-D481.	14.5	122
1687	15 years of PhosphoSitePlusÂ®: integrating post-translationally modified sites, disease variants and isoforms. <i>Nucleic Acids Research</i> , 2019, 47, D433-D441.	14.5	208
1688	Î€-Î€ stacking interaction is a key factor for the stability of GH11 xylanases at low pH. <i>International Journal of Biological Macromolecules</i> , 2019, 124, 895-902.	7.5	7
1689	Computational analysis of the <i>Plasmodiophora brassicae</i> genome: mitochondrial sequence description and metabolic pathway database design. <i>Genomics</i> , 2019, 111, 1629-1640.	2.9	27
1690	Sex-related gonadal gene expression differences in the Russian sturgeon (<i>Acipenser gueldenstaedtii</i>) grown in stable aquaculture conditions. <i>Animal Reproduction Science</i> , 2019, 200, 75-85.	1.5	15
1691	Quantitative Proteomics Identification of Seminal Fluid Proteins in Male <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, S46-S58.	3.8	66
1692	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	14.5	94
1693	Exploring Protein Conformational Diversity. <i>Methods in Molecular Biology</i> , 2019, 1851, 353-365.	0.9	2

#	ARTICLE	IF	CITATIONS
1694	Towards region-specific propagation of protein functions. <i>Bioinformatics</i> , 2019, 35, 1737-1744.	4.1	7
1695	The global prevalence and genetic spectrum of lysosomal acid lipase deficiency: A rare condition that mimics NAFLD. <i>Journal of Hepatology</i> , 2019, 70, 142-150.	3.7	50
1696	The genetic architecture of aniridia and Gillespie syndrome. <i>Human Genetics</i> , 2019, 138, 881-898.	3.8	51
1697	Mechanistic insights into high mobility group box-1 (HMGB1)-induced Toll-like receptor 4 (TLR4) dimer formation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3721-3730.	3.5	17
1698	Identifying and validating blood mRNA biomarkers for acute and chronic insufficient sleep in humans: a machine learning approach. <i>Sleep</i> , 2019, 42, .	1.1	35
1699	Updates in Rhea: SPARQLing biochemical reaction data. <i>Nucleic Acids Research</i> , 2019, 47, D596-D600.	14.5	54
1700	An analysis of codon bias in six red yeast species. <i>Yeast</i> , 2019, 36, 53-64.	1.7	8
1701	KAT6A Syndrome: genotypeâ€“phenotype correlation in 76 patients with pathogenic KAT6A variants. <i>Genetics in Medicine</i> , 2019, 21, 850-860.	2.4	68
1702	The Encyclopedia of Proteome Dynamics: the KinoViewer. <i>Bioinformatics</i> , 2019, 35, 1441-1442.	4.1	9
1703	<scp>BASTA</scp> â€“ Taxonomic classification of sequences and sequence bins using last common ancestor estimations. <i>Methods in Ecology and Evolution</i> , 2019, 10, 100-103.	5.2	83
1704	Development of new Coumarin-based profluorescent substrates for human cytochrome P450 enzymes. <i>Xenobiotica</i> , 2019, 49, 1015-1024.	1.1	16
1705	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 2267-2290.	6.5	99
1706	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	6.5	186
1707	Bioinformatics on a national scale: an example from Switzerland. <i>Briefings in Bioinformatics</i> , 2019, 20, 361-369.	6.5	9
1708	Characteristics and evolution of the ecosystem of software tools supporting research in molecular biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 1329-1336.	6.5	5
1709	Prader-Willi syndrome and Angelman syndrome: Visualisation of the molecular pathways for two chromosomal disorders. <i>World Journal of Biological Psychiatry</i> , 2019, 20, 670-682.	2.6	13
1710	Identification of anti-filarial leads against aspartate semialdehyde dehydrogenase of <i>Wolbachia</i> endosymbiont of <i>Brugia malayi</i>: combined molecular docking and molecular dynamics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 394-410.	3.5	31
1711	Identification of new benzamide inhibitor against Î±-subunit of tryptophan synthase from <i>Mycobacterium tuberculosis</i> through structure-based virtual screening, anti-tuberculosis activity and molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1043-1053.	3.5	20

#	ARTICLE	IF	CITATIONS
1712	Global proteomic and functional analysis of <i>Crotalus durissus collilineatus</i> individual venom variation and its impact on envenoming. <i>Journal of Proteomics</i> , 2019, 191, 153-165.	2.4	42
1713	A Draft Map of the Human Ovarian Proteome for Tissue Engineering and Clinical Applications. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S159-S173.	3.8	35
1714	Prediction of deleterious mutations in coding regions of mammals with transfer learning. <i>Evolutionary Applications</i> , 2019, 12, 18-28.	3.1	13
1715	Orthosteric and benzodiazepine cavities of the $\alpha 1\beta 2\gamma 2$ GABAA receptor: insights from experimentally validated in silico methods. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1597-1615.	3.5	11
1716	Toward completion of the Earth's proteome: an update a decade later. <i>Briefings in Bioinformatics</i> , 2019, 20, 463-470.	6.5	3
1717	Drug knowledge bases and their applications in biomedical informatics research. <i>Briefings in Bioinformatics</i> , 2019, 20, 1308-1321.	6.5	29
1718	Bioinformatics for precision oncology. <i>Briefings in Bioinformatics</i> , 2019, 20, 778-788.	6.5	49
1719	Comprehensive review and empirical analysis of hallmarks of DNA-, RNA- and protein-binding residues in protein chains. <i>Briefings in Bioinformatics</i> , 2019, 20, 1250-1268.	6.5	84
1720	Small leucine-rich proteoglycans and matrix metalloproteinase-14: Key partners?. <i>Matrix Biology</i> , 2019, 75-76, 271-285.	3.6	55
1721	The disordered charged biased proteins in the human diseasome. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 44-49.	3.6	3
1722	Bridging the gaps: using an NHP model to predict single dose radiation absorption in humans. <i>International Journal of Radiation Biology</i> , 2020, 96, 47-56.	1.8	7
1723	Plasma protein biomarkers and their association with mutually exclusive cardiovascular phenotypes: the FIBRO-TARGETS case-control analyses. <i>Clinical Research in Cardiology</i> , 2020, 109, 22-33.	3.3	19
1724	Genetic association in female stress urinary incontinence based on proteomic findings: a case-control study. <i>International Urogynecology Journal</i> , 2020, 31, 117-122.	1.4	2
1725	DPH1 syndrome: two novel variants and structural and functional analyses of seven missense variants identified in syndromic patients. <i>European Journal of Human Genetics</i> , 2020, 28, 64-75.	2.8	15
1726	ragp: Pipeline for mining of plant hydroxyproline-rich glycoproteins with implementation in R. <i>Glycobiology</i> , 2020, 30, 19-35.	2.5	10
1727	Mapping Taste-Relevant Food Peptidomes by Means of Sequential Window Acquisition of All Theoretical Fragment Ion-Mass Spectrometry. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 10287-10298.	5.2	13
1728	Pierce into the Native Structure of Ata, a Trimeric Autotransporter of <i>Acinetobacter baumannii</i> ATCC 17978. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 1269-1282.	1.9	8
1729	Comparative Transcriptomics Analyses across Species, Organs, and Developmental Stages Reveal Functionally Constrained lncRNAs. <i>Molecular Biology and Evolution</i> , 2020, 37, 240-259.	8.9	30

#	ARTICLE	IF	CITATIONS
1730	Resources to Discover and Use Short Linear Motifs in Viral Proteins. Trends in Biotechnology, 2020, 38, 113-127.	9.3	26
1731	PhaSepDB: a database of liquidâ€“liquid phase separation related proteins. Nucleic Acids Research, 2020, 48, D354-D359.	14.5	157
1732	Protein-Protein Interaction Networks. Methods in Molecular Biology, 2020, , .	0.9	3
1733	Detection of Nonhematologic Neoplasms by Routine Flow Cytometry Analysis. American Journal of Clinical Pathology, 2020, 153, 99-104.	0.7	10
1734	XMAN v2â€“a database of <i>Homo sapiens</i> mutated peptides. Bioinformatics, 2020, 36, 1311-1313.	4.1	12
1735	Proteomic Analysis of Infants Undergoing Cardiopulmonary Bypass Using Contemporary Ontological Tools. Journal of Surgical Research, 2020, 246, 83-92.	1.6	6
1736	Seaweed natural products modify the host inflammatory response via Nrf2 signaling and alter colon microbiota composition and gene expression. Free Radical Biology and Medicine, 2020, 146, 306-323.	2.9	13
1737	Mass Spectrometry Data Analysis in Proteomics. Methods in Molecular Biology, 2020, , .	0.9	3
1738	PerMemDB: A database for eukaryotic peripheral membrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183076.	2.6	14
1739	A structure-based approach towards the identification of novel antichagasic compounds: <i>Trypanosoma cruzi</i> carbonic anhydrase inhibitors. Journal of Enzyme Inhibition and Medicinal Chemistry, 2020, 35, 21-30.	5.2	13
1740	Impact of oxidative stress SNPs and dietary antioxidant quality score on prostate cancer. International Journal of Food Sciences and Nutrition, 2020, 71, 500-508.	2.8	8
1741	<i>ANKLE1</i> N ⁶ -Methyladenosine-related variant is associated with colorectal cancer risk by maintaining the genomic stability. International Journal of Cancer, 2020, 146, 3281-3293.	5.1	35
1742	Structural and functional analysis of â€œnon-smellyâ€•proteins. Cellular and Molecular Life Sciences, 2020, 77, 2423-2440.	5.4	16
1743	A Unique Conformational Distortion Mechanism Drives Lipocalin 2 Binding to Bacterial Siderophores. ACS Chemical Biology, 2020, 15, 234-242.	3.4	12
1744	The sweet side of venom: Glycosylated prothrombin activating metalloproteases from <i>Dispholidus typus</i> (boomslang) and <i>Thelotornis mossambicanus</i> (twig snake). Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2020, 227, 108625.	2.6	11
1745	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	14.5	87
1746	Protein Nanotechnology. Methods in Molecular Biology, 2020, , .	0.9	4
1747	The ABCD database: a repository for chemically defined antibodies. Nucleic Acids Research, 2020, 48, D261-D264.	14.5	46

#	ARTICLE	IF	CITATIONS
1748	Proteomic Analysis Reveals Anti-Fibrotic Effects of Blue Light Photobiomodulation on Fibroblasts. <i>Lasers in Surgery and Medicine</i> , 2020, 52, 358-372.	2.1	6
1749	Vampirovibrio chlorellavorus draft genome sequence, annotation, and preliminary characterization of pathogenicity determinants. <i>Phycological Research</i> , 2020, 68, 23-29.	1.6	3
1750	Using What We Already Have: Uncovering New Drug Repurposing Strategies in Existing Omics Data. <i>Annual Review of Pharmacology and Toxicology</i> , 2020, 60, 333-352.	9.4	39
1751	Protein functional annotation of simultaneously improved stability, accuracy and false discovery rate achieved by a sequence-based deep learning. <i>Briefings in Bioinformatics</i> , 2020, 21, 1437-1447.	6.5	105
1752	Enabling Massive XML-Based Biological Data Management in HBase. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1994-2004.	3.0	12
1753	Targeting B7-1 in immunotherapy. <i>Medicinal Research Reviews</i> , 2020, 40, 654-682.	10.5	44
1754	A Novel Homozygous Missense Variant in the NAGA Gene with Extreme Intrafamilial Phenotypic Heterogeneity. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 45-55.	2.3	2
1755	Identification of Genes Underlying the Resistance to <i>Melampsora larici-populina</i> in an <i>R</i> Gene Supercluster of the <i>Populus deltoides</i> Genome. <i>Plant Disease</i> , 2020, 104, 1133-1143.	1.4	6
1756	A Genome Resource for Several North American <i>Venturia inaequalis</i> Isolates with Multiple Fungicide Resistance Phenotypes. <i>Phytopathology</i> , 2020, 110, 544-546.	2.2	17
1757	Histidine Phosphorylation. <i>Methods in Molecular Biology</i> , 2020, , .	0.9	2
1758	The utility of reptile blood transcriptomes in molecular ecology. <i>Molecular Ecology Resources</i> , 2020, 20, 308-317.	4.8	17
1759	Autologous Exosome Transfer: A New Personalised Treatment Concept to Prevent Colitis in a Murine Model. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 841-855.	1.3	24
1760	NHP-immunome: A translational research-oriented database of non-human primate immune system proteins. <i>Cellular Immunology</i> , 2020, 347, 103999.	3.0	1
1761	A contemporary view on the molecular basis of neurodevelopmental disorders. , 2020, , 57-78.		0
1762	Clinical and genetic risk factors for aromatase inhibitor-associated arthralgia in breast cancer survivors. <i>Breast</i> , 2020, 49, 48-54.	2.2	12
1763	Metatranscriptomics yields new genomic resources and sensitive detection of infections for diverse blood parasites. <i>Molecular Ecology Resources</i> , 2020, 20, 14-28.	4.8	25
1764	RCSB Protein Data Bank: Enabling biomedical research and drug discovery. <i>Protein Science</i> , 2020, 29, 52-65.	7.6	223
1765	Machine learning techniques for protein function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 397-413.	2.6	90

#	ARTICLE	IF	CITATIONS
1766	Elucidation of role of an acetyltransferase like protein in paromomycin resistance in <i>Leishmania donovani</i> using <i>in silico</i> and <i>in vitro</i> approaches. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4449-4460.	3.5	0
1767	Adaptive Radiation of the Flukes of the Family Fasciolidae Inferred from Genome-Wide Comparisons of Key Species. Molecular Biology and Evolution, 2020, 37, 84-99.	8.9	28
1768	Accuracy of protein-level disorder predictions. Briefings in Bioinformatics, 2020, 21, 1509-1522.	6.5	36
1769	Nutritional component analyses of kiwifruit in different development stages by metabolomic and transcriptomic approaches. Journal of the Science of Food and Agriculture, 2020, 100, 2399-2409.	3.5	33
1770	Concentration Determination of >200 Proteins in Dried Blood Spots for Biomarker Discovery and Validation. Molecular and Cellular Proteomics, 2020, 19, 540-553.	3.8	27
1771	Prediction of human-virus protein-protein interactions through a sequence embedding-based machine learning method. Computational and Structural Biotechnology Journal, 2020, 18, 153-161.	4.1	98
1772	Monoclonal antibody-based sandwich ELISA for the detection of mammalian meats. Food Control, 2020, 110, 107045.	5.5	19
1773	EGY3: homologue of S2P protease located in chloroplasts. Plant Biology, 2020, 22, 735-743.	3.8	11
1774	Malus niedzwetzkyana (Dieck) Langenf transcriptome comparison and phylogenetic analysis with Malus sieversii (Ledeb) Roem. Genetic Resources and Crop Evolution, 2020, 67, 313-323.	1.6	3
1775	Discovering nuclear targeting signal sequence through protein language learning and multivariate analysis. Analytical Biochemistry, 2020, 591, 113565.	2.4	25
1776	Is the E.Âcoli Homolog of the Formate/Nitrite Transporter Family an Anion Channel? A Computational Study. Biophysical Journal, 2020, 118, 846-860.	0.5	3
1777	NMR-based investigation into protein phosphorylation. International Journal of Biological Macromolecules, 2020, 145, 53-63.	7.5	15
1778	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. Journal of Molecular Biology, 2020, 432, 3379-3387.	4.2	46
1779	Shot-gun proteomics: why thousands of unidentified signals matter. FEMS Yeast Research, 2020, 20, .	2.3	14
1780	Comparative genomics reveals divergent thermal selection in warmâ€•and coldâ€•tolerant marine mussels. Molecular Ecology, 2020, 29, 519-535.	3.9	24
1781	Detecting sequence variants in clinically important protozoan parasites. International Journal for Parasitology, 2020, 50, 1-18.	3.1	2
1782	Reinforcement Learning for Bioretrosynthesis. ACS Synthetic Biology, 2020, 9, 157-168.	3.8	77
1783	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. Journal of Computational Biology, 2020, 27, 1283-1294.	1.6	0

#	ARTICLE	IF	CITATIONS
1784	Multiple antibodies targeting tumor-specific mutations redirect immune cells to inhibit tumor growth and increase survival in experimental animal models. <i>Clinical and Translational Oncology</i> , 2020, 22, 1094-1104.	2.4	2
1785	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	14.5	13
1786	Barley long non-coding RNAs (lncRNA) responsive to excess boron. <i>Genomics</i> , 2020, 112, 1947-1955.	2.9	20
1787	Emulsifying peptides from potato protein predicted by bioinformatics: Stabilization of fish oil-in-water emulsions. <i>Food Hydrocolloids</i> , 2020, 101, 105529.	10.7	45
1788	LINCS Data Portal 2.0: next generation access point for perturbation-response signatures. <i>Nucleic Acids Research</i> , 2020, 48, D431-D439.	14.5	112
1789	Diversity & tractability revisited in collaborative small molecule phenotypic screening library design. <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115192.	3.0	6
1790	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	5.7	10
1791	Gingimaps: Protein Localization in the Oral Pathogen <i>Porphyrromonas gingivalis</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2020, 84, .	6.6	18
1792	PHARMIP: An insilico method to predict genetics that underpin adverse drug reactions. <i>MethodsX</i> , 2020, 7, 100775.	1.6	6
1793	A comparative synthesis of transcriptomic analyses reveals major differences between WSSV-susceptible <i>Litopenaeus vannamei</i> and WSSV-refractory <i>Macrobrachium rosenbergii</i> . <i>Developmental and Comparative Immunology</i> , 2020, 104, 103564.	2.3	23
1794	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. <i>Nature Ecology and Evolution</i> , 2020, 4, 250-260.	7.8	38
1795	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	17.5	273
1796	Quantization of SnO2 dots: Apoptosis and intrinsic effect of quantum dots for myoblast cancer cells with caspase 3/7 genes. <i>Ceramics International</i> , 2020, 46, 6383-6395.	4.8	3
1797	Predâ€MutHTP: Prediction of diseaseâ€causing and neutral mutations in human transmembrane proteins. <i>Human Mutation</i> , 2020, 41, 581-590.	2.5	21
1798	Systematic analysis of alterations in the ubiquitin proteolysis system reveals its contribution to driver mutations in cancer. <i>Nature Cancer</i> , 2020, 1, 122-135.	13.2	30
1799	Ligand binding and activation of UTP-activated G protein-coupled P2Y2 and P2Y4 receptors elucidated by mutagenesis, pharmacological and computational studies. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129501.	2.4	6
1800	Expression and function of the stromal cell-derived factor-1 (SDF-1) and CXC chemokine receptor 4 (CXCR4) in the swine ovarian follicle. <i>Domestic Animal Endocrinology</i> , 2020, 71, 106404.	1.6	8
1801	Association of polymorphism in heat shock protein 70 genes with type 2 diabetes in Bangladeshi population. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1073.	1.2	8

#	ARTICLE	IF	CITATIONS
1802	mitoXplorer, a visual data mining platform to systematically analyze and visualize mitochondrial expression dynamics and mutations. <i>Nucleic Acids Research</i> , 2020, 48, 605-632.	14.5	47
1803	Bioprofiles and mechanistic pathways associated with Cheyne-Stokes respiration: insights from the SERVE-HF trial. <i>Clinical Research in Cardiology</i> , 2020, 109, 881-891.	3.3	5
1804	Proteomic and Metabolic Elucidation of Solar-Powered Biomanufacturing by Bio-Abiotic Hybrid System. <i>CheM</i> , 2020, 6, 234-249.	11.7	60
1805	SCGid: a consensus approach to contig filtering and genome prediction from single-cell sequencing libraries of uncultured eukaryotes. <i>Bioinformatics</i> , 2020, 36, 1994-2000.	4.1	2
1806	Multi-step bioconversion of annonalide by <i>Fusarium oxysporum</i> f. sp. <i>tracheiphilum</i> and theoretical investigation of the decarboxylase pathway. <i>Journal of Molecular Structure</i> , 2020, 1204, 127514.	3.6	9
1807	Elimination of bitter-off taste of stevioside through structure modification and computational interventions. <i>Journal of Theoretical Biology</i> , 2020, 486, 110094.	1.7	26
1808	Genomic landscape and genetic manipulation of the black soldier fly <i>Hermetia illucens</i> , a natural waste recycler. <i>Cell Research</i> , 2020, 30, 50-60.	12.0	136
1809	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. <i>Nature Methods</i> , 2020, 17, 41-44.	19.0	882
1810	Towards discovery of new leishmanicidal scaffolds able to inhibit <i>Leishmania</i> GSK-3. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2020, 35, 199-210.	5.2	12
1811	Multi-omics approaches to human biological age estimation. <i>Mechanisms of Ageing and Development</i> , 2020, 185, 111192.	4.6	32
1812	Structural and Functional Analyses of Human ChaC2 in Glutathione Metabolism. <i>Biomolecules</i> , 2020, 10, 31.	4.0	12
1813	Exercise immunology: Future directions. <i>Journal of Sport and Health Science</i> , 2020, 9, 432-445.	6.5	73
1814	BITS2019: the sixteenth annual meeting of the Italian society of bioinformatics. <i>BMC Bioinformatics</i> , 2020, 21, 363.	2.6	1
1815	Executable biochemical space for specification and analysis of biochemical systems. <i>PLoS ONE</i> , 2020, 15, e0238838.	2.5	4
1816	Physico-chemical characterization and topological analysis of pathogenesis-related proteins from <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> using in-silico approaches. <i>PLoS ONE</i> , 2020, 15, e0239836.	2.5	32
1817	On-chip protein separation with single-molecule resolution. <i>Scientific Reports</i> , 2020, 10, 15313.	3.3	6
1818	Molecular and cellular paradigms of multidrug resistance in cancer. <i>Cancer Reports</i> , 2022, 5, e1291.	1.4	56
1819	Storage, partitioning, indexing and retrieval in Big RDF frameworks: A survey. <i>Computer Science Review</i> , 2020, 38, 100309.	15.3	10

#	ARTICLE	IF	CITATIONS
1820	Rapid evolution of genome-wide gene expression and plasticity during saline to freshwater invasions by the copepod <i>Eurytemora affinis</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 4835-4856.	3.9	19
1821	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	3.6	14
1822	New Lineage of Microbial Predators Adds Complexity to Reconstructing the Evolutionary Origin of Animals. <i>Current Biology</i> , 2020, 30, 4500-4509.e5.	3.9	24
1823	Single-nucleotide polymorphism of the DNA cytosine deaminase APOBEC3H haplotype I leads to enzyme destabilization and correlates with lung cancer. <i>NAR Cancer</i> , 2020, 2, zcaa023.	3.1	13
1824	In Silico Prediction of the Effects of Nonsynonymous Single Nucleotide Polymorphisms in the Human Catechol-O-Methyltransferase (COMT) Gene. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 227-239.	1.8	4
1825	Polyphyletic origin, intracellular invasion, and meiotic genes in the putatively asexual agamococcidians (Apicomplexa incertae sedis). <i>Scientific Reports</i> , 2020, 10, 15847.	3.3	10
1826	Identification of osteoporosis markers through bioinformatic functional analysis of serum proteome. <i>Medicine (United States)</i> , 2020, 99, e22172.	1.0	5
1827	In silico analysis of the functional and structural consequences of SNPs in human ARX gene associated with EIEE1. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100447.	3.4	7
1828	Late first trimester circulating microparticle proteins predict the risk of preeclampsia ≥ 35 weeks and suggest phenotypic differences among affected cases. <i>Scientific Reports</i> , 2020, 10, 17353.	3.3	9
1829	A Network Pharmacology Technique to Investigate the Synergistic Mechanisms of <i>Salvia miltiorrhiza</i> and <i>Radix puerariae</i> in Treatment of Cardio-Cerebral Vascular Diseases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-18.	1.2	6
1830	Dendritic Cells and Microglia Have Non-redundant Functions in the Inflamed Brain with Protective Effects of Type 1 cDCs. <i>Cell Reports</i> , 2020, 33, 108291.	6.4	39
1831	Presynaptic PRRT2 Deficiency Causes Cerebellar Dysfunction and Paroxysmal Kinesigenic Dyskinesia. <i>Neuroscience</i> , 2020, 448, 272-286.	2.3	22
1832	A disintegrin and metalloproteinase domain 17-epidermal growth factor receptor signaling contributes to oral cancer pain. <i>Pain</i> , 2020, 161, 2330-2343.	4.2	8
1833	Effects of Single-Nucleotide Polymorphisms in Calmodulin-Dependent Protein Kinase Kinase 2 (CAMKK2): A Comprehensive Study. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-9.	1.3	1
1834	Improved preparation of group-specific component (Gc) protein to derive macrophage activating factor. <i>Protein Expression and Purification</i> , 2020, 175, 105714.	1.3	0
1835	Sequence alignment generation using intermediate sequence search for homology modeling. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2043-2050.	4.1	2
1836	Transcriptome dataset for RNA-seq analysis of axolotl embryonic oropharyngeal endoderm explants. <i>Data in Brief</i> , 2020, 32, 106126.	1.0	1
1837	In-silico prediction of role of chitosan, chondroitin sulphate and agar in process of wound healing towards scaffold development. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100406.	3.4	6

#	ARTICLE	IF	CITATIONS
1838	Computational and drug target analysis of functional single nucleotide polymorphisms associated with Haemoglobin Subunit Beta (HBB) gene. Computers in Biology and Medicine, 2020, 125, 104018.	7.0	1
1839	Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. Nature Methods, 2020, 17, 985-988.	19.0	23
1840	<i>In silico</i> and <i>in vitro</i> investigations on the protein-protein interactions of glutathione S-transferases with mitogen-activated protein kinase 8 and apoptosis signal-regulating kinase 1. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1430-1440.	3.5	6
1841	The articles.ELM resource: simplifying access to protein linear motif literature by annotation, text-mining and classification. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	5
1842	Data-driven rational biosynthesis design: from molecules to cell factories. Briefings in Bioinformatics, 2020, 21, 1238-1248.	6.5	9
1843	Comparative genomics and transcriptomics of 4 Paragonimus species provide insights into lung fluke parasitism and pathogenesis. GigaScience, 2020, 9, .	6.4	18
1844	Selective Hydrolysis of Terminal Glycosidic Bond in α -Acid Glycoprotein Promoted by Keggins and Wells's Dawson Type Heteropolyacids. Chemistry - A European Journal, 2020, 26, 16463-16471.	3.3	4
1845	Shared up-regulation and contrasting down-regulation of gene expression distinguish desiccation-tolerant from intolerant green algae. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17438-17445.	7.1	22
1846	SNAREs bind the Rhg1 SNAP and mediate soybean cyst nematode resistance. Plant Journal, 2020, 104, 318-331.	5.7	24
1847	Investigation on the Mechanism of Qubi Formula in Treating Psoriasis Based on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-13.	1.2	6
1848	Computational identification of receptor-like kinases and receptor-like proteins in legumes. BMC Genomics, 2020, 21, 459.	2.8	16
1849	Computational systematic selectivity of the Fasalog inhibitors between ROCK-I and ROCK-II kinase isoforms in Alzheimer's disease. Computational Biology and Chemistry, 2020, 87, 107314.	2.3	4
1850	Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases. Genomics, Proteomics and Bioinformatics, 2020, 18, 91-103.	6.9	14
1851	Shikonin induces tumor apoptosis in glioma cells via endoplasmic reticulum stress, and Bax/Bak mediated mitochondrial outer membrane permeability. Journal of Ethnopharmacology, 2020, 263, 113059.	4.1	22
1852	DeepHelicon: Accurate prediction of inter-helical residue contacts in transmembrane proteins by residual neural networks. Journal of Structural Biology, 2020, 212, 107574.	2.8	11
1853	Mapping Coeliac Toxic Motifs in the Prolamin Seed Storage Proteins of Barley, Rye, and Oats Using a Curated Sequence Database. Frontiers in Nutrition, 2020, 7, 87.	3.7	18
1854	The gain-of-function allele <i>bamA</i> _{E470K} bypasses the essential requirement for BamD in β -barrel outer membrane protein assembly. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18737-18743.	7.1	23
1855	The barley lectin, horcolin, binds high-mannose glycans in a multivalent fashion, enabling high-affinity, specific inhibition of cellular HIV infection. Journal of Biological Chemistry, 2020, 295, 12111-12129.	3.4	8

#	ARTICLE	IF	CITATIONS
1856	Heat9 is an infection responsive gene that affects cytokine production in alveolar epithelial cells. PLoS ONE, 2020, 15, e0236195.	2.5	4
1857	Chemical genetic analysis of FTY720 and Ca^{2+} -sensitive mutants reveals a functional connection between FTY720 and membrane trafficking. Genes To Cells, 2020, 25, 637-645.	1.2	1
1858	Using phosphoproteomics data to understand cellular signaling: a comprehensive guide to bioinformatics resources. Clinical Proteomics, 2020, 17, 27.	2.1	35
1859	Liver transcriptome resources of four commercially exploited teleost species. Scientific Data, 2020, 7, 214.	5.3	4
1860	Attractor Concepts to Evaluate the Transcriptome-wide Dynamics Guiding Anaerobic to Aerobic State Transition in Escherichia coli. Scientific Reports, 2020, 10, 5878.	3.3	12
1861	TraPS-Varl: Identifying genetic variants altering phosphotyrosine based signalling motifs. Scientific Reports, 2020, 10, 8453.	3.3	1
1862	Phosphodiesterase Inhibitors for Alzheimer's Disease: A Systematic Review of Clinical Trials and Epidemiology with a Mechanistic Rationale. Journal of Alzheimer's Disease Reports, 2020, 4, 185-215.	2.2	59
1863	Spatiotemporal Proteomic Analysis of Stress Granule Disassembly Using APEX Reveals Regulation by SUMOylation and Links to ALS Pathogenesis. Molecular Cell, 2020, 80, 876-891.e6.	9.7	154
1864	Assessing the Ability of Developmentally Precocious Estrogen Signaling to Recapitulate Ovarian Transcriptomes and Follicle Dynamics in Alligators from a Contaminated Lake. Environmental Health Perspectives, 2020, 128, 117003.	6.0	8
1865	PATH ^{cre8} : A Tool That Facilitates the Searching for Heterologous Biosynthetic Routes. ACS Synthetic Biology, 2020, 9, 3217-3227.	3.8	7
1866	E3 Ubiquitin Ligase APC/CCdh1 Negatively Regulates FAH Protein Stability by Promoting Its Polyubiquitination. International Journal of Molecular Sciences, 2020, 21, 8719.	4.1	3
1867	A Network Pharmacology-Based Strategy for Unveiling the Mechanisms of Tripterygium Wilfordii Hook F against Diabetic Kidney Disease. Journal of Diabetes Research, 2020, 2020, 1-14.	2.3	10
1868	Modelling of pathogen-host systems using deeper ORF annotations and transcriptomics to inform proteomics analyses. Computational and Structural Biotechnology Journal, 2020, 18, 2836-2850.	4.1	7
1869	Top-Down Proteomics of Endogenous Membrane Proteins Enabled by Cloud Point Enrichment and Multidimensional Liquid Chromatography-Mass Spectrometry. Analytical Chemistry, 2020, 92, 15726-15735.	6.5	24
1870	Solving a furan fatty acid biosynthesis puzzle. Journal of Biological Chemistry, 2020, 295, 9802-9803.	3.4	4
1871	Identification of the anti-breast cancer targets of triterpenoids in Liquidambaris Fructus and the hints for its traditional applications. BMC Complementary Medicine and Therapies, 2020, 20, 369.	2.7	7
1872	Role of cardiac drugs and flavonoids on the IRE1-JNK pathway as revealed by re-ranked molecular docking scores, MM/PBSA and umbrella sampling. Journal of Biomolecular Structure and Dynamics, 2022, 40, 3428-3450.	3.5	2
1873	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. Cell Reports, 2020, 33, 108450.	6.4	37

#	ARTICLE	IF	CITATIONS
1874	Structural and conformational changes induced by missense variants in the zinc finger domains of GATA3 involved in breast cancer. RSC Advances, 2020, 10, 39640-39653.	3.6	8
1875	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. Frontiers in Environmental Science, 2020, 8, .	3.3	7
1876	Impact of Porcine Arterivirus, Influenza B, and Their Coinfection on Antiviral Response in the Porcine Lung. Pathogens, 2020, 9, 934.	2.8	8
1877	The identification and characterisation of novel bioactive peptides derived from porcine liver. Current Research in Food Science, 2020, 3, 314-321.	5.8	18
1878	Genome Analysis of <i>Candidatus</i> Regiella insecticola Strain TUt, Facultative Bacterial Symbiont of the Pea Aphid <i>Acyrtosiphon pisum</i> . Microbiology Resource Announcements, 2020, 9, .	0.6	1
1879	Computational Prediction of Antiangiogenesis Synergistic Mechanisms of Total Saponins of Panax japonicus Against Rheumatoid Arthritis. Frontiers in Pharmacology, 2020, 11, 566129.	3.5	4
1880	Bringing New Methods to the Seed Proteomics Platform: Challenges and Perspectives. International Journal of Molecular Sciences, 2020, 21, 9162.	4.1	19
1881	Mechanism of Action of Bu-Fei-Yi-Shen Formula in Treating Chronic Obstructive Pulmonary Disease Based on Network Pharmacology Analysis and Molecular Docking Validation. BioMed Research International, 2020, 2020, 1-12.	1.9	8
1882	Parthenolide inhibits the growth of non-small cell lung cancer by targeting epidermal growth factor receptor. Cancer Cell International, 2020, 20, 561.	4.1	20
1883	Succinylation Site Prediction Based on Protein Sequences Using the IFS-LightGBM (BO) Model. Computational and Mathematical Methods in Medicine, 2020, 2020, 1-15.	1.3	17
1884	A human cell atlas of fetal gene expression. Science, 2020, 370, .	12.6	436
1885	ConCysFind: a pipeline tool to predict conserved amino acids of protein sequences across the plant kingdom. BMC Bioinformatics, 2020, 21, 490.	2.6	3
1886	Triage of documents containing protein interactions affected by mutations using an NLP based machine learning approach. BMC Genomics, 2020, 21, 773.	2.8	6
1887	Molecular signatures of the rediae, cercariae and adult stages in the complex life cycles of parasitic flatworms (Digenea: Psilostomatidae). Parasites and Vectors, 2020, 13, 559.	2.5	4
1888	AimB Is a Small Protein Regulator of Cell Size and MreB Assembly. Biophysical Journal, 2020, 119, 593-604.	0.5	3
1889	Structural Biological Characteristics of CK1-Like Protein Kinase Isoforms Associated with Regulation of Plant Microtubules. Cytology and Genetics, 2020, 54, 293-304.	0.5	0
1890	Effect of using a nitrogen atmosphere on enzyme hydrolysis at high corn stover loadings in an agitated reactor. Biotechnology Progress, 2020, 36, e3059.	2.6	11
1891	COSMO: A dynamic programming algorithm for multicriteria codon optimization. Computational and Structural Biotechnology Journal, 2020, 18, 1811-1818.	4.1	6

#	ARTICLE	IF	CITATIONS
1892	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	14.5	410
1893	Computational Design and Experimental Confirmation of a Head-to-Tail Cyclic Peptide to Target Human Bone Morphogenic Protein 2 based on its Type-IA Receptor. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, , .	0.8	0
1894	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	2.8	23
1895	Sexually Dimorphic Crosstalk at the Maternal-Fetal Interface. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e4831-e4847.	3.6	48
1896	Predicting the Realâ€Valued Interâ€Residue Distances for Proteins. <i>Advanced Science</i> , 2020, 7, 2001314.	11.2	42
1897	Prediction of Neuropeptides from Sequence Information Using Ensemble Classifier and Hybrid Features. <i>Journal of Proteome Research</i> , 2020, 19, 3732-3740.	3.7	31
1898	Characterization of a SPM-1 metallo-beta-lactamase-producing <i>Pseudomonas aeruginosa</i> by comparative genomics and phenotypic analysis. <i>Scientific Reports</i> , 2020, 10, 13192.	3.3	9
1899	Comprehensive chemotaxonomic and genomic profiling of a biosynthetically talented Australian fungus, <i>Aspergillus burnettii</i> sp. nov.. <i>Fungal Genetics and Biology</i> , 2020, 143, 103435.	2.1	19
1900	Leveraging computational genomics to understand the molecular basis of metal homeostasis. <i>New Phytologist</i> , 2020, 228, 1472-1489.	7.3	4
1901	Shedding the Light on <i>Litopenaeus vannamei</i> Differential Muscle and Hepatopancreas Immune Responses in White Spot Syndrome Virus (WSSV) Exposure. <i>Genes</i> , 2020, 11, 805.	2.4	12
1902	(Phospho)proteomic Profiling of Microsatellite Unstable CRC Cells Reveals Alterations in Nuclear Signaling and Cholesterol Metabolism Caused by Frameshift Mutation of NMD Regulator UPF3A. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5234.	4.1	6
1903	TEX15 is an essential executor of MIWI2-directed transposon DNA methylation and silencing. <i>Nature Communications</i> , 2020, 11, 3739.	12.8	44
1904	A detailed in silico analysis of the amylolytic family GH126 and its possible relatedness to family GH76. <i>Carbohydrate Research</i> , 2020, 494, 108082.	2.3	7
1905	Metabolomics as an Emerging Tool in the Search for Astrobiologically Relevant Biomarkers. <i>Astrobiology</i> , 2020, 20, 1251-1261.	3.0	16
1906	Tol-Pal System and Rgs Proteins Interact to Promote Unipolar Growth and Cell Division in <i>Sinorhizobium meliloti</i> . <i>MBio</i> , 2020, 11, .	4.1	18
1907	Modelling and Recognition of Protein Contact Networks by Multiple Kernel Learning and Dissimilarity Representations. <i>Entropy</i> , 2020, 22, 794.	2.2	5
1908	From pan-genome to protein dynamics: A computational hierarchical quest to identify drug target in multi-drug resistant <i>Burkholderia cepacia</i> . <i>Journal of Molecular Liquids</i> , 2020, 317, 113904.	4.9	2
1909	GapMind: Automated Annotation of Amino Acid Biosynthesis. <i>MSystems</i> , 2020, 5, .	3.8	40

#	ARTICLE	IF	CITATIONS
1910	Full-length transcriptome sequences of ridgetail white prawn <i>Exopalaemon carinicauda</i> provide insight into gene expression dynamics during thermal stress. <i>Science of the Total Environment</i> , 2020, 747, 141238.	8.0	13
1911	Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data. <i>Genome Biology</i> , 2020, 21, 190.	8.8	67
1912	Bioactive Conformational Ensemble Server and Database. A Public Framework to Speed Up <i>In Silico</i> Drug Discovery. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 6586-6597.	5.3	10
1913	Comparative Genome Analysis Reveals <i>Cyanidiococcus</i> gen. nov., A New Extremophilic Red Algal Genus Sister to <i>Cyanidioschyzon</i> (<i>Cyanidioschyzonaceae</i> , <i>Rhodophyta</i>). <i>Journal of Phycology</i> , 2020, 56, 1428-1442.	2.3	22
1914	GiTx1 (β -theraphotoxin-Gi1a), a novel toxin from the venom of Brazilian tarantula <i>Grammostola iheringi</i> (Mygalomorphae, Theraphosidae): Isolation, structural assessments and activity on voltage-gated ion channels. <i>Biochimie</i> , 2020, 176, 138-149.	2.6	1
1915	A review of computational drug repositioning: strategies, approaches, opportunities, challenges, and directions. <i>Journal of Cheminformatics</i> , 2020, 12, 46.	6.1	194
1916	How to Illuminate the Dark Proteome Using the Multi-omic OpenProt Resource. <i>Current Protocols in Bioinformatics</i> , 2020, 71, e103.	25.8	4
1917	Immunoinformatics-guided design of an epitope-based vaccine against severe acute respiratory syndrome coronavirus 2 spike glycoprotein. <i>Computers in Biology and Medicine</i> , 2020, 124, 103967.	7.0	62
1918	Transcriptomic profiling of the medicinal plant <i>Clitoria ternatea</i> : identification of potential genes in cyclotide biosynthesis. <i>Scientific Reports</i> , 2020, 10, 12658.	3.3	11
1919	Identification of potential <i>Leishmania chagasi</i> superoxide dismutase allosteric modulators by structure-based computational approaches: homology modelling, molecular dynamics and pharmacophore-based virtual screening. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 7000-7016.	3.5	3
1920	JAGN1, tetraspanins, and Erv proteins: is common topology indicative of common function in cargo sorting?. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 319, C667-C674.	4.6	2
1921	S-layer associated proteins contribute to the adhesive and immunomodulatory properties of <i>Lactobacillus acidophilus</i> NCFM. <i>BMC Microbiology</i> , 2020, 20, 248.	3.3	18
1922	Characterization of an acid rock drainage microbiome and transcriptome at the Ely Copper Mine Superfund site. <i>PLoS ONE</i> , 2020, 15, e0237599.	2.5	7
1923	Pan-cancer proteogenomic analysis reveals long and circular noncoding RNAs encoding peptides. <i>NAR Cancer</i> , 2020, 2, zcaa015.	3.1	18
1924	p39-associated Cdk5 activity regulates dendritic morphogenesis. <i>Scientific Reports</i> , 2020, 10, 18746.	3.3	9
1925	Proximity labeling in mammalian cells with TurboID and split-TurboID. <i>Nature Protocols</i> , 2020, 15, 3971-3999.	12.0	171
1926	The Dynamic Proteome of Oligodendrocyte Lineage Differentiation Features Planar Cell Polarity and Macroautophagy Pathways. <i>GigaScience</i> , 2020, 9, .	6.4	10
1927	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. <i>Open Biology</i> , 2020, 10, 200149.	3.6	7

#	ARTICLE	IF	CITATIONS
1928	Vulpeculin: a novel and abundant lipocalin in the urine of the common brushtail possum, <i>Trichosurus vulpecula</i>. Open Biology, 2020, 10, 200218.	3.6	2
1929	Immuno-Informatics based Peptides: An Approach for Vaccine Development against Outer Membrane Proteins of Pseudomonas Genus. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	1
1930	SPOTONE: Hot Spots on Protein Complexes with Extremely Randomized Trees via Sequence-Only Features. International Journal of Molecular Sciences, 2020, 21, 7281.	4.1	12
1931	Oxidant-induced glutathionylation at protein disulfide bonds. Free Radical Biology and Medicine, 2020, 160, 513-525.	2.9	14
1932	Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. Mycobiology, 2020, 48, 373-382.	1.7	9
1933	Benchmarking gene ontology function predictions using negative annotations. Bioinformatics, 2020, 36, i210-i218.	4.1	12
1934	Transcriptomic data on the transgenerational exposure of the keystone amphipod Gammarus locusta to simvastatin. Data in Brief, 2020, 32, 106248.	1.0	7
1935	On the Optimization of Embedding Spaces via Information Granulation for Pattern Recognition. , 2020, , .		6
1936	Chromatin accessibility dynamics of Chlamydia-infected epithelial cells. Epigenetics and Chromatin, 2020, 13, 45.	3.9	6
1937	Long non-coding RNAs in plants: emerging modulators of gene activity in development and stress responses. Planta, 2020, 252, 92.	3.2	57
1938	Network pharmacology-based investigation on the mechanisms of action of Morinda officinalis How. in the treatment of osteoporosis. Computers in Biology and Medicine, 2020, 127, 104074.	7.0	26
1939	The adenoviral protein E4orf4: a probing tool to decipher mechanical stress-induced nuclear envelope remodeling in tumor cells. Cell Cycle, 2020, 19, 2963-2981.	2.6	0
1940	Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. BMC Bioinformatics, 2020, 21, 469.	2.6	14
1941	<i>GNAO1</i>organizes the cytoskeletal remodeling and firing of developing neurons. FASEB Journal, 2020, 34, 16601-16621.	0.5	14
1942	Molecular insights into the powerful mucus-based adhesion of limpets (<i>Patella vulgata</i> L.). Open Biology, 2020, 10, 200019.	3.6	23
1943	VPTMdb: a viral posttranslational modification database. Briefings in Bioinformatics, 2021, 22, .	6.5	9
1944	RNA-binding and prion domains: the Yin and Yang of phase separation. Nucleic Acids Research, 2020, 48, 9491-9504.	14.5	57
1945	Characterization of the <i>F</i> Locus Responsible for Floral Anthocyanin Production in Potato. G3: Genes, Genomes, Genetics, 2020, 10, 3871-3879.	1.8	7

#	ARTICLE	IF	CITATIONS
1946	TargetDB: A target information aggregation tool and tractability predictor. PLoS ONE, 2020, 15, e0232644.	2.5	11
1947	Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. Analytical Chemistry, 2020, 92, 13672-13676.	6.5	1
1948	Structure of a nucleotide pyrophosphatase/phosphodiesterase (NPP) from <i>Euphorbia characias</i> characterized by small-angle X-ray scattering: clues for the general organization of plant NPPs. Acta Crystallographica Section D: Structural Biology, 2020, 76, 857-867.	2.3	1
1949	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. Genome Biology, 2020, 21, 229.	8.8	38
1950	Identification of destabilizing SNPs in SARS-CoV2-ACE2 protein and spike glycoprotein: implications for virus entry mechanisms. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1205-1215.	3.5	12
1951	The FTO Gene and Diseases: The Role of Genetic Polymorphism, Epigenetic Modifications, and Environmental Factors. Russian Journal of Genetics, 2020, 56, 1025-1043.	0.6	5
1952	N-GlycoGo: Predicting Protein N-Glycosylation Sites on Imbalanced Data Sets by Using Heterogeneous and Comprehensive Strategy. IEEE Access, 2020, 8, 165944-165950.	4.2	9
1953	Extension of the taxonomic coverage of the family GH126 outside Firmicutes and in silico characterization of its non-catalytic terminal domains. 3 Biotech, 2020, 10, 420.	2.2	5
1954	Effect of sequence padding on the performance of deep learning models in archaeal protein functional prediction. Scientific Reports, 2020, 10, 14634.	3.3	21
1955	High-resolution proteomics reveals differences in the proteome of spelt and bread wheat flour representing targets for research on wheat sensitivities. Scientific Reports, 2020, 10, 14677.	3.3	12
1956	A Cytokine Protein Identification Model Based on the Compressed PseKRAAC Features. IEEE Access, 2020, 8, 141422-141431.	4.2	0
1957	Mining and Statistical Modeling of Natural and Variant Class IIa Bacteriocins Elucidate Activity and Selectivity Profiles across Species. Applied and Environmental Microbiology, 2020, 86, .	3.1	5
1958	Vitamin D3 receptor polymorphisms regulate T cells and T cell-dependent inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24986-24997.	7.1	14
1959	Functional characterization of rare NRXN1 variants identified in autism spectrum disorders and schizophrenia. Journal of Neurodevelopmental Disorders, 2020, 12, 25.	3.1	17
1960	An allosteric site on MKP5 reveals a strategy for small-molecule inhibition. Science Signaling, 2020, 13, eaba3043.	3.6	12
1961	Functionally uncoupled transcription–translation in <i>Bacillus subtilis</i> . Nature, 2020, 585, 124-128.	27.8	109
1962	Sex differences in circulating proteins in heart failure with preserved ejection fraction. Biology of Sex Differences, 2020, 11, 47.	4.1	12
1963	Literature search – Exploring in silico protein toxicity prediction methods to support the food and feed risk assessment. EFSA Supporting Publications, 2020, 17, 1875E.	0.7	1

#	ARTICLE	IF	CITATIONS
1964	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	3.5	62
1965	Chromosome-level genome assembly of the female western mosquitofish (<i>Gambusia affinis</i>). <i>GigaScience</i> , 2020, 9, .	6.4	5
1966	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. <i>Genome Biology</i> , 2020, 21, 217.	8.8	11
1967	ANDDigest: a new web-based module of ANDSystem for the search of knowledge in the scientific literature. <i>BMC Bioinformatics</i> , 2020, 21, 228.	2.6	19
1968	Isolation and characterisation of <i>Leishmania donovani</i> protein antigens from urine of visceral leishmaniasis patients. <i>PLoS ONE</i> , 2020, 15, e0238840.	2.5	4
1969	Torin 2 Derivative, NCATS-SM3710, Has Potent Multistage Antimalarial Activity through Inhibition of <i>P. falciparum</i> Phosphatidylinositol 4-Kinase (<i>Pf</i> PI4KIII ²). <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 948-964.	4.9	19
1970	Mechanisms of indigo naturalis on treating ulcerative colitis explored by GEO gene chips combined with network pharmacology and molecular docking. <i>Scientific Reports</i> , 2020, 10, 15204.	3.3	45
1971	FLUTE: Fast and reliable knowledge retrieval from biomedical literature. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	13
1972	Large-scale prediction and analysis of protein sub-mitochondrial localization with DeepMito. <i>BMC Bioinformatics</i> , 2020, 21, 266.	2.6	6
1973	Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution. <i>Communications Biology</i> , 2020, 3, 480.	4.4	31
1974	Study on the Mechanisms of Banxia Xiexin Decoction in Treating Diabetic Gastroparesis Based on Network Pharmacology. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 487-498.	3.6	10
1975	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1740.	3.5	27
1976	Pain-CKB, A Pain-Domain-Specific Chemogenomics Knowledgebase for Target Identification and Systems Pharmacology Research. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4429-4435.	5.4	3
1977	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020, 584, 635-639.	27.8	96
1978	Prediction of Therapeutic Peptides Using Machine Learning: Computational Models, Datasets, and Feature Encodings. <i>IEEE Access</i> , 2020, 8, 148570-148594.	4.2	17
1979	PINCER: improved CRISPR/Cas9 screening by efficient cleavage at conserved residues. <i>Nucleic Acids Research</i> , 2020, 48, 9462-9477.	14.5	6
1980	Mining potentially actionable kinase gene fusions in cancer cell lines with the KuNG FU database. <i>Scientific Data</i> , 2020, 7, 420.	5.3	2
1981	Network-based approach highlighting interplay among anti-hypertensives: target coding-genes: diseases. <i>Scientific Reports</i> , 2020, 10, 20152.	3.3	0

#	ARTICLE	IF	CITATIONS
1982	AnOxPePred: using deep learning for the prediction of antioxidative properties of peptides. Scientific Reports, 2020, 10, 21471.	3.3	71
1983	Neural Network and Random Forest Models in Protein Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1772-1781.	3.0	11
1984	Alteration of Proteotranscriptomic Landscape Reveals the Transcriptional Regulatory Circuits Controlling Key-Signaling Pathways and Metabolic Reprogramming During Tumor Evolution. Frontiers in Cell and Developmental Biology, 2020, 8, 586479.	3.7	6
1985	Comparison of the central human and mouse platelet signaling cascade by systems biological analysis. BMC Genomics, 2020, 21, 897.	2.8	12
1986	Artificial Intelligence-Based Application to Explore Inhibitors of Neurodegenerative Diseases. Frontiers in Neuroinformatics, 2020, 14, 617327.	2.8	5
1987	Discovery and Structure-Activity Relationships of Novel Template, Truncated 1 α ,25-Dihydroxyvitamin D ₃ Homologated Adenosine Derivatives as Pure Dual PPAR α / γ Modulators. Journal of Medicinal Chemistry, 2020, 63, 16012-16027.	6.4	15
1988	Genetic architecture of host proteins involved in SARS-CoV-2 infection. Nature Communications, 2020, 11, 6397.	12.8	71
1989	Maternal diet alters human milk oligosaccharide composition with implications for the milk metagenome. Scientific Reports, 2020, 10, 22092.	3.3	81
1990	New information of dopaminergic agents based on quantum chemistry calculations. Scientific Reports, 2020, 10, 21581.	3.3	16
1991	Non-adaptive Evolution of Trimeric Autotransporters in Brucellaceae. Frontiers in Microbiology, 2020, 11, 560667.	3.5	3
1992	Deciphering the Role of Filamin B Calponin-Homology Domain in Causing the Larsen Syndrome, Boomerang Dysplasia, and Atelosteogenesis Type I Spectrum Disorders via a Computational Approach. Molecules, 2020, 25, 5543.	3.8	10
1993	Systematic Data Analysis and Diagnostic Machine Learning Reveal Differences between Compounds with Single- and Multitarget Activity. Molecular Pharmaceutics, 2020, 17, 4652-4666.	4.6	14
1994	Trametinib Induces the Stabilization of a Dual GNAQ p.Gly48Leu- and FGFR4 p.Cys172Gly-Mutated Uveal Melanoma. The Role of Molecular Modelling in Personalized Oncology. International Journal of Molecular Sciences, 2020, 21, 8021.	4.1	3
1995	The Cyclically Seasonal Drosophila subobscura Inversion O7 Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. Frontiers in Genetics, 2020, 11, 565836.	2.3	4
1996	Identification and characterization of a rare variant in apolipoprotein A-IV, p.(V336M), and evaluation of HDL functionality in a Greek cohort with extreme HDL cholesterol levels. Archives of Biochemistry and Biophysics, 2020, 696, 108655.	3.0	1
1997	Potential novel proteomic biomarkers for diagnosis of vertebral osteomyelitis identified using an immunomics protein array technique. Medicine (United States), 2020, 99, e22852.	1.0	1
1998	Expression of a novel brain specific isoform of C3G is regulated during development. Scientific Reports, 2020, 10, 18838.	3.3	8
1999	Proteomic analysis of platelet-rich and platelet-poor plasma. Regenerative Therapy, 2020, 15, 226-235.	3.0	13

#	ARTICLE	IF	CITATIONS
2000	Transcriptomics reveals specific molecular mechanisms underlying transgenerational immunity in <i>Manduca sexta</i> . Ecology and Evolution, 2020, 10, 11251-11261.	1.9	6
2001	The Cellular Response to Lanthanum Is Substrate Specific and Reveals a Novel Route for Glycerol Metabolism in <i>Pseudomonas putida</i> KT2440. MBio, 2020, 11, .	4.1	17
2002	Comparative Computational Modeling of Agonist Binding to the Leukotriene Receptors BLT1 and BLT2. Molecular Biology, 2020, 54, 299-309.	1.3	0
2003	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. Cell Systems, 2020, 10, 333-350.e14.	6.2	48
2004	Computational approach for collection and prediction of molecular initiating events in developmental toxicity. Reproductive Toxicology, 2020, 94, 55-64.	2.9	2
2005	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. Bioinformatics, 2020, 36, 4088-4090.	4.1	42
2006	Quantitative analysis of amino acid metabolism in liver cancer links glutamate excretion to nucleotide synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10294-10304.	7.1	45
2007	Salivary proteome signatures in the early and middle stages of human pregnancy with term birth outcome. Scientific Reports, 2020, 10, 8022.	3.3	13
2008	Tyrosinase-Targeting Gallacetophenone Inhibits Melanogenesis in Melanocytes and Human Skin-Equivalents. International Journal of Molecular Sciences, 2020, 21, 3144.	4.1	12
2009	Characterization and identification of antimicrobial peptides with different functional activities. Briefings in Bioinformatics, 2020, 21, 1098-1114.	6.5	83
2010	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. ISME Journal, 2020, 14, 2164-2178.	9.8	33
2011	Identification of promising compounds from curry tree with cyclooxygenase inhibitory potential using a combination of machine learning, molecular docking, dynamics simulations and binding free energy calculations. Molecular Simulation, 2020, 46, 812-822.	2.0	9
2012	BpForms and BcForms: a toolkit for concretely describing non-canonical polymers and complexes to facilitate global biochemical networks. Genome Biology, 2020, 21, 117.	8.8	8
2013	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. Science Translational Medicine, 2020, 12, .	12.4	60
2014	Anti-vimentin, anti-TUFM, anti-NAP1L1 and anti-DPYSL2 nanobodies display cytotoxic effect and reduce glioblastoma cell migration. Therapeutic Advances in Medical Oncology, 2020, 12, 175883592091530.	3.2	25
2015	A Rapid, Sensitive, Low-Cost Assay for Detecting Hydrogenotrophic Methanogens in Anaerobic Digesters Using Loop-Mediated Isothermal Amplification. Microorganisms, 2020, 8, 740.	3.6	5
2016	Balancing selection in Pattern Recognition Receptor signalling pathways is associated with gene function and pleiotropy in a wild rodent. Molecular Ecology, 2020, 29, 1990-2003.	3.9	8
2017	Chaperone client proteins evolve slower than non-client proteins. Functional and Integrative Genomics, 2020, 20, 621-631.	3.5	6

#	ARTICLE	IF	CITATIONS
2018	First Report of CR1 Polymorphisms and Soluble CR1 Levels Associated with Late Onset Alzheimerâ€™s Disease (LOAD) in Latin America. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1338-1344.	2.3	6
2019	Rhodoxanthin synthase from honeysuckle; a membrane diiron enzyme catalyzes the multistep conversion of l ² -carotene to rhodoxanthin. <i>Science Advances</i> , 2020, 6, eaay9226.	10.3	7
2020	MyoMiner: explore gene co-expression in normal and pathological muscle. <i>BMC Medical Genomics</i> , 2020, 13, 67.	1.5	7
2021	The Bioinformatic and In Vitro Studies of Clostridioides Difficile Aminopeptidase M24 Revealed the Immunoreactive KKGK Peptide. <i>Cells</i> , 2020, 9, 1146.	4.1	2
2022	Eight novel variants in the <i>SLC34A2</i> gene in pulmonary alveolar microlithiasis. <i>European Respiratory Journal</i> , 2020, 55, 1900806.	6.7	14
2023	RNA-protein coevolution study of Gemin5 uncovers the role of the PXSS motif of RBS1 domain for RNA binding. <i>RNA Biology</i> , 2020, 17, 1331-1341.	3.1	10
2024	Binding modes of cabazitaxel with the different human Î²-tubulin isotypes: DFT and MD studies. <i>Journal of Molecular Modeling</i> , 2020, 26, 162.	1.8	6
2025	Integrated omics in Drosophila uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	12.8	23
2026	PredDBP-Stack: Prediction of DNA-Binding Proteins from HMM Profiles using a Stacked Ensemble Method. <i>BioMed Research International</i> , 2020, 2020, 1-8.	1.9	6
2027	Comprehensive analysis of Translationally Controlled Tumor Protein (TCTP) provides insights for lineage-specific evolution and functional divergence. <i>PLoS ONE</i> , 2020, 15, e0232029.	2.5	3
2028	Computational Investigation of APOBEC3H Substrate Orientation and Selectivity. <i>Journal of Physical Chemistry B</i> , 2020, 124, 3903-3908.	2.6	1
2029	Reversal of Regioselectivity in Zincâ€Dependent Mediumâ€Chain Alcohol Dehydrogenase from Rhodococcus erythropolis toward Octanone Derivatives. <i>ChemBioChem</i> , 2020, 21, 2957-2965.	2.6	6
2030	ABC Transporter DerAB of Lactobacillus casei Mediates Resistance against Insect-Derived Defensins. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	3
2031	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020, 16, e1007775.	3.2	11
2032	Viral hijacking of the TENT4â€ZCCHC14 complex protects viral RNAs via mixed tailing. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 581-588.	8.2	42
2033	In Silico Subtractive Proteomics Approach for Identification of Potential Drug Targets in Staphylococcus saprophyticus. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 3644.	2.6	22
2034	Draft Genome of the Macadamia Husk Spot Pathogen, Pseudocercospora macadamiae. <i>Phytopathology</i> , 2020, 110, 1503-1506.	2.2	2
2035	Structural basis for membrane insertion by the human ER membrane protein complex. <i>Science</i> , 2020, 369, 433-436.	12.6	127

#	ARTICLE	IF	CITATIONS
2036	Comprehensive analysis of the secreted proteome of adult <i>Necator americanus</i> hookworms. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008237.	3.0	25
2037	Bacteriophage genotyping using BOXA repetitive-PCR. <i>BMC Microbiology</i> , 2020, 20, 154.	3.3	1
2038	Understanding the protein sequence and structural adaptation in extremophilic organisms through machine learning techniques. , 2020, , 307-314.		0
2039	Dataset of transcriptome assembly of date palm embryogenic calli and functional annotation. <i>Data in Brief</i> , 2020, 31, 105760.	1.0	4
2040	Genome sequence of <i>Kobresia littledalei</i> , the first chromosome-level genome in the family Cyperaceae. <i>Scientific Data</i> , 2020, 7, 175.	5.3	20
2041	A Heterogeneous Information Network Model for Long Non-Coding RNA Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 255-266.	3.0	2
2042	The role of 3'UTR-protein complexes in the regulation of protein multifunctionality and subcellular localization. <i>Nucleic Acids Research</i> , 2020, 48, 6491-6502.	14.5	7
2043	Intrinsic disorder in protein sense-antisense recognition. <i>Journal of Molecular Recognition</i> , 2020, 33, e2868.	2.1	7
2044	Exploring the mechanism of TCM formulae in the treatment of different types of coronary heart disease by network pharmacology and machine learning. <i>Pharmacological Research</i> , 2020, 159, 105034.	7.1	56
2045	Assessing predictors for new post translational modification sites: A case study on hydroxylation. <i>PLoS Computational Biology</i> , 2020, 16, e1007967.	3.2	10
2046	Time-course Transcriptome of <i>Parageobacillus thermoglucosidasius</i> DSM 6285 Grown in the Presence of Carbon Monoxide and Air. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3870.	4.1	6
2047	Genome sequence and comparative analysis of reindeer (<i>Rangifer tarandus</i>) in northern Eurasia. <i>Scientific Reports</i> , 2020, 10, 8980.	3.3	30
2048	In silico vaccine design against <i>Chlamydia trachomatis</i> infection. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 39.	2.1	9
2049	Prediction of protein-binding residues: dichotomy of sequence-based methods developed using structured complexes versus disordered proteins. <i>Bioinformatics</i> , 2020, 36, 4729-4738.	4.1	16
2050	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	14.5	41
2051	Essential roles for deubiquitination in <i>Leishmania</i> life cycle progression. <i>PLoS Pathogens</i> , 2020, 16, e1008455.	4.7	39
2052	DRUGPATH: The Drug Gene Pathway Meta-Database. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3171.	4.1	3
2053	A Proline Derivative-Enriched Fraction from <i>Sideroxylon obtusifolium</i> Protects the Hippocampus from Intracerebroventricular Pilocarpine-Induced Injury Associated with Status Epilepticus in Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4188.	4.1	6

#	ARTICLE	IF	CITATIONS
2054	Differential Urinary Proteome Analysis for Predicting Prognosis in Type 2 Diabetes Patients with and without Renal Dysfunction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4236.	4.1	30
2055	In Silico Analysis of FDA Drugs as P2X4 Modulators for the Treatment of Alcohol Use Disorder. <i>Molecular Informatics</i> , 2020, 39, e1900111.	2.5	2
2056	A bacterial biosynthetic pathway for methylated furan fatty acids. <i>Journal of Biological Chemistry</i> , 2020, 295, 9786-9801.	3.4	18
2057	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. <i>Journal of Proteome Research</i> , 2020, 19, 3478-3486.	3.7	19
2058	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	8.8	72
2059	Analysis of Virus and Host Proteomes During Productive HSV-1 and VZV Infection in Human Epithelial Cells. <i>Frontiers in Microbiology</i> , 2020, 11, 1179.	3.5	16
2060	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. <i>Aging Cell</i> , 2020, 19, e13158.	6.7	27
2061	iTRAQ-Based Proteomic Profile Analysis of the Hepatopancreas of Caribbean Spiny Lobsters Infected With <i>Panulirus argus</i> Virus 1: Metabolic and Physiological Implications. <i>Frontiers in Microbiology</i> , 2020, 11, 1084.	3.5	6
2062	The Human Body as a Super Network: Digital Methods to Analyze the Propagation of Aging. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 136.	3.4	24
2063	The Role of Bone Morphogenetic Protein Signaling in Non-Alcoholic Fatty Liver Disease. <i>Scientific Reports</i> , 2020, 10, 9831.	3.3	10
2064	A novel artificial intelligence protocol to investigate potential leads for Parkinson's disease. <i>RSC Advances</i> , 2020, 10, 22939-22958.	3.6	12
2065	Paradoxical activation of the protein kinase-transcription factor ERK5 by ERK5 kinase inhibitors. <i>Nature Communications</i> , 2020, 11, 1383.	12.8	30
2066	Cell cycle transcriptomics of <i>Capsaspora</i> provides insights into the evolution of cyclin-CDK machinery. <i>PLoS Genetics</i> , 2020, 16, e1008584.	3.5	8
2067	CD5L Constitutes a Novel Biomarker for Integrated Hepatic Thyroid Hormone Action. <i>Thyroid</i> , 2020, 30, 908-923.	4.5	8
2068	Deciphering the Active Compounds and Mechanisms of Qixuehe Capsule on Qi Stagnation and Blood Stasis Syndrome: A Network Pharmacology Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-18.	1.2	2
2069	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. <i>PLoS Biology</i> , 2020, 18, e3000631.	5.6	51
2070	Edgetic perturbation signatures represent known and novel cancer biomarkers. <i>Scientific Reports</i> , 2020, 10, 4350.	3.3	5
2071	Comprehensive in silico screening and molecular dynamics studies of missense mutations in Sjogren-Larsson syndrome associated with the ALDH3A2 gene. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 120, 349-377.	2.3	21

#	ARTICLE	IF	CITATIONS
2072	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	27.8	328
2073	Expression and distribution of CD151 as a partner of alpha6 integrin in male germ cells. <i>Scientific Reports</i> , 2020, 10, 4374.	3.3	9
2075	Design of bioactive peptides derived from CART sequence isolated from the toadfish <i>Thalassophryne nattereri</i> . <i>3 Biotech</i> , 2020, 10, 162.	2.2	4
2076	Identification of region-specific astrocyte subtypes at single cell resolution. <i>Nature Communications</i> , 2020, 11, 1220.	12.8	444
2077	Relational dynamics obtained through simulation studies of thioredoxin reductase: From a multi-drug resistant <i>Entamoeba histolytica</i> . <i>Journal of Molecular Liquids</i> , 2020, 307, 112939.	4.9	4
2078	Pharmacological Mechanisms Underlying the Neuroprotective Effects of <i>Alpinia oxyphylla</i> Miq. on Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2071.	4.1	41
2079	Design, Synthesis, and Biological Evaluation of Quinazolin-4-one-Based Hydroxamic Acids as Dual PI3K/HDAC Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4256-4292.	6.4	59
2080	Structural Genomics of SARS-CoV-2 Indicates Evolutionary Conserved Functional Regions of Viral Proteins. <i>Viruses</i> , 2020, 12, 360.	3.3	206
2081	Emergence of an evolutionary innovation: Gene expression differences associated with the transition between oviparity and viviparity. <i>Molecular Ecology</i> , 2020, 29, 1315-1327.	3.9	16
2082	Functional colour genes and signals of selection in colour-polymorphic salamanders. <i>Molecular Ecology</i> , 2020, 29, 1284-1299.	3.9	15
2083	Fibroblast-specific genome-scale modelling predicts an imbalance in amino acid metabolism in Refsum disease. <i>FEBS Journal</i> , 2020, 287, 5096-5113.	4.7	8
2084	Hepatic transcriptome of the freeze-tolerant <i>Cope's gray treefrog</i> , <i>Dryophytes chrysoscelis</i> : responses to cold acclimation and freezing. <i>BMC Genomics</i> , 2020, 21, 226.	2.8	17
2085	In silico Analysis of the tryptophan hydroxylase 2 (TPH2) protein variants related to psychiatric disorders. <i>PLoS ONE</i> , 2020, 15, e0229730.	2.5	14
2086	Protein Secondary Structure Prediction: A Review of Progress and Directions. <i>Current Bioinformatics</i> , 2020, 15, 90-107.	1.5	37
2087	Automated recognition of functional compound-protein relationships in literature. <i>PLoS ONE</i> , 2020, 15, e0220925.	2.5	3
2088	Exploring the mechanism of action Xianlingubao Prescription in the treatment of osteoporosis by network pharmacology. <i>Computational Biology and Chemistry</i> , 2020, 85, 107240.	2.3	50
2089	Two small, cysteine-rich and cationic antifungal proteins from <i>Penicillium chrysogenum</i> : A comparative study of PAF and PAFB. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183246.	2.6	20
2090	Genome sequencing of human in vitro fertilisation embryos for pathogenic variation screening. <i>Scientific Reports</i> , 2020, 10, 3795.	3.3	15

#	ARTICLE	IF	CITATIONS
2091	Laser capture microdissection coupled mass spectrometry (LCM-MS) for spatially resolved analysis of formalin-fixed and stained human lung tissues. <i>Clinical Proteomics</i> , 2020, 17, 24.	2.1	37
2092	From bag-of-genes to bag-of-genomes: metabolic modelling of communities in the era of metagenome-assembled genomes. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1722-1734.	4.1	52
2093	Identifying Protein Biomarkers in Blood for Alzheimer's Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 472.	3.7	7
2094	Pan-Proteomic Analysis and Elucidation of Protein Abundance among the Closely Related <i>Brucella</i> Species, <i>Brucella abortus</i> and <i>Brucella melitensis</i> . <i>Biomolecules</i> , 2020, 10, 836.	4.0	6
2095	The Arg/N-Degron Pathway—A Potential Running Back in Fine-Tuning the Inflammatory Response?. <i>Biomolecules</i> , 2020, 10, 903.	4.0	5
2096	X-ray Structure-Based Chemoinformatic Analysis Identifies Promiscuous Ligands Binding to Proteins from Different Classes with Varying Shapes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3782.	4.1	7
2097	Data and Text Mining Help Identify Key Proteins Involved in the Molecular Mechanisms Shared by SARS-CoV-2 and HIV-1. <i>Molecules</i> , 2020, 25, 2944.	3.8	12
2098	Pharmacological inhibition of lysine-specific demethylase 1 (LSD1) induces global transcriptional deregulation and ultrastructural alterations that impair viability in <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008332.	3.0	11
2099	Site of Action of Brain Neurosteroid Pregnenolone Sulfate at the N-Methyl-D-Aspartate Receptor. <i>Journal of Neuroscience</i> , 2020, 40, 5922-5936.	3.6	18
2100	A fully-automated method discovers loss of mouse-lethal and human-monogenic disease genes in 58 mammals. <i>Nucleic Acids Research</i> , 2020, 48, e91-e91.	14.5	7
2101	Targeted sequencing of genes associated with the mismatch repair pathway in patients with endometrial cancer. <i>PLoS ONE</i> , 2020, 15, e0235613.	2.5	4
2102	Molecular basis of the beta-lactamase protein using comparative modelling, drug screening and molecular dynamics studies to understand the resistance of β -lactam antibiotics. <i>Journal of Molecular Modeling</i> , 2020, 26, 200.	1.8	1
2103	Network pharmacology and molecular docking analysis on molecular targets and mechanisms of Huashi Baidu formula in the treatment of COVID-19. <i>Drug Development and Industrial Pharmacy</i> , 2020, 46, 1345-1353.	2.0	153
2104	Protein Interactions of the Mechanosensory Proteins Wsc2 and Wsc3 for Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3121-3135.	1.8	4
2105	The genome, transcriptome, and proteome of the fish parasite <i>Pomphorhynchus laevis</i> (Acanthocephala). <i>PLoS ONE</i> , 2020, 15, e0232973.	2.5	19
2106	Results of targeted next-generation sequencing in children with cystic kidney diseases often change the clinical diagnosis. <i>PLoS ONE</i> , 2020, 15, e0235071.	2.5	12
2107	Immunochemical analysis of pepsin-digested fish tropomyosin. <i>Food Control</i> , 2020, 118, 107427.	5.5	13
2108	Regulation of cellular senescence by eukaryotic members of the FAH superfamily — A role in calcium homeostasis?. <i>Mechanisms of Ageing and Development</i> , 2020, 190, 111284.	4.6	4

#	ARTICLE	IF	CITATIONS
2109	Identification and classification of differentially expressed genes reveal potential molecular signature associated with SARS-CoV-2 infection in lung adenocarcinoma cells. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100384.	3.4	15
2110	Genomic Analysis of Bovine <i>Staphylococcus aureus</i> Isolates from Milk To Elucidate Diversity and Determine the Distributions of Antimicrobial and Virulence Genes and Their Association with Mastitis. <i>MSystems</i> , 2020, 5, .	3.8	35
2111	Survey and Validation of tRNA Modifications and Their Corresponding Genes in <i>Bacillus subtilis</i> sp Subtilis Strain 168. <i>Biomolecules</i> , 2020, 10, 977.	4.0	21
2112	Ubiquitylation of the ER-Shaping Protein Lunapark via the CRL3KLHL12 Ubiquitin Ligase Complex. <i>Cell Reports</i> , 2020, 31, 107664.	6.4	12
2113	Impact of the Protein Data Bank on antineoplastic approvals. <i>Drug Discovery Today</i> , 2020, 25, 837-850.	6.4	24
2115	Enhancing Host-Cell Protein Detection in Protein Therapeutics Using HILIC Enrichment and Proteomic Analysis. <i>Analytical Chemistry</i> , 2020, 92, 10327-10335.	6.5	20
2116	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. <i>Molecular Informatics</i> , 2020, 39, e2000033.	2.5	4
2117	The possible role of a bacterial aspartate β -decarboxylase in the biosynthesis of alamandine. <i>Medical Hypotheses</i> , 2020, 144, 110038.	1.5	5
2118	Using AnABlast for intergenic sORF prediction in the <i>Caenorhabditis elegans</i> genome. <i>Bioinformatics</i> , 2020, 36, 4827-4832.	4.1	6
2119	Landscape of Eukaryotic Transmembrane Beta Barrel Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 1209-1221.	3.7	5
2120	PlaPPISite: a comprehensive resource for plant protein-protein interaction sites. <i>BMC Plant Biology</i> , 2020, 20, 61.	3.6	25
2121	SmartGraph: a network pharmacology investigation platform. <i>Journal of Cheminformatics</i> , 2020, 12, 5.	6.1	10
2122	Identifying Synergistic Mechanisms of Multiple Ingredients in Shuangbai Tablets against Proteinuria by Virtual Screening and a Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	1.2	4
2123	Review: Nutritional regulation of intestinal starch and protein assimilation in ruminants. <i>Animal</i> , 2020, 14, s17-s28.	3.3	23
2124	Comparison of the Transcriptome Response within the Swine Tracheobronchial Lymphnode Following Infection with PRRSV, PCV-2 or IAV-S.. <i>Pathogens</i> , 2020, 9, 99.	2.8	7
2125	Predicting lncRNA-Protein Interactions With miRNAs as Mediators in a Heterogeneous Network Model. <i>Frontiers in Genetics</i> , 2019, 10, 1341.	2.3	27
2126	New groups of protein homologues in the α -amylase family GH57 closely related to α -glucan branching enzymes and 4- α -glucanotransferases. <i>Genetica</i> , 2020, 148, 77-86.	1.1	5
2127	Phage protein receptors have multiple interaction partners and high expressions. <i>Bioinformatics</i> , 2020, 36, 2975-2979.	4.1	12

#	ARTICLE	IF	CITATIONS
2128	Carnelian uncovers hidden functional patterns across diverse study populations from whole metagenome sequencing reads. <i>Genome Biology</i> , 2020, 21, 47.	8.8	14
2130	Using proteomics for an insight into the performance of activated sludge in a lab-scale WWTP. <i>International Biodeterioration and Biodegradation</i> , 2020, 149, 104934.	3.9	10
2131	Cone snail analogs of the pituitary hormones oxytocin/vasopressin and their carrier protein neurophysin. Proteomic and transcriptomic identification of conopressins and conophysins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140391.	2.3	10
2132	Exploration and Evaluation of Machine Learning-Based Models for Predicting Enzymatic Reactions. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1833-1843.	5.4	17
2133	Enhanced clinical phenotyping by mechanistic bioprofiling in heart failure with preserved ejection fraction: insights from the MEDIA-DHF study (The Metabolic Road to Diastolic Heart Failure). <i>Biomarkers</i> , 2020, 25, 201-211.	1.9	26
2134	Alteration of retinal metabolism and oxidative stress may implicate myopic eye growth: Evidence from discovery and targeted proteomics in an animal model. <i>Journal of Proteomics</i> , 2020, 221, 103684.	2.4	19
2135	An initial comparative genomic autopsy of wasting disease in sea stars. <i>Molecular Ecology</i> , 2020, 29, 1087-1102.	3.9	22
2136	A Hybrid Model for Predicting Pattern Recognition Receptors Using Evolutionary Information. <i>Frontiers in Immunology</i> , 2020, 11, 71.	4.8	15
2137	FeGenie: A Comprehensive Tool for the Identification of Iron Genes and Iron Gene Neighborhoods in Genome and Metagenome Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 37.	3.5	195
2138	Phosphorylated vimentin as an immunotherapeutic target against metastatic colorectal cancer. <i>Cancer Immunology, Immunotherapy</i> , 2020, 69, 989-999.	4.2	15
2139	What Could Go Wrong? A Practical Guide to Single-Particle Cryo-EM: From Biochemistry to Atomic Models. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2458-2469.	5.4	25
2140	Comparative genetic and physiological characterisation of <i>Pectinatus</i> species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , 2020, 90, 103462.	4.2	6
2141	Enzymatic hydrolysis of pea protein: Interactions and protein fractions involved in fermentation induced gels and their influence on rheological properties. <i>Food Hydrocolloids</i> , 2020, 105, 105793.	10.7	45
2142	Widespread patterns of gene loss in the evolution of the animal kingdom. <i>Nature Ecology and Evolution</i> , 2020, 4, 519-523.	7.8	89
2143	Prolonged Heat Stress of <i>Lactobacillus paracasei</i> GCRL163 Improves Binding to Human Colorectal Adenocarcinoma HT-29 Cells and Modulates the Relative Abundance of Secreted and Cell Surface-Located Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 1824-1846.	3.7	7
2144	Modification of the head proteome of nurse honeybees (<i>Apis mellifera</i>) exposed to field-relevant doses of pesticides. <i>Scientific Reports</i> , 2020, 10, 2190.	3.3	17
2145	Identifying the drivers of computationally detected correlated evolution among sites under antibiotic selection. <i>Evolutionary Applications</i> , 2020, 13, 781-793.	3.1	3
2146	Transcriptome analysis of near-isogenic lines for glume hairiness of wheat. <i>Gene</i> , 2020, 739, 144517.	2.2	7

#	ARTICLE	IF	CITATIONS
2147	Causes and consequences of mitochondrial proteome size variation in animals. <i>Mitochondrion</i> , 2020, 52, 100-107.	3.4	2
2148	Computational Identification of the Proteins Associated With Quorum Sensing and Biofilm Formation in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3011.	3.5	19
2149	Alternate approach to stroke phenotyping identifies a genetic risk locus for small vessel stroke. <i>European Journal of Human Genetics</i> , 2020, 28, 963-972.	2.8	12
2150	A novel artificial intelligence protocol for finding potential inhibitors of acute myeloid leukemia. <i>Journal of Materials Chemistry B</i> , 2020, 8, 2063-2081.	5.8	12
2151	A multi-omics investigation of the molecular characteristics and classification of six metabolic syndrome relevant diseases. <i>Theranostics</i> , 2020, 10, 2029-2046.	10.0	35
2152	High-throughput quantification of protein structural change reveals potential mechanisms of temperature adaptation in <i>Mytilus</i> mussels. <i>BMC Evolutionary Biology</i> , 2020, 20, 28.	3.2	11
2154	Computational Method for Structure-Based Analysis of SAR Transfer. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1388-1396.	6.4	4
2155	Diversity spectrum analysis identifies mutation-specific effects of cancer driver genes. <i>Communications Biology</i> , 2020, 3, 6.	4.4	9
2156	Mining histone methyltransferases and demethylases from whole genome sequence. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	2
2157	Comprehensive transcriptomic analysis of papillary thyroid cancer: potential biomarkers associated with tumor progression. <i>Journal of Endocrinological Investigation</i> , 2020, 43, 911-923.	3.3	14
2158	Genome based characterization of <i>Kitasatospora</i> sp. MMS16-BH015, a multiple heavy metal resistant soil actinobacterium with high antimicrobial potential. <i>Gene</i> , 2020, 733, 144379.	2.2	13
2159	A competency question-oriented approach for the transformation of semi-structured bioinformatics data into linked open data. <i>Engineering Applications of Artificial Intelligence</i> , 2020, 90, 103495.	8.1	1
2160	Making sense out of missense mutations: Mechanistic dissection of Notch receptors through structureâ€function studies in <i>Drosophila</i> . <i>Development Growth and Differentiation</i> , 2020, 62, 15-34.	1.5	14
2161	N-Linked Surface Glycan Biosynthesis, Composition, Inhibition, and Function in Cnidarian-Dinoflagellate Symbiosis. <i>Microbial Ecology</i> , 2020, 80, 223-236.	2.8	17
2162	Identification of emulsifier potato peptides by bioinformatics: application to omega-3 delivery emulsions and release from potato industry side streams. <i>Scientific Reports</i> , 2020, 10, 690.	3.3	41
2163	Growth Mode and Physiological State of Cells Prior to Biofilm Formation Affect Immune Evasion and Persistence of <i>Staphylococcus aureus</i> . <i>Microorganisms</i> , 2020, 8, 106.	3.6	18
2164	Rational design and improvement of the dimerizationâ€disrupting peptide selectivity between ROCKâ€I and ROCKâ€II kinase isoforms in cerebrovascular diseases. <i>Journal of Molecular Recognition</i> , 2020, 33, e2835.	2.1	7
2165	Building de novo reference genome assemblies of complex eukaryotic microorganisms from single nuclei. <i>Scientific Reports</i> , 2020, 10, 1303.	3.3	22

#	ARTICLE	IF	CITATIONS
2166	Hesperidin improves insulin resistance via down-regulation of inflammatory responses: Biochemical analysis and in silico validation. PLoS ONE, 2020, 15, e0227637.	2.5	20
2167	Critiquing Protein Family Classification Models Using Sufficient Input Subsets. Journal of Computational Biology, 2020, 27, 1219-1231.	1.6	7
2168	Multiplex quantitation of 270 plasma protein markers to identify a signature for early detection of colorectal cancer. European Journal of Cancer, 2020, 127, 30-40.	2.8	19
2169	Nucleoside-modified AdoMet analogues for differential methyltransferase targeting. Chemical Communications, 2020, 56, 2115-2118.	4.1	27
2170	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. Applied and Environmental Microbiology, 2020, 86, .	3.1	27
2171	In Silico Identification of a Key Residue for Substrate Recognition of the Riboflavin Membrane Transporter RFVT3. Journal of Chemical Information and Modeling, 2020, 60, 1368-1375.	5.4	4
2172	Venomomics of the ectoparasitoid wasp <i>Bracon nigricans</i> . BMC Genomics, 2020, 21, 34.	2.8	20
2173	In Silico Target Identification and Molecular Docking Studies of Natural Cytotoxic Compound Borivilianoside H. Current Biotechnology, 2020, 8, 127-137.	0.4	2
2174	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. Molecular and Cellular Proteomics, 2020, 19, 554-568.	3.8	38
2175	Emerging role of tumor-related functional peptides encoded by lncRNA and circRNA. Molecular Cancer, 2020, 19, 22.	19.2	330
2176	Multiple protein-DNA interfaces unravelled by evolutionary information, physico-chemical and geometrical properties. PLoS Computational Biology, 2020, 16, e1007624.	3.2	18
2177	Comprehensive understanding of <i>Saccharomyces cerevisiae</i> phenotypes with whole-cell model WM_S288C. Biotechnology and Bioengineering, 2020, 117, 1562-1574.	3.3	23
2178	Characterization of cancer-related somatic mutations in the adenosine A2B receptor. European Journal of Pharmacology, 2020, 880, 173126.	3.5	15
2179	Post-translational Modification Crosstalk and Hotspots in Sirtuin Interactors Implicated in Cardiovascular Diseases. Frontiers in Genetics, 2020, 11, 356.	2.3	25
2180	Using an integrative machine learning approach utilising homology modelling to clinically interpret genetic variants: CACNA1F as an exemplar. European Journal of Human Genetics, 2020, 28, 1274-1282.	2.8	11
2181	QSAR without borders. Chemical Society Reviews, 2020, 49, 3525-3564.	38.1	427
2182	Adaptations of <i>Escherichia coli</i> strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162.	2.6	5
2183	SSCpred: Single-Sequence-Based Protein Contact Prediction Using Deep Fully Convolutional Network. Journal of Chemical Information and Modeling, 2020, 60, 3295-3303.	5.4	8

#	ARTICLE	IF	CITATIONS
2184	The Function of Tafazzin, a Mitochondrial Phospholipidâ€“Lysophospholipid Acyltransferase. <i>Journal of Molecular Biology</i> , 2020, 432, 5043-5051.	4.2	29
2185	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. <i>BMC Genomics</i> , 2020, 21, 293.	2.8	47
2186	Proteomic fingerprints of damage in extracellular matrix assemblies. <i>Matrix Biology Plus</i> , 2020, 5, 100027.	3.5	19
2187	Structure of the Native Muscle-type Nicotinic Receptor and Inhibition by Snake Venom Toxins. <i>Neuron</i> , 2020, 106, 952-962.e5.	8.1	138
2188	Crosstalk between Ubiquitination and Other Post-translational Protein Modifications in Plant Immunity. <i>Plant Communications</i> , 2020, 1, 100041.	7.7	49
2189	Functional cooperation of the glycine synthase-reductase and Woodâ€“Ljungdahl pathways for autotrophic growth of <i>Clostridium drakei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7516-7523.	7.1	88
2190	An integrated approach to unravel a crucial structural property required for the function of the insect steroidogenic Halloween protein Noppera-bo. <i>Journal of Biological Chemistry</i> , 2020, 295, 7154-7167.	3.4	14
2191	Salivary protein candidates for biomarkers of oral disorders in alcohol and tobacco dependents. <i>Oral Diseases</i> , 2020, 26, 1200-1208.	3.0	8
2192	Human Colon Mucosal Biofilms and Murine Host Communicate via Altered mRNA and microRNA Expression during Cancer. <i>MSystems</i> , 2020, 5, .	3.8	25
2193	The Role of Genetic Variation of BMI, Body Composition, and Fat Distribution for Mental Traits and Disorders: A Look-Up and Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2020, 11, 373.	2.3	20
2194	A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. <i>Genes</i> , 2020, 11, 407.	2.4	45
2195	Structural Characterization of Carbonic Anhydrase VIII and Effects of Missense Single Nucleotide Variations to Protein Structure and Function. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2764.	4.1	11
2196	Integrative and quantitative view of the CtrA regulatory network in a stalked budding bacterium. <i>PLoS Genetics</i> , 2020, 16, e1008724.	3.5	8
2197	Noncompetitive tightâ€“binding inhibition of <i>Anticarsia gemmatilis</i> trypsins by <i>Adenanthera pavonina</i> protease inhibitor affects larvae survival. <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 104, e21687.	1.5	10
2198	Structural characterization of the Pet c 1.0201 PR-10 protein isolated from roots of <i>Petroselinum crispum</i> (Mill.) Fuss. <i>Phytochemistry</i> , 2020, 175, 112368.	2.9	3
2199	Revealing Acquired Resistance Mechanisms of Kinase-Targeted Drugs Using an on-the-Fly, Function-Site Interaction Fingerprint Approach. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 3152-3161.	5.3	8
2200	Energetic contributions of amino acid residues and its crossâ€“talk to delineate ligandâ€“binding mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1207-1225.	2.6	16
2201	Analysis of apoplastic proteins expressed during net form net blotch of barley. <i>Journal of Plant Diseases and Protection</i> , 2020, 127, 683-694.	2.9	8

#	ARTICLE	IF	CITATIONS
2202	Monoclonal antibody-based sandwich enzyme-linked immunosorbent assay for porcine hemoglobin quantification. Food Chemistry, 2020, 324, 126880.	8.2	14
2203	Computational Chemistry on a Budget: Supporting Drug Discovery with Limited Resources. Journal of Medicinal Chemistry, 2020, 63, 10158-10169.	6.4	37
2204	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. Nature Communications, 2020, 11, 1801.	12.8	153
2205	Iron is a ligand of SecA-like metal-binding domains in vivo. Journal of Biological Chemistry, 2020, 295, 7516-7528.	3.4	3
2206	Alternative proteins are functional regulators in cell reprogramming by PKA activation. Nucleic Acids Research, 2020, 48, 7864-7882.	14.5	24
2207	HMMPred: Accurate Prediction of DNA-Binding Proteins Based on HMM Profiles and XGBoost Feature Selection. Computational and Mathematical Methods in Medicine, 2020, 2020, 1-10.	1.3	27
2208	MetaEukâ€”sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. Microbiome, 2020, 8, 48.	11.1	119
2209	Deletion of S-Layer Associated Ig-Like Domain Protein Disrupts the Lactobacillus acidophilus Cell Surface. Frontiers in Microbiology, 2020, 11, 345.	3.5	14
2210	Nuclear and Chloroplast Sequences Resolve the Enigmatic Origin of the Concord Grape. Frontiers in Plant Science, 2020, 11, 263.	3.6	17
2211	Identification and characterization of parvalbumin-like protein in Trichophyton violaceum. Fungal Biology, 2020, 124, 592-600.	2.5	2
2212	GPS-Palm: a deep learning-based graphic presentation system for the prediction of<i>S</i>-palmitoylation sites in proteins. Briefings in Bioinformatics, 2021, 22, 1836-1847.	6.5	64
2213	Potential Pathogenic Genes Prioritization Based on Protein Domain Interaction Network Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1026-1034.	3.0	13
2214	MPTherm: database for membrane protein thermodynamics for understanding folding and stability. Briefings in Bioinformatics, 2021, 22, 2119-2125.	6.5	18
2215	Setting the basis of best practices and standards for curation and annotation of logical models in biologyâ€”highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25
2216	Systematic evaluation of machine learning methods for identifying humanâ€”pathogen proteinâ€”protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	23
2217	The secreted inhibitor of invasive cell growth CREG1 is negatively regulated by cathepsin proteases. Cellular and Molecular Life Sciences, 2021, 78, 733-755.	5.4	2
2218	Data science-driven analyses of drugs inducing hypertension as an adverse effect. Molecular Diversity, 2021, 25, 801-810.	3.9	1
2219	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in Bioinformatics, 2021, 22, 1656-1678.	6.5	66

#	ARTICLE	IF	CITATIONS
2220	Radiation of nitrogenâ€metabolizing enzymes across the tree of life tracks environmental transitions in Earth history. <i>Geobiology</i> , 2021, 19, 18-34.	2.4	36
2221	Design and synthesis of novel pyrazole-phenyl semicarbazone derivatives as potential Î±-glucosidase inhibitor: Kinetics and molecular dynamics simulation study. <i>International Journal of Biological Macromolecules</i> , 2021, 166, 1082-1095.	7.5	33
2222	Phage Proteins Required for Tail Fiber Assembly Also Bind Specifically to the Surface of Host Bacterial Strains. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	18
2223	The Secretome landscape of <i>Escherichia coli</i> O157:H7: Deciphering the cell-surface, outer membrane vesicle and extracellular subproteomes. <i>Journal of Proteomics</i> , 2021, 232, 104025.	2.4	8
2224	The Potential Role of Preoperative Pain, Catastrophizing, and Differential Gene Expression on Pain Outcomes after Pediatric Spinal Fusion. <i>Pain Management Nursing</i> , 2021, 22, 44-49.	0.9	12
2225	Integrative biomarker detection on high-dimensional gene expression data sets: a survey on prior knowledge approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
2226	Contributions of de novo variants to systemic lupus erythematosus. <i>European Journal of Human Genetics</i> , 2021, 29, 184-193.	2.8	6
2227	Functions of Bacterial tRNA Modifications: From Ubiquity to Diversity. <i>Trends in Microbiology</i> , 2021, 29, 41-53.	7.7	67
2228	Rational drug discovery: Ellagic acid as a potent dualâ€target inhibitor against hepatitis C virus genotype 3 (HCV G3) NS3 enzymes. <i>Chemical Biology and Drug Design</i> , 2021, 97, 28-40.	3.2	6
2229	Mutations in transmembrane proteins: diseases, evolutionary insights, prediction and comparison with globular proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
2230	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021, 41, 1039-1055.	3.3	5
2231	A Review of Prostanoid Receptors: Expression, Characterization, Regulation, and Mechanism of Action. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 155-184.	3.4	31
2232	Transcriptome differential expression analysis reveals the activated genes in <i>Litopenaeus vannamei</i> shrimp families of superior growth performance. <i>Aquaculture</i> , 2021, 531, 735871.	3.5	22
2233	Allelic polymorphisms in a glycosyltransferase gene shape glycan repertoire in the <i>O</i> -linked protein glycosylation system of <i>Neisseria</i> . <i>Glycobiology</i> , 2021, 31, 477-491.	2.5	6
2234	Complete genome sequence of the biocontrol agent <i>Serratia marcescens</i> strain N4â€5 uncovers an assembly artefact. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 245-250.	2.0	3
2235	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 940-952.	3.0	18
2236	A systematic evaluation of bioinformatics tools for identification of long noncoding RNAs. <i>Rna</i> , 2021, 27, 80-98.	3.5	19
2237	Network Effects of the 15q13.3 Microdeletion on the Transcriptome and Epigenome in Human-Induced Neurons. <i>Biological Psychiatry</i> , 2021, 89, 497-509.	1.3	17

#	ARTICLE	IF	CITATIONS
2238	Strongyloides stercoralis proteome: A reverse approach to the identification of potential immunogenic candidates. Microbial Pathogenesis, 2021, 152, 104545.	2.9	8
2239	Deep illumina miRNA sequencing provides insights into the mechanism underlying grass carp reovirus infection. Aquaculture Research, 2021, 52, 463-470.	1.8	0
2240	Repurposed drugs and nutraceuticals targeting envelope protein: A possible therapeutic strategy against COVID-19. Genomics, 2021, 113, 1129-1140.	2.9	22
2241	CSDB_GT, a curated glycosyltransferase database with close-to-full coverage on three most studied nonanimal species. Glycobiology, 2021, 31, 524-529.	2.5	6
2242	Structure-based discovery and redesign of TGF α 21 Elbow epitope recognition by its type α II receptor in hypertrophic scarring biotherapy. Journal of Molecular Recognition, 2021, 34, e2881.	2.1	1
2243	Proteome-Scale Detection of Differential Conservation Patterns at Protein and Subprotein Levels with BLUR. Genome Biology and Evolution, 2021, 13, .	2.5	3
2244	MoonProt 3.0: an update of the moonlighting proteins database. Nucleic Acids Research, 2021, 49, D368-D372.	14.5	38
2245	Shedding Light on the Ghost Proteome. Trends in Biochemical Sciences, 2021, 46, 239-250.	7.5	20
2246	Heterozygous, Polyploid, Giant Bacterium, <i>Achromatium</i> , Possesses an Identical Functional Inventory Worldwide across Drastically Different Ecosystems. Molecular Biology and Evolution, 2021, 38, 1040-1059.	8.9	4
2247	Alcohol stress on cyanobacterial membranes: New insights revealed by transcriptomics. Gene, 2021, 764, 145055.	2.2	4
2248	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. Frontiers in Plant Science, 2020, 11, 600278.	3.6	44
2249	Machine learning for metabolic engineering: A review. Metabolic Engineering, 2021, 63, 34-60.	7.0	135
2250	Classification of the glyphosate target enzyme (5-enolpyruvylshikimate-3-phosphate synthase) for assessing sensitivity of organisms to the herbicide. Journal of Hazardous Materials, 2021, 408, 124556.	12.4	55
2251	Protein cost allocation explains metabolic strategies in Escherichia coli. Journal of Biotechnology, 2021, 327, 54-63.	3.8	12
2252	Systematic Analysis of Phosphatidylinositol-5-phosphate-Interacting Proteins Using Yeast Proteome Microarrays. Analytical Chemistry, 2021, 93, 868-877.	6.5	5
2253	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	14.5	4,709
2254	A second shell residue modulates a conserved ATP-binding site with radically different affinities for ATP. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129766.	2.4	4
2255	Is there a causal relationship between trehalose consumption and Clostridioides difficile infection?. Current Opinion in Gastroenterology, 2021, 37, 9-14.	2.3	1

#	ARTICLE	IF	CITATIONS
2256	Direct seminal fluid identification by protease-free high-resolution mass spectrometry. <i>Journal of Forensic Sciences</i> , 2021, 66, 1017-1023.	1.6	4
2257	The Transcription Regulator and c-di-GMP Phosphodiesterase PdeL Represses Motility in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	5
2258	Proteoform Identification by Combining RNA-Seq and Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 261-269.	3.7	7
2259	Whole-exome sequencing of non-BRCA1/BRCA2 mutation carrier cases at high-risk for hereditary breast/ovarian cancer. <i>Human Mutation</i> , 2021, 42, 290-299.	2.5	32
2260	Evidence of sporulation capability of the ubiquitous oil reservoir microbe <i>Halanaerobium congolense</i> . <i>Geomicrobiology Journal</i> , 2021, 38, 283-293.	2.0	5
2261	Improved protein model quality assessment by integrating sequential and pairwise features using deep learning. <i>Bioinformatics</i> , 2021, 36, 5361-5367.	4.1	11
2262	SCycDB: A curated functional gene database for metagenomic profiling of sulphur cycling pathways. <i>Molecular Ecology Resources</i> , 2021, 21, 924-940.	4.8	52
2263	TOA: A software package for automated functional annotation in non-model plant species. <i>Molecular Ecology Resources</i> , 2021, 21, 621-636.	4.8	10
2264	Navigating the Global Protein-Protein Interaction Landscape Using iRefWeb. <i>Methods in Molecular Biology</i> , 2021, 2199, 191-207.	0.9	2
2265	Evaluation of gene expression and protein structural modeling involved in persister cell formation in <i>Salmonella Typhimurium</i> . <i>Brazilian Journal of Microbiology</i> , 2021, 52, 207-217.	2.0	2
2266	Transcriptomes of Major Proximal Tubule Cell Culture Models. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 86-97.	6.1	35
2267	CAVA: A Visual Analytics System for Exploratory Columnar Data Augmentation Using Knowledge Graphs. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021, 27, 1731-1741.	4.4	11
2268	Proteome-scale analysis of phase-separated proteins in immunofluorescence images. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
2269	How to use the MEROPS database and website to help understand peptidase specificity. <i>Protein Science</i> , 2021, 30, 83-92.	7.6	44
2270	SMI-BLAST: a novel supervised search framework based on PSI-BLAST for protein remote homology detection. <i>Bioinformatics</i> , 2021, 37, 913-920.	4.1	19
2271	Revealing secrets of the enigmatic omega subunit of bacterial RNA polymerase. <i>Molecular Microbiology</i> , 2021, 115, 1-11.	2.5	16
2272	The Methods and Tools for Intrinsic Disorder Prediction and their Application to Systems Medicine. , 2021, , 159-169.		3
2274	A Network Pharmacology Approach to Estimate Potential Targets of the Active Ingredients of Epimedium for Alleviating Mild Cognitive Impairment and Treating Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	1.2	13

#	ARTICLE	IF	CITATIONS
2275	CausalBuilder: bringing the MI2CAST causal interaction annotation standard to the curator. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	3
2276	Transcriptional response of <i>Asarum heterotropoides</i> Fr. Schmidt var. <i>mandshuricum</i> (Maxim.) Kitag. leaves grown under full and partial daylight conditions. BMC Genomics, 2021, 22, 16.	2.8	1
2277	ADP-ribose and analogues bound to the deMARYlating macrodomain from the bat coronavirus HKU4. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
2280	Conformational Landscape of Cytochrome P450 Reductase Interactions. International Journal of Molecular Sciences, 2021, 22, 1023.	4.1	8
2281	Horizon Scanning for Plant Health: report on 2017â€2020 activities. EFSA Supporting Publications, 2021, 18, 2010E.	0.7	5
2282	Deciphering the architecture and interactome of hnRNP proteins and enigmRBPs. Molecular Omics, 2021, 17, 503-516.	2.8	1
2283	Arabidopsis REI-LIKE proteins activate ribosome biogenesis during cold acclimation. Scientific Reports, 2021, 11, 2410.	3.3	19
2284	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. Scientific Reports, 2021, 11, 1990.	3.3	32
2285	Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	8
2286	Safe-in-Man Broad Spectrum Antiviral Agents. Advances in Experimental Medicine and Biology, 2021, 1322, 313-337.	1.6	1
2287	Integrated molecular characterisation of the MAPK pathways in human cancers reveals pharmacologically vulnerable mutations and gene dependencies. Communications Biology, 2021, 4, 9.	4.4	32
2288	Insight into membraneless organelles and their associated proteins: Drivers, Clients and Regulators. Computational and Structural Biotechnology Journal, 2021, 19, 3964-3977.	4.1	24
2289	A Novel Method for Identification of Glutarylation Sites Combining Borderline-SMOTE With Tomek Links Technique in Imbalanced Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2632-2641.	3.0	19
2290	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	21.4	117
2291	From Homology Modeling to the Hit Identification and Drug Repurposing: A Structure-Based Approach in the Discovery of Novel Potential Anti-Obesity Compounds. Methods in Molecular Biology, 2021, 2266, 263-277.	0.9	3
2292	Conformational Changes of Thyroid Receptors in Response to Antagonists. Journal of Chemical Information and Modeling, 2021, 61, 1010-1019.	5.4	4
2293	A Method for Analysis of by Coupled with Mass. Methods in Molecular Biology, 2021, 2276, 383-396.	0.9	0
2294	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	6.5	37

#	ARTICLE	IF	CITATIONS
2295	Short loop functional commonality identified in leukaemia proteome highlights crucial protein sub-networks. NAR Genomics and Bioinformatics, 2021, 3, lqab010.	3.2	0
2296	Resources for Docking-Based Virtual Screening. , 2021, , 179-203.		1
2297	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. Nature Microbiology, 2021, 6, 354-365.	13.3	109
2298	Network pharmacology-based analysis for unraveling potential cancer-related molecular targets of Egyptian propolis phytoconstituents accompanied with molecular docking and <i>in vitro</i> studies. RSC Advances, 2021, 11, 11610-11626.	3.6	22
2299	HPLC-MS identification and expression of <i>Candida</i> drug-resistance proteins from African HIV-infected patients. AIMS Microbiology, 2021, 7, 320-335.	2.2	1
2300	Making fundamental scientific discoveries by combining information from literature, databases, and computational tools – An example. Computational and Structural Biotechnology Journal, 2021, 19, 3027-3033.	4.1	9
2301	Molecular basis of tail-anchored integral membrane protein recognition by the cochaperone Sgt2. Journal of Biological Chemistry, 2021, 296, 100441.	3.4	15
2302	MODOMICS: An Operational Guide to the Use of the RNA Modification Pathways Database. Methods in Molecular Biology, 2021, 2284, 481-505.	0.9	35
2303	Transcription-translation error: In-silico investigation of the structural and functional impact of deleterious single nucleotide polymorphisms in GULP1 gene. Informatics in Medicine Unlocked, 2021, 22, 100503.	3.4	0
2304	The mammalian cholesterol synthesis enzyme squalene monooxygenase is proteasomally truncated to a constitutively active form. Journal of Biological Chemistry, 2021, 296, 100731.	3.4	17
2305	BioMaster: An Integrated Database and Analytic Platform to Provide Comprehensive Information About BioBrick Parts. Frontiers in Microbiology, 2021, 12, 593979.	3.5	5
2306	Epitope-based peptide vaccine against Bombali Ebolavirus viral protein 40: An immunoinformatics combined with molecular docking studies. Informatics in Medicine Unlocked, 2021, 25, 100694.	3.4	6
2307	Evaluating accessibility, usability and interoperability of genome-scale metabolic models for diverse yeasts species. FEMS Yeast Research, 2021, 21, .	2.3	6
2308	SNF-NN: computational method to predict drug-disease interactions using similarity network fusion and neural networks. BMC Bioinformatics, 2021, 22, 28.	2.6	29
2309	Genome sequence and transcriptome profiles of pathogenic fungus Paecilomyces penicillatus reveal its interactions with edible fungus Morchella importuna. Computational and Structural Biotechnology Journal, 2021, 19, 2607-2617.	4.1	11
2310	FMODB: The World's First Database of Quantum Mechanical Calculations for Biomacromolecules Based on the Fragment Molecular Orbital Method. Journal of Chemical Information and Modeling, 2021, 61, 777-794.	5.4	24
2311	Identifying the molecular targets and mechanisms of xuebijing injection for the treatment of COVID-19 via network pharmacology and molecular docking. Bioengineered, 2021, 12, 2274-2287.	3.2	17
2312	PIM-induced phosphorylation of Notch3 promotes breast cancer tumorigenicity in a CSL-independent fashion. Journal of Biological Chemistry, 2021, 296, 100593.	3.4	9

#	ARTICLE	IF	CITATIONS
2313	IBDDDB: a manually curated and text-mining-enhanced database of genes involved in inflammatory bowel disease. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	8
2314	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. BMC Bioinformatics, 2021, 22, 11.	2.6	61
2316	An Ebola, Neisseria and Trypanosoma human protein interaction census reveals a conserved human protein cluster targeted by various human pathogens. Computational and Structural Biotechnology Journal, 2021, 19, 5292-5308.	4.1	4
2317	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
2318	UbiNet 2.0: a verified, classified, annotated and updated database of E3 ubiquitin ligaseâ€“substrate interactions. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	27
2320	Diiron Enzyme Structure and Catalysis. , 2021, , 455-499.		2
2321	Practical Considerations Relating to Routine Clinical Biomarker Testing for Nonâ€“small Cell Lung Cancer: Focus on Testing for RET Fusions. Frontiers in Medicine, 2020, 7, 562480.	2.6	6
2322	GPR101, an orphan G-protein coupled receptor, with roles in growth, puberty, and possibly appetite regulation. , 2021, , 79-88.		0
2323	Semankey: A Semantics-Driven Approach for Querying RDF Repositories Using Keywords. IEEE Access, 2021, 9, 91282-91302.	4.2	4
2324	Software Options for the Analysis of MS-Proteomic Data. Methods in Molecular Biology, 2021, 2361, 35-59.	0.9	3
2325	Databases for Proteinâ€“Protein Interactions. Methods in Molecular Biology, 2021, 2361, 229-248.	0.9	6
2327	Protonation states at different pH, conformational changes and impact of glycosylation in synapsin Ia. Physical Chemistry Chemical Physics, 2021, 23, 16718-16729.	2.8	4
2328	In silico and in vitro insights into tyrosinase inhibitors with a 2-thioxooxazoline-4-one template. Computational and Structural Biotechnology Journal, 2021, 19, 37-50.	4.1	18
2329	Investigating ¹² -Lactam Drug Targets in <i>Mycobacterium tuberculosis</i> Using Chemical Probes. ACS Infectious Diseases, 2021, 7, 461-470.	3.8	19
2330	A protocol for adding knowledge to Wikidata: aligning resources on human coronaviruses. BMC Biology, 2021, 19, 12.	3.8	14
2331	Food Constituent and Food Metabolite Databases. , 2021, , 2-18.		2
2332	Ensemble-AMPPred: Robust AMP Prediction and Recognition Using the Ensemble Learning Method with a New Hybrid Feature for Differentiating AMPs. Genes, 2021, 12, 137.	2.4	20
2333	The Interplay of Cholesterol and Ligand Binding in hTSPO from Classical Molecular Dynamics Simulations. Molecules, 2021, 26, 1250.	3.8	5

#	ARTICLE	IF	CITATIONS
2334	Study of Endogen Substrates, Drug Substrates and Inhibitors Binding Conformations on MRP4 and Its Variants by Molecular Docking and Molecular Dynamics. <i>Molecules</i> , 2021, 26, 1051.	3.8	9
2335	Protein structure search to support the development of protein structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 648-658.	2.6	7
2336	A novel homozygous nonsense mutation in the CA2 gene (c.368G>A, p.W123X) linked to carbonic anhydrase II deficiency syndrome in a Chinese family. <i>Metabolic Brain Disease</i> , 2021, 36, 589-599.	2.9	5
2337	Generative chemistry: drug discovery with deep learning generative models. <i>Journal of Molecular Modeling</i> , 2021, 27, 71.	1.8	63
2338	Polymorphism Detection of GDF9 Gene and Its Association with Litter Size in Luzhong Mutton Sheep (<i>Ovis aries</i>). <i>Animals</i> , 2021, 11, 571.	2.3	21
2340	<scp>In silico</scp> screening and molecular dynamics simulation of deleterious <scp>PAH</scp> mutations responsible for phenylketonuria genetic disorder. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 683-696.	2.6	3
2341	Crystal structures of adenylylated and unadenylylated P_{II} protein GlnK from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 325-335.	2.3	4
2342	Role of PFKFB3 and PFKFB4 in Cancer: Genetic Basis, Impact on Disease Development/Progression, and Potential as Therapeutic Targets. <i>Cancers</i> , 2021, 13, 909.	3.7	67
2343	A modeling framework for embedding-based predictions for compoundâ€™ viral protein activity. <i>Bioinformatics</i> , 2021, 37, 2544-2555.	4.1	5
2344	A survey of human histone <scp>H1</scp> subtypes interaction networks: Implications for histones <scp>H1</scp> functioning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 792-810.	2.6	1
2345	Identification of novel lipid droplet factors that regulate lipophagy and cholesterol efflux in macrophage foam cells. <i>Autophagy</i> , 2021, 17, 3671-3689.	9.1	90
2346	Genes underlying species differences in cuticular hydrocarbon production between <i>Drosophila melanogaster</i> and <i>D. simulans</i> . <i>Genome</i> , 2021, 64, 87-95.	2.0	2
2349	Network pharmacologyâ€™based study to explore the mechanism of the Yiqi Gubiao pill in lung cancer treatment. <i>Oncology Letters</i> , 2021, 21, 321.	1.8	4
2350	Computational Assessment of Combination Therapy of Androgen Receptor-Targeting Compounds. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1001-1009.	5.4	4
2351	The glycoconjugate ontology (GlycoCoO) for standardizing the annotation of glycoconjugate data and its application. <i>Glycobiology</i> , 2021, 31, 741-750.	2.5	7
2352	A High-Quality Reference Genome for a Parasitic Bivalve with Doubly Uniparental Inheritance (Bivalvia: Tj ETQq1 1 0.784314,ggBT /Over 2.5	2.5	21
2353	A Molecular Interaction Map of <i>Klebsiella pneumoniae</i> and Its Human Host Reveals Potential Mechanisms of Host Cell Subversion. <i>Frontiers in Microbiology</i> , 2021, 12, 613067.	3.5	8
2354	Genome-wide DNA methylation dynamics during epigenetic reprogramming in the porcine germline. <i>Clinical Epigenetics</i> , 2021, 13, 27.	4.1	7

#	ARTICLE	IF	CITATIONS
2355	Mapping proteolytic neo-N termini at the surface of living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	27
2356	Electric Blue: Molecular Evolution of Three-Finger Toxins in the Long-Clained Coral Snake Species <i>Calliophis bivirgatus</i> . <i>Toxins</i> , 2021, 13, 124.	3.4	9
2357	Molecular dynamics, residue network analysis, and cross-correlation matrix to characterize the deleterious missense mutations in GALE causing galactosemia III. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 201-219.	1.8	23
2358	Genome annotation of disease-causing microorganisms. <i>Briefings in Bioinformatics</i> , 2021, 22, 845-854.	6.5	13
2360	Novel Two-Component System-Like Elements Reveal Functional Domains Associated with Restrictionâ€“Modification Systems and paraMORC ATPases in Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	4
2361	Transcriptome analysis reveals major transcriptional changes during regrowth after mowing of red clover (<i>Trifolium pratense</i>). <i>BMC Plant Biology</i> , 2021, 21, 95.	3.6	10
2362	Pharaoh Cuttlefish, <i>Sepia pharaonis</i> , Genome Reveals Unique Reflectin Camouflage Gene Set. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	10
2363	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	1
2364	Comprehensive in silico analysis and molecular dynamics of the superoxide dismutase 1 (SOD1) variants related to amyotrophic lateral sclerosis. <i>PLoS ONE</i> , 2021, 16, e0247841.	2.5	24
2365	Differential Splicing of Skipped Exons Predicts Drug Response in Cancer Cell Lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 901-912.	6.9	0
2366	Discovery of Protein Modifications Using Differential Tandem Mass Spectrometry Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 1835-1848.	3.7	13
2367	Hepatic steatosis and steatohepatitis: a functional meta-analysis of sex-based differences in transcriptomic studies. <i>Biology of Sex Differences</i> , 2021, 12, 29.	4.1	18
2368	MaCPepDB: A Database to Quickly Access All Tryptic Peptides of the UniProtKB. <i>Journal of Proteome Research</i> , 2021, 20, 2145-2150.	3.7	6
2369	Cardiovascular informatics: building a bridge to data harmony. <i>Cardiovascular Research</i> , 2021, , .	3.8	4
2370	A Second Look at FAIR in Proteomic Investigations. <i>Journal of Proteome Research</i> , 2021, 20, 2182-2186.	3.7	2
2371	Molecular and genomic characterization of a novel equine molluscum contagiosum-like virus. <i>Journal of General Virology</i> , 2021, 102, .	2.9	7
2372	Genomic signatures of drift and selection driven by predation and human pressure in an insular lizard. <i>Scientific Reports</i> , 2021, 11, 6136.	3.3	5
2373	Approaches to Identify and Characterise the Post-Transcriptional Roles of lncRNAs in Cancer. <i>Non-coding RNA</i> , 2021, 7, 19.	2.6	6

#	ARTICLE	IF	CITATIONS
2374	Evidence for <i>CAT</i> gene being functionally involved in the susceptibility of COVID-19. <i>FASEB Journal</i> , 2021, 35, e21384.	0.5	6
2375	A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. <i>Cell Reports</i> , 2021, 34, 108856.	6.4	101
2376	Toward Characterising the Cellular 3D-Proteome. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	3
2378	Linear B-Cell Epitope Prediction for In Silico Vaccine Design: A Performance Review of Methods Available via Command-Line Interface. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3210.	4.1	60
2379	Integration of Data from Liquid–Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3017.	4.1	29
2380	gapseq: informed prediction of bacterial metabolic pathways and reconstruction of accurate metabolic models. <i>Genome Biology</i> , 2021, 22, 81.	8.8	103
2381	Crystal structure of timothy grass allergen Phl p 12.0101 reveals an unusual profilin dimer. <i>Acta Biochimica Polonica</i> , 2021, 68, 15-22.	0.5	3
2384	The ST11 domain is a flexible alpha-helical fold with a hydrophobic groove. <i>Protein Science</i> , 2021, 30, 882-898.	7.6	15
2385	DeepHBSP: A Deep Learning Framework for Predicting Human Blood-Secretory Proteins Using Transfer Learning. <i>Journal of Computer Science and Technology</i> , 2021, 36, 234-247.	1.5	1
2386	Dihydrouridine synthesis in tRNAs is under reductive evolution in Mollicutes. <i>RNA Biology</i> , 2021, 18, 2278-2289.	3.1	7
2387	Integrative network analyses of transcriptomics data reveal potential drug targets for acute radiation syndrome. <i>Scientific Reports</i> , 2021, 11, 5585.	3.3	4
2388	MANTI: Automated Annotation of Protein N-Termini for Rapid Interpretation of N-Terminome Data Sets. <i>Analytical Chemistry</i> , 2021, 93, 5596-5605.	6.5	9
2389	Mayday sustains trans-synaptic BMP signaling required for synaptic maintenance with age. <i>ELife</i> , 2021, 10, .	6.0	5
2391	Evolution of mammalian longevity: age-related increase in autophagy in bats compared to other mammals. <i>Aging</i> , 2021, 13, 7998-8025.	3.1	16
2392	Swiss-PO: a new tool to analyze the impact of mutations on protein three-dimensional structures for precision oncology. <i>Npj Precision Oncology</i> , 2021, 5, 19.	5.4	9
2393	Dissemination of novel Tn7 family transposons carrying genes for synthesis and uptake of fimsbactin siderophores among <i>Acinetobacter baumannii</i> isolates. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10
2394	Ensemble of Multiple Classifiers for Multilabel Classification of Plant Protein Subcellular Localization. <i>Life</i> , 2021, 11, 293.	2.4	13
2395	Hepatitis B virus X protein promotes vimentin expression via LIM and SH3 domain protein 1 to facilitate epithelial-mesenchymal transition and hepatocarcinogenesis. <i>Cell Communication and Signaling</i> , 2021, 19, 33.	6.5	14

#	ARTICLE	IF	CITATIONS
2396	Systematic inhibitor selectivity between PARP1 and PARP2 enzymes: Molecular implications for ovarian cancer personalized therapy. <i>Journal of Molecular Recognition</i> , 2021, 34, e2891.	2.1	6
2398	Initial Insights Into the Genetic Epidemiology of SARS-CoV-2 Isolates From Kerala Suggest Local Spread From Limited Introductions. <i>Frontiers in Genetics</i> , 2021, 12, 630542.	2.3	11
2399	Deciphering potential pharmacological mechanism of Sha-Shen-Mai-Dong decoction on primary Sjogren's syndrome. <i>BMC Complementary Medicine and Therapies</i> , 2021, 21, 79.	2.7	3
2400	Discovery and engineering of small SlugCas9 with broad targeting range and high specificity and activity. <i>Nucleic Acids Research</i> , 2021, 49, 4008-4019.	14.5	33
2401	The very early evolution of protein translocation across membranes. <i>PLoS Computational Biology</i> , 2021, 17, e1008623.	3.2	13
2402	A comprehensive molecular characterization of the 8q22.2 region reveals the prognostic relevance of OSR2 mRNA in muscle invasive bladder cancer. <i>PLoS ONE</i> , 2021, 16, e0248342.	2.5	4
2403	Analyzing the potential therapeutic mechanism of Huashi Baidu Decoction on severe COVID-19 through integrating network pharmacological methods. <i>Journal of Traditional and Complementary Medicine</i> , 2021, 11, 180-187.	2.7	22
2404	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. <i>Nature Genetics</i> , 2021, 53, 445-454.	21.4	61
2405	A potential interaction between the SARS-CoV-2 spike protein and nicotinic acetylcholine receptors. <i>Biophysical Journal</i> , 2021, 120, 983-993.	0.5	43
2406	Subcellular photosynthesis in hot desert habitats. <i>Environmental Microbiology</i> , 2021, 23, 3867-3880.	3.8	10
2407	Chromosome Walking: A Novel Approach to Analyse Amino Acid Content of Human Proteins Ordered by Gene Position. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3511.	2.5	1
2408	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	2.8	14
2409	A comprehensive review of the imbalance classification of protein post-translational modifications. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	26
2411	Origin and evolution of nonulosonic acid synthases and their relationship with bacterial pathogenicity revealed by a large-scale phylogenetic analysis. <i>Microbial Genomics</i> , 2021, 7, .	2.0	3
2412	Increased expression of peptides from non-coding genes in cancer proteomics datasets suggests potential tumor neoantigens. <i>Communications Biology</i> , 2021, 4, 496.	4.4	20
2413	In Silico Analysis of the Molecular-Level Impact of SMPD1 Variants on Niemann-Pick Disease Severity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4516.	4.1	4
2414	Assessing the functional relevance of splice isoforms. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab044.	3.2	13
2415	An integrative drug repositioning framework discovered a potential therapeutic agent targeting COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 165.	17.1	89

#	ARTICLE	IF	CITATIONS
2416	ARTEMIS: A Novel Mass-Spec Platform for HLA-Restricted Self and Disease-Associated Peptide Discovery. <i>Frontiers in Immunology</i> , 2021, 12, 658372.	4.8	7
2419	Spatially interacting phosphorylation sites and mutations in cancer. <i>Nature Communications</i> , 2021, 12, 2313.	12.8	12
2421	Bacterial avidins are a widely distributed protein family in Actinobacteria, Proteobacteria and Bacteroidetes. <i>Bmc Ecology and Evolution</i> , 2021, 21, 53.	1.6	7
2422	Screening of Twelve Pea (<i>Pisum sativum</i> L.) Cultivars and Their Isolates Focusing on the Protein Characterization, Functionality, and Sensory Profiles. <i>Foods</i> , 2021, 10, 758.	4.3	26
2423	Spatial Distribution of Private Gene Mutations in Clear Cell Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 2163.	3.7	10
2424	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	8
2425	MAPLE: A Microbiome Analysis Pipeline Enabling Optimal Peptide Search and Comparative Taxonomic and Functional Analysis. <i>Journal of Proteome Research</i> , 2021, 20, 2882-2894.	3.7	4
2426	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	12.6	358
2428	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	14.5	25
2429	In silico T cell epitope identification for SARS-CoV-2: Progress and perspectives. <i>Advanced Drug Delivery Reviews</i> , 2021, 171, 29-47.	13.7	52
2430	A putative novel starch-binding domain revealed by in silico analysis of the N-terminal domain in bacterial amylomaltases from the family GH77. <i>3 Biotech</i> , 2021, 11, 229.	2.2	7
2432	CAZymes in <i>Maribacter dokdonensis</i> 62â€™1 From the Patagonian Shelf: Genomics and Physiology Compared to Related Flavobacteria and a Co-occurring <i>Alteromonas</i> Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 628055.	3.5	13
2433	Ethylmalonic acid impairs bioenergetics by disturbing succinate and glutamate oxidation and induces mitochondrial permeability transition pore opening in rat cerebellum. <i>Journal of Neurochemistry</i> , 2021, 158, 262-281.	3.9	3
2434	Machine learning reveals that structural features distinguishing promiscuous and non-promiscuous compounds depend on target combinations. <i>Scientific Reports</i> , 2021, 11, 7863.	3.3	14
2435	Phylogenetic analysis of Harmonin homology domains. <i>BMC Bioinformatics</i> , 2021, 22, 190.	2.6	5
2437	Behavior of Chemokine Receptor 6 (CXCR6) in Complex with CXCL16 Soluble form Chemokine by Molecular Dynamic Simulations: General Proteinâ€™Ligand Interaction Model and 3D-QSAR Studies of Synthetic Antagonists. <i>Life</i> , 2021, 11, 346.	2.4	4
2438	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. <i>Cell Reports</i> , 2021, 35, 109032.	6.4	23
2439	Improving integrative 3D modeling into lowâ€™to mediumâ€™resolution electron microscopy structures with evolutionary couplings. <i>Protein Science</i> , 2021, 30, 1006-1021.	7.6	2

#	ARTICLE	IF	CITATIONS
2440	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
2441	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	19.0	187
2442	Protein-Based Immunome Wide Association Studies (PIWAS) for the Discovery of Significant Disease-Associated Antigens. <i>Frontiers in Immunology</i> , 2021, 12, 625311.	4.8	13
2443	EnhFFL: A database of enhancer mediated feed-forward loops for human and mouse. <i>Precision Clinical Medicine</i> , 2021, 4, 129-135.	3.3	3
2444	Peptide location fingerprinting reveals modification-associated biomarker candidates of ageing in human tissue proteomes. <i>Aging Cell</i> , 2021, 20, e13355.	6.7	9
2446	The f subunit of human ATP synthase is essential for normal mitochondrial morphology and permeability transition. <i>Cell Reports</i> , 2021, 35, 109111.	6.4	22
2447	Cholesterol recognition motifs in the transmembrane domain of the tyrosine kinase receptor family: The case of TRKB. <i>European Journal of Neuroscience</i> , 2021, 53, 3311-3322.	2.6	15
2448	The human cytomegalovirus protein UL147A downregulates the most prevalent MICA allele: MICA*008, to evade NK cell-mediated killing. <i>PLoS Pathogens</i> , 2021, 17, e1008807.	4.7	10
2449	Adaptive Proteome Diversification by Nonsynonymous A-to-I RNA Editing in Coleoid Cephalopods. <i>Molecular Biology and Evolution</i> , 2021, 38, 3775-3788.	8.9	22
2450	Resilience in Greenland intertidal <i>Mytilus</i> : The hidden stress defense. <i>Science of the Total Environment</i> , 2021, 767, 144366.	8.0	25
2452	Analysis of Zika virus capsid-Aedes aegypti mosquito interactome reveals pro-viral host factors critical for establishing infection. <i>Nature Communications</i> , 2021, 12, 2766.	12.8	19
2453	The symbiotic relationship between <i>Caenorhabditis elegans</i> and members of its microbiome contributes to worm fitness and lifespan extension. <i>BMC Genomics</i> , 2021, 22, 364.	2.8	12
2455	Urolithin and Reduced Urolithin Derivatives as Potent Inhibitors of Tyrosinase and Melanogenesis: Importance of the 4-Substituted Resorcinol Moiety. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5616.	4.1	8
2456	Exploring the Mechanism of Total Flavonoids of <i>Drynariae Rhizoma</i> to Improve Large Bone Defects by Network Pharmacology and Experimental Assessment. <i>Frontiers in Pharmacology</i> , 2021, 12, 603734.	3.5	11
2458	Study on the Intentional Choice Mechanism of Course Selection Based on Swarm Intelligence Algorithm. <i>Scientific Programming</i> , 2021, 2021, 1-6.	0.7	2
2460	Comprehensive analysis of the lysine acetylome and succinylome in the hippocampus of gut microbiota-dysbiosis mice. <i>Journal of Advanced Research</i> , 2021, 30, 27-38.	9.5	26
2461	Identification METTL18 as a Potential Prognosis Biomarker and Associated With Immune Infiltrates in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 665192.	2.8	11
2462	<i>Agrobacterium tumefaciens</i> Growth Pole Ring Protein: C Terminus and Internal Apolipoprotein Homologous Domains Are Essential for Function and Subcellular Localization. <i>MBio</i> , 2021, 12, .	4.1	9

#	ARTICLE	IF	CITATIONS
2463	Modelling of an autonomous Nav1.5 channel system as a part of in silico pharmacology study. Journal of Molecular Modeling, 2021, 27, 182.	1.8	3
2465	A New Sequential Forward Feature Selection (SFFS) Algorithm for Mining Best Topological and Biological Features to Predict Protein Complexes from Protein-Protein Interaction Networks (PPINs). Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 371-388.	3.6	8
2466	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	4.1	19
2467	Myeloid-derived growth factor regulates neutrophil motility in interstitial tissue damage. Journal of Cell Biology, 2021, 220, .	5.2	18
2468	ML-AdVInfect: A Machine-Learning Based Adenoviral Infection Predictor. Frontiers in Molecular Biosciences, 2021, 8, 647424.	3.5	10
2469	hu.MAP 2.0: integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies. Molecular Systems Biology, 2021, 17, e10016.	7.2	82
2470	Prospecting Biomarkers for Diagnostic and Therapeutic Approaches in Pythiosis. Journal of Fungi (Basel, Switzerland), 2021, 7, 423.	3.5	2
2471	Neutrophil-to-lymphocyte ratio and outcomes in patients with new-onset or worsening heart failure with reduced and preserved ejection fraction. ESC Heart Failure, 2021, 8, 3168-3179.	3.1	33
2472	Rational Molecular Profiling of Receptor-Associated Late Transducer Peptide Selectivity Across Her/Rtk Kinases. International Journal of Peptide Research and Therapeutics, 2021, 27, 1945-1951.	1.9	4
2473	A zinc finger protein gene signature enables bladder cancer treatment stratification. Aging, 2021, 13, 13023-13038.	3.1	2
2475	IDSME ChemWebRDF: SPARQLing small-molecule datasets. Journal of Cheminformatics, 2021, 13, 38.	6.1	10
2476	Recent advances in top-down proteome sample processing ahead of MS analysis. Mass Spectrometry Reviews, 2023, 42, 457-495.	5.4	24
2477	Xanthonones Active against Multidrug Resistance and Virulence Mechanisms of Bacteria. Antibiotics, 2021, 10, 600.	3.7	24
2478	Complementing the pulp proteome via sampling with a picosecond infrared laser (PIRL). Clinical Oral Investigations, 2021, 25, 6757-6768.	3.0	0
2479	Measuring pathway database coverage of the phosphoproteome. PeerJ, 2021, 9, e11298.	2.0	1
2480	Comparative Genomics of Peroxisome Biogenesis Proteins: Making Sense of the PEX Proteins. Frontiers in Cell and Developmental Biology, 2021, 9, 654163.	3.7	48
2481	Sex chromosome transformation and the origin of a male-specific X chromosome in the creeping vole. Science, 2021, 372, 592-600.	12.6	20
2482	Prediction of human-Streptococcus pneumoniae protein-protein interactions using logistic regression. Computational Biology and Chemistry, 2021, 92, 107492.	2.3	6

#	ARTICLE	IF	CITATIONS
2483	Assessment of protein-protein interfaces in cryo-EM derived assemblies. <i>Nature Communications</i> , 2021, 12, 3399.	12.8	20
2484	Network Pharmacology-Based Approach to Investigate the Molecular Targets of Rhubarb for Treating Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-8.	1.2	12
2485	Immunoinformatics prediction of potential B-cell and T-cell epitopes as effective vaccine candidates for eliciting immunogenic responses against Epstein-Barr virus. <i>Biomedical Journal</i> , 2021, 44, 317-337.	3.1	11
2486	Identification of sequence changes in myosin II that adjust muscle contraction velocity. <i>PLoS Biology</i> , 2021, 19, e3001248.	5.6	9
2487	A Network Pharmacology Approach to Reveal the Underlying Mechanisms of Zuogui Yin in the Treatment of Male Infertility. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 803-813.	1.1	2
2488	A novel homozygous missense variant in the NAXE gene in an Iranian family with progressive encephalopathy with brain edema and leukoencephalopathy. <i>Acta Neurologica Belgica</i> , 2022, 122, 1201-1210.	1.1	10
2490	Updating MoonProt From Home: An Online Student Research Project During the COVID-19 Pandemic. <i>The Biophysicist</i> , 2021, 2, 23-27.	0.3	2
2491	Structured data sets of compounds with multi-target and corresponding single-target activity from biological assays. <i>Future Science OA</i> , 2021, 7, FSO685.	1.9	2
2492	Biocatalysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	255
2493	Predicting anticancer hyperfoods with graph convolutional networks. <i>Human Genomics</i> , 2021, 15, 33.	2.9	9
2494	Study on the Molecular Mechanism of the Herbal Couple Sparganii Rhizoma-Curcumae Rhizoma in the Treatment of Lung Cancer Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	1.2	5
2495	Antimicrobial Activity of a Library of Thioxanones and Their Potential as Efflux Pump Inhibitors. <i>Pharmaceuticals</i> , 2021, 14, 572.	3.8	11
2497	Pectin Modification in Seed Coat Mucilage by <i>In Vivo</i> Expression of Rhamnogalacturonan-I- and Homogalacturonan-Degrading Enzymes. <i>Plant and Cell Physiology</i> , 2021, 62, 1912-1926.	3.1	8
2498	Functional and genomic characterization of <i>Komagataeibacter uvaceti</i> FXV3, a multiple stress resistant bacterium producing increased levels of cellulose. <i>Biotechnology Reports (Amsterdam)</i> , 2021, 10, 100743.	1.4	10
2499	The proteome of the human endolymphatic sac endolymph. <i>Scientific Reports</i> , 2021, 11, 11850.	3.3	5
2500	State-of-the-Art Biocatalysis. <i>ACS Central Science</i> , 2021, 7, 1105-1116.	11.3	59
2501	Immune Tolerance-Adjusted Personalized Immunogenicity Prediction for Pompe Disease. <i>Frontiers in Immunology</i> , 2021, 12, 636731.	4.8	10
2502	Analysis of High Molecular Mass Compounds from the Spider <i>Pamphobeteus verdolaga</i> Venom Gland. A Transcriptomic and MS ID Approach. <i>Toxins</i> , 2021, 13, 453.	3.4	1

#	ARTICLE	IF	CITATIONS
2503	A SARS-CoV-2 “human metalloproteome interaction map. <i>Journal of Inorganic Biochemistry</i> , 2021, 219, 111423.	3.5	23
2508	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. <i>IScience</i> , 2021, 24, 102762.	4.1	11
2509	Toward a Coronavirus Knowledge Graph. <i>Genes</i> , 2021, 12, 998.	2.4	7
2510	Mutagenic Analysis of the Putative ABCC6 Substrate-Binding Cavity Using a New Homology Model. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6910.	4.1	8
2511	Environmental dimensions of the protein corona. <i>Nature Nanotechnology</i> , 2021, 16, 617-629.	31.5	173
2512	Accurate annotation of protein coding sequences with IDTAXA. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab080.	3.2	0
2513	Chimera Spectrum Diagnostics for Peptides Using Two-Dimensional Partial Covariance Mass Spectrometry. <i>Molecules</i> , 2021, 26, 3728.	3.8	6
2514	Ayurveda botanicals in COVID-19 management: An in silico multi-target approach. <i>PLoS ONE</i> , 2021, 16, e0248479.	2.5	60
2515	Spatially Enriched Paralog Rearrangements Argue Functionally Diverse Ribosomes Arise during Cold Acclimation in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6160.	4.1	10
2516	Purification and quantitative proteomic analysis of cell bodies and protrusions. <i>STAR Protocols</i> , 2021, 2, 100462.	1.2	0
2517	A Comprehensive Molecular Epidemiological Analysis of SARS-CoV-2 Infection in Cyprus from April 2020 to January 2021: Evidence of a Highly Polyphyletic and Evolving Epidemic. <i>Viruses</i> , 2021, 13, 1098.	3.3	11
2518	Investigating the active compounds and mechanism of HuaShi XuanFei formula for prevention and treatment of COVID-19 based on network pharmacology and molecular docking analysis. <i>Molecular Diversity</i> , 2022, 26, 1175-1190.	3.9	14
2519	LSTM-PHV: prediction of human-virus protein-protein interactions by LSTM with word2vec. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	44
2520	Genetic Control of Human Infection with SARS-CoV-2. <i>Russian Journal of Genetics</i> , 2021, 57, 627-641.	0.6	3
2521	Protein Secondary Structure Prediction With a Reductive Deep Learning Method. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 687426.	4.1	18
2522	CLARINET: Efficient learning of dynamic network models from literature. <i>Bioinformatics Advances</i> , 0, , .	2.4	5
2524	S2L-PSIBLAST: a supervised two-layer search framework based on PSI-BLAST for protein remote homology detection. <i>Bioinformatics</i> , 2021, 37, 4321-4327.	4.1	7
2525	Genome-scale comparative analysis for host resistance against sea lice between Atlantic salmon and rainbow trout. <i>Scientific Reports</i> , 2021, 11, 13231.	3.3	9

#	ARTICLE	IF	CITATIONS
2526	UniBind: maps of high-confidence direct TF-DNA interactions across nine species. BMC Genomics, 2021, 22, 482.	2.8	36
2527	A Tissue-Specific Landscape of Alternative Polyadenylation, lncRNAs, TFs, and Gene Co-expression Networks in Liriodendron chinense. Frontiers in Plant Science, 2021, 12, 705321.	3.6	12
2528	Expression Patterns and Functional Characterization of Arabidopsis <i>Galactose Oxidase-Like</i> Genes Suggest Specialized Roles for Galactose Oxidases in Plants. Plant and Cell Physiology, 2021, 62, 1927-1943.	3.1	8
2529	Discovering and Summarizing Relationships Between Chemicals, Genes, Proteins, and Diseases in PubChem. Frontiers in Research Metrics and Analytics, 2021, 6, 689059.	1.9	14
2530	GWAS-Top Polymorphisms Associated With Late-Onset Alzheimer Disease in Brazil: Pointing Out Possible New Culprits Among Non-Coding RNAs. Frontiers in Molecular Biosciences, 2021, 8, 632314.	3.5	3
2531	Genome assembly of the popular Korean soybean cultivar Hwangkeum. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	5
2532	A genome sequence resource for the genus <i>Passiflora</i>, the genome of the wild diploid species <i>Passiflora organensis</i>. Plant Genome, 2021, 14, e20117.	2.8	8
2534	Comparison of anti-inflammatory effects of Lonicerae Japonicae Flos and Lonicerae Flos based on network pharmacology. Chinese Herbal Medicines, 2021, 13, 332-341.	3.0	7
2535	Chironomus ramosus Larval Microbiome Composition Provides Evidence for the Presence of Detoxifying Enzymes. Microorganisms, 2021, 9, 1571.	3.6	10
2536	Differential Domain Distribution of gnomAD- and Disease-Linked Connexin Missense Variants. International Journal of Molecular Sciences, 2021, 22, 7832.	4.1	7
2537	Yesprit and Yeaseq: Applications for designing primers and browsing sequences for research using the four <i>Schizosaccharomyces</i> species. Yeast, 2021, 38, 583-591.	1.7	2
2538	The clinical importance of tandem exon duplication-derived substitutions. Nucleic Acids Research, 2021, 49, 8232-8246.	14.5	11
2539	Acteoside exerts neuroprotection effects in the model of Parkinson's disease via inducing autophagy: Network pharmacology and experimental study. European Journal of Pharmacology, 2021, 903, 174136.	3.5	15
2540	Non-Specific Binding and Cross-Reaction of ELISA: A Case Study of Porcine Hemoglobin Detection. Foods, 2021, 10, 1708.	4.3	16
2542	In vitro and in silico analysis reveals antifungal activity and potential targets of curcumin on Paracoccidioides spp.. Brazilian Journal of Microbiology, 2021, 52, 1897-1911.	2.0	8
2543	Integrated in silico MS-based phosphoproteomics and network enrichment analysis of RASopathy proteins. Orphanet Journal of Rare Diseases, 2021, 16, 303.	2.7	1
2544	The origin and radiation of the phosphoprotein phosphatase (PPP) enzymes of Eukaryotes. Scientific Reports, 2021, 11, 13681.	3.3	2
2545	Transfer learning via multi-scale convolutional neural layers for human-virus protein-protein interaction prediction. Bioinformatics, 2021, 37, 4771-4778.	4.1	33

#	ARTICLE	IF	CITATIONS
2547	First detection of OsHV-1 in the cephalopod <i>Octopus vulgaris</i> . Is the octopus a dead-end for OsHV-1?. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107553.	3.2	5
2548	De novo transcriptome analysis of white teak (<i>Gmelina arborea</i> Roxb) wood reveals critical genes involved in xylem development and secondary metabolism. <i>BMC Genomics</i> , 2021, 22, 494.	2.8	1
2549	Innate-like self-reactive B cells infiltrate human renal allografts during transplant rejection. <i>Nature Communications</i> , 2021, 12, 4372.	12.8	34
2550	Ranked choice voting for representative transcripts with TRaCE. <i>Bioinformatics</i> , 2021, 38, 261-264.	4.1	4
2551	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	12.6	2,843
2552	GABA-receptive microglia selectively sculpt developing inhibitory circuits. <i>Cell</i> , 2021, 184, 4048-4063.e32.	28.9	142
2553	Comparative study of His- and Non-His-tagged CLIC proteins, reveals changes in their enzymatic activity. <i>Biochemistry and Biophysics Reports</i> , 2021, 26, 101015.	1.3	2
2554	Reciprocal interaction between SIRT6 and APC/C regulates genomic stability. <i>Scientific Reports</i> , 2021, 11, 14253.	3.3	4
2555	Trehalose-Induced Remodelling of the Human Microbiota Affects <i>Clostridioides difficile</i> Infection Outcome in an In Vitro Colonic Model: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 670935.	3.9	18
2556	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021, 39, 1563-1573.	17.5	115
2558	Polymorphisms at site 469 of B-RAF protein associated with skin melanoma may be correlated with dabrafenib resistance: An <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10862-10877.	3.5	1
2559	Comprehensive Analysis of the Systemic Transcriptomic Alternations and Inflammatory Response during the Occurrence and Progress of COVID-19. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-17.	4.0	13
2560	Structure-â€‘sequence features based prediction of phosphosites of serine/threonine protein kinases of <i>Mycobacterium tuberculosis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 131-141.	2.6	3
2562	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using ChIP-exo. <i>Nucleic Acids Research</i> , 2021, 49, 9696-9710.	14.5	30
2565	Sequence-specific dynamics of DNA response elements and their flanking sites regulate the recognition by AP-1 transcription factors. <i>Nucleic Acids Research</i> , 2021, 49, 9280-9293.	14.5	21
2566	Pim Kinases as Therapeutic Targets in Early Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2021, 73, 1820-1830.	5.6	14
2567	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1786.	1.2	5
2568	Data on the first functionally-annotated de novo transcriptome assembly for North American flying squirrels (genus <i>Glaucomys</i>). <i>Data in Brief</i> , 2021, 37, 107267.	1.0	1

#	ARTICLE	IF	CITATIONS
2569	Metabolites from Marine-Derived Fungi as Potential Antimicrobial Adjuvants. <i>Marine Drugs</i> , 2021, 19, 475.	4.6	14
2570	The COMPARE Database: A Public Resource for Allergen Identification, Adapted for Continuous Improvement. <i>Frontiers in Allergy</i> , 2021, 2, 700533.	2.8	24
2571	Rethinking water treatment targets: Bacteria regrowth under unprovable conditions. <i>Water Research</i> , 2021, 201, 117374.	11.3	17
2572	Allosteric regulation within the highly interconnected structural scaffold of <scp>AraC</scp>/<scp>XylS</scp> homologs tolerates a wide range of amino acid changes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 186-199.	2.6	0
2574	Characterization of iron reducibility of soy protein amyloid fibrils and their applications in iron fortification. <i>Food Chemistry</i> , 2021, 353, 129420.	8.2	23
2575	Distribution and diversity of dimetal-carboxylate halogenases in cyanobacteria. <i>BMC Genomics</i> , 2021, 22, 633.	2.8	5
2577	An extensive and dynamic trans-omic network illustrating prominent regulatory mechanisms in response to insulin in the liver. <i>Cell Reports</i> , 2021, 36, 109569.	6.4	7
2578	Potential <i>Arabidopsis thaliana</i> glucosinolate genes identified from the co-expression modules using graph clustering approach. <i>PeerJ</i> , 2021, 9, e11876.	2.0	7
2579	The coral symbiont <i>Candidatus</i> Aquarickettsia is variably abundant in threatened Caribbean acroporids and transmitted horizontally. <i>ISME Journal</i> , 2022, 16, 400-411.	9.8	21
2580	Drug repurposing for COVID-19 using computational screening: Is Fostamatinib/R406 a potential candidate?. <i>Methods</i> , 2022, 203, 564-574.	3.8	18
2582	Packpred: Predicting the Functional Effect of Missense Mutations. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 646288.	3.5	7
2583	ACO2 clinicobiological dataset with extensive phenotype ontology annotation. <i>Scientific Data</i> , 2021, 8, 205.	5.3	2
2584	Escherichia coli AraJ boosts utilization of arabinose in metabolically engineered cyanobacterium Synechocystis sp. PCC 6803. <i>AMB Express</i> , 2021, 11, 115.	3.0	2
2585	Novel Anti-Melanogenic Compounds, (Z)-5-(Substituted Benzylidene)-4-thioxothiazolidin-2-one Derivatives: In Vitro and In Silico Insights. <i>Molecules</i> , 2021, 26, 4963.	3.8	6
2586	Properties of peptides released from salmon and carp via simulated human-like gastrointestinal digestion described applying quantitative parameters. <i>PLoS ONE</i> , 2021, 16, e0255969.	2.5	8
2587	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
2588	Molecular Aspects and Structure Activity Relationship of Oxytocin Agonists and Antagonistâ€™s Role in Health. , 0, , .		0
2589	Improved pathogenicity prediction for rare human missense variants. <i>American Journal of Human Genetics</i> , 2021, 108, 1891-1906.	6.2	51

#	ARTICLE	IF	CITATIONS
2590	Peptide Location Fingerprinting Reveals Tissue Region-Specific Differences in Protein Structures in an Ageing Human Organ. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10408.	4.1	9
2593	Wittig reagents for chemoselective sulfenic acid ligation enables global site stoichiometry analysis and redox-controlled mitochondrial targeting. <i>Nature Chemistry</i> , 2021, 13, 1140-1150.	13.6	37
2594	Bacteria-driven phthalic acid ester biodegradation: Current status and emerging opportunities. <i>Environment International</i> , 2021, 154, 106560.	10.0	66
2596	Selection of the Optimal L-asparaginase II Against Acute Lymphoblastic Leukemia: An In Silico Approach. <i>Jmirx Med</i> , 2021, 2, e29844.	0.4	11
2598	The effects of Tbx15 and Pax1 on facial and other physical morphology in mice. <i>FASEB BioAdvances</i> , 2021, 3, 1011-1019.	2.4	4
2600	Global Transcriptome Characterization and Assembly of the Thermophilic Ascomycete <i>Chaetomium thermophilum</i> . <i>Genes</i> , 2021, 12, 1549.	2.4	3
2602	Diverse phosphate and auxin transport loci distinguish phosphate tolerant from sensitive <i>Arabidopsis</i> accessions. <i>Plant Physiology</i> , 2021, 187, 2656-2673.	4.8	9
2605	MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885.	2.0	0
2606	In Silico Analysis of Fungal and Chloride-Dependent α -Amylases within the Family GH13 with Identification of Possible Secondary Surface-Binding Sites. <i>Molecules</i> , 2021, 26, 5704.	3.8	4
2607	Genome-wide prediction of cauliflower miRNAs and lncRNAs and their roles in post-transcriptional gene regulation. <i>Planta</i> , 2021, 254, 72.	3.2	2
2608	The Human Gut Resistome up to Extreme Longevity. <i>MSphere</i> , 2021, 6, e0069121.	2.9	12
2609	Neuroigin-3 and neuroigin-4X form nanoscopic clusters and regulate growth cone organization and size. <i>Human Molecular Genetics</i> , 2022, 31, 674-691.	2.9	4
2610	A New Subfamily of Glycoside Hydrolase Family 30 with Strict Xylobiohydrolase Function. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 714238.	3.5	6
2611	Proteogenomic analysis of pancreatic cancer subtypes. <i>PLoS ONE</i> , 2021, 16, e0257084.	2.5	5
2612	Contraceptive and infertility target DataBase (CITDBase): A contraceptive drug development tool for targeting and analysis of human reproductive specific tissues. <i>Biology of Reproduction</i> , 2021, , .	2.7	3
2613	Gene-gene relationships in an <i>Escherichia coli</i> accessory genome are linked to function and mobility. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
2614	Swine plasma peptides obtained using pepsin: <i>in silico</i> and <i>in vitro</i> properties and biological activities. <i>Biocatalysis and Biotransformation</i> , 2023, 41, 108-122.	2.0	1
2616	Unique somatic variants in DNA from urine exosomes of individuals with bladder cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 22, 360-376.	4.1	10

#	ARTICLE	IF	CITATIONS
2617	The function of twister ribozyme variants in non-LTR retrotransposition in <i>Schistosoma mansoni</i> . Nucleic Acids Research, 2021, 49, 10573-10588.	14.5	3
2618	Catalytic and binding sites prediction in globular proteins through discrete Markov chains and network centrality measures. Physical Biology, 2021, 18, 066002.	1.8	0
2620	Immunogenic amino acid motifs and linear epitopes of COVID-19 mRNA vaccines. PLoS ONE, 2021, 16, e0252849.	2.5	11
2621	Mitochondria-localized AMPK responds to local energetics and contributes to exercise and energetic stress-induced mitophagy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	75
2622	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. Nature Communications, 2021, 12, 5773.	12.8	29
2623	Mutational spectrum of BRAF gene in colorectal cancer patients in Saudi Arabia. Saudi Journal of Biological Sciences, 2021, 28, 5906-5912.	3.8	8
2624	Proteome based mapping and molecular docking revealed DnaA as a potential drug target against <i>Shigella sonnei</i> . Saudi Journal of Biological Sciences, 2021, 29, 1147-1159.	3.8	3
2625	Hepatic Regulator of G Protein Signaling 6 (RGS6) drives non-alcoholic fatty liver disease by promoting oxidative stress and ATM-dependent cell death. Redox Biology, 2021, 46, 102105.	9.0	17
2626	Biallelic <i>AOPEP</i> Loss-of-Function Variants Cause Progressive Dystonia with Prominent Limb Involvement. Movement Disorders, 2022, 37, 137-147.	3.9	14
2627	Interaction of epigallocatechin-gallate and chlorhexidine with <i>Streptococcus mutans</i> stimulated odontoblast-like cells: Cytotoxicity, Interleukin-1 β and co-species proteomic analyses. Archives of Oral Biology, 2021, 131, 105268.	1.8	4
2628	Mig6 not only inhibits EGFR and HER2 but also targets HER3 and HER4 in a differential specificity: Implications for targeted esophageal cancer therapy. Biochimie, 2021, 190, 132-142.	2.6	10
2629	Comprehensive structure-activity-relationship studies of sensory active compounds in licorice (<i>Glycyrrhiza glabra</i>). Food Chemistry, 2021, 364, 130420.	8.2	15
2630	Fuzzy Jaccard Index: A robust comparison of ordered lists. Applied Soft Computing Journal, 2021, 113, 107849.	7.2	7
2631	Mobilization of seed storage proteins is crucial to high vigor in common bean seeds. Ciencia Rural, 2022, 52, .	0.5	2
2632	Computational Modeling of Protein Three-Dimensional Structure: Methods and Resources. , 2021, , 155-178.		4
2633	Proteomic profile of vitreous in patients with tubercular uveitis. Tuberculosis, 2021, 126, 102036.	1.9	8
2634	Network Pharmacology-Based Analysis on the Mechanism of Action of Ephedrae Herba-Cinnamomi Ramulus Couplet Medicines in the Treatment for Psoriasis. Medical Science Monitor, 2021, 27, e927421.	1.1	4
2635	Coxsackievirus B3 Infection of Human iPSC Lines and Derived Primary Germ-Layer Cells Regarding Receptor Expression. International Journal of Molecular Sciences, 2021, 22, 1220.	4.1	3

#	ARTICLE	IF	CITATIONS
2636	Convergence of sphingolipid desaturation across over 500 million years of plant evolution. <i>Nature Plants</i> , 2021, 7, 219-232.	9.3	31
2637	CE16 acetylsterases: in silico analysis, catalytic machinery prediction and comparison with related SGNH hydrolases. <i>3 Biotech</i> , 2021, 11, 84.	2.2	6
2638	CHD2-Related CNS Pathologies. <i>International Journal of Molecular Sciences</i> , 2021, 22, 588.	4.1	20
2639	Challenge of post-COVID era: management of cardiovascular complications in asymptomatic carriers of SARS-CoV-2. <i>Heart Failure Reviews</i> , 2022, 27, 239-249.	3.9	6
2640	Capturing Protein Domain Structure and Function Using Self-Supervision on Domain Architectures. <i>Algorithms</i> , 2021, 14, 28.	2.1	3
2641	Integrative multiomics analysis of <i>Premolis semirufa</i> caterpillar venom in the search for molecules leading to a joint disease. <i>Scientific Reports</i> , 2021, 11, 1995.	3.3	2
2642	Predicting bacteriophage hosts based on sequences of annotated receptor-binding proteins. <i>Scientific Reports</i> , 2021, 11, 1467.	3.3	50
2643	Origin of the Phosphoprotein Phosphatase (PPP) sequence family in Bacteria: Critical ancestral sequence changes, radiation patterns and substrate binding features. <i>BBA Advances</i> , 2021, 1, 100005.	1.6	3
2644	Integrative computational approach identifies drug targets in CD4+ T-cell-mediated immune disorders. <i>Npj Systems Biology and Applications</i> , 2021, 7, 4.	3.0	18
2645	Computational Phosphorylation Network Reconstruction: An Update on Methods and Resources. <i>Methods in Molecular Biology</i> , 2021, 2358, 203-219.	0.9	1
2646	Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk. <i>ELife</i> , 2021, 10, .	6.0	38
2647	Combination of lyophilized adipose-derived stem cell concentrated conditioned medium and polysaccharide hydrogel in the inhibition of hypertrophic scarring. <i>Stem Cell Research and Therapy</i> , 2021, 12, 23.	5.5	18
2648	Automatization and self-maintenance of the O-GlcNAcome catalog: a smart scientific database. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	10
2649	AutoPVS1: An automatic classification tool for PVS1 interpretation of null variants. <i>Human Mutation</i> , 2020, 41, 1488-1498.	2.5	34
2650	Protein Thermal Stability Engineering Using HoTMuSiC. <i>Methods in Molecular Biology</i> , 2020, 2112, 59-73.	0.9	15
2651	Bioinformatic Application of Fluorescence-Based In Vivo RNA Regional Accessibility Data to Identify Novel sRNA Targets. <i>Methods in Molecular Biology</i> , 2020, 2113, 41-71.	0.9	2
2652	Calculation of False Discovery Rate for Peptide and Protein Identification. <i>Methods in Molecular Biology</i> , 2020, 2051, 145-159.	0.9	2
2653	Strategies for Increasing Protein Stability. <i>Methods in Molecular Biology</i> , 2020, 2073, 163-181.	0.9	21

#	ARTICLE	IF	CITATIONS
2654	Explore Protein-Protein Interactions for Cancer Target Discovery Using the OncoPPI Portal. <i>Methods in Molecular Biology</i> , 2020, 2074, 145-164.	0.9	7
2655	Embedding Alternative Conformations of Proteins in Protein-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2020, 2074, 113-124.	0.9	9
2656	Proteoinformatics and Agricultural Biotechnology Research: Applications and Challenges. , 2019, , 1-27.		1
2657	Data Portals and Analysis. , 2019, , 169-196.		1
2658	Tobacco Resources in the Sol Genomics Network and Nicotiana Metabolic Databases. <i>Compendium of Plant Genomes</i> , 2020, , 59-71.	0.5	3
2659	Data Journeys Beyond Databases in Systems Biology: Cytoscape and NDEx. , 2020, , 121-143.		3
2660	Unsupervised Grammar Induction for Revealing the Internal Structure of Protein Sequence Motifs. <i>Lecture Notes in Computer Science</i> , 2020, , 299-309.	1.3	1
2661	Community-Based Semantic Subgroup Discovery. <i>Lecture Notes in Computer Science</i> , 2018, , 182-196.	1.3	7
2662	Protein Structure Prediction Using Coarse-Grained Models. <i>Springer Series on Bio- and Neurosystems</i> , 2019, , 27-59.	0.2	3
2663	Genomics and Transcriptomics Advance in Plant Sciences. <i>Energy, Environment, and Sustainability</i> , 2019, , 419-448.	1.0	5
2664	In silico identification of potential inhibitors against human 2'-5'-oligoadenylate synthetase (OAS) proteins. <i>Computational Biology and Chemistry</i> , 2020, 85, 107211.	2.3	9
2665	Fungal α -amylases from three GH13 subfamilies: their sequence-structural features and evolutionary relationships. <i>International Journal of Biological Macromolecules</i> , 2020, 159, 763-772.	7.5	13
2666	Gonadal transcriptomic analysis of the mud crab <i>Scylla olivacea</i> infected with rhizocephalan parasite <i>Sacculina beauforti</i> . <i>Genomics</i> , 2020, 112, 2959-2969.	2.9	13
2667	Improved Method for Determining Absolute Phosphorylation Stoichiometry Using Bayesian Statistics and Isobaric Labeling. <i>Journal of Proteome Research</i> , 2017, 16, 4217-4226.	3.7	25
2668	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. <i>Nature Communications</i> , 2018, 9, 2419.	12.8	374
2669	A biochemically-interpretable machine learning classifier for microbial GWAS. <i>Nature Communications</i> , 2020, 11, 2580.	12.8	51
2670	Analysis of impact metrics for the Protein Data Bank. <i>Scientific Data</i> , 2018, 5, 180212.	5.3	24
2671	A reference set of curated biomedical data and metadata from clinical case reports. <i>Scientific Data</i> , 2018, 5, 180258.	5.3	22

#	ARTICLE	IF	CITATIONS
2672	Generation of a zebrafish SWATH-MS spectral library to quantify 10,000 proteins. <i>Scientific Data</i> , 2019, 6, 190011.	5.3	37
2673	The sequence and de novo assembly of <i>Oxygymnocypris stewartii</i> genome. <i>Scientific Data</i> , 2019, 6, 190009.	5.3	29
2674	Enabling Methods to Elucidate the Effects of Metal-based Anticancer Agents. 2-Oxoglutarate-Dependent Oxygenases, 2019, , 246-270.	0.8	8
2675	The challenge of detecting modifications on proteins. <i>Essays in Biochemistry</i> , 2020, 64, 135-153.	4.7	11
2676	High-resolution crystal structures of two prototypical $\hat{1}^2$ - and $\hat{1}^3$ -herpesviral nuclear egress complexes unravel the determinants of subfamily specificity. <i>Journal of Biological Chemistry</i> , 2020, 295, 3189-3201.	3.4	28
2677	Using ChEMBL web services for building applications and data processing workflows relevant to drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 757-767.	5.0	24
2678	Topological features of integrin adhesion complexes revealed by multiplexed proximity biotinylation. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	48
2679	Proteinâ€Sol: a web tool for predicting protein solubility from sequence. <i>Bioinformatics</i> , 2017, 33, 3098-3100.	4.1	404
2680	Comparative Genomics of Strictly Vertically Transmitted, Feminizing Microsporidia Endosymbionts of Amphipod Crustaceans. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	12
2681	LegumelP V3: from models to cropsâ€an integrative gene discovery platform for translational genomics in legumes. <i>Nucleic Acids Research</i> , 2021, 49, D1472-D1479.	14.5	25
2682	<i>Blastococcus atacamensis</i> sp. nov., a novel strain adapted to life in the Yungay core region of the Atacama Desert. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2712-2721.	1.7	33
2683	<i>Kyrpidia spormannii</i> sp. nov., a thermophilic, hydrogen-oxidizing, facultative autotroph, isolated from hydrothermal systems at S�o Miguel Island, and emended description of the genus <i>Kyrpidia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3735-3740.	1.7	28
2684	Transfer of <i>Meiothermus chliarophilus</i> (Tenreiro et al. 1995) Nobre et al. 1996, <i>Meiothermus roseus</i> Ming et al. 2016, <i>Meiothermus terrae</i> Yu et al. 2014 and <i>Meiothermus timidus</i> Pires et al. 2005, to <i>Calidithermus</i> gen. nov., as <i>Calidithermus chliarophilus</i> comb. nov., <i>Calidithermus roseus</i> comb. nov., <i>Calidithermus terrae</i> comb. nov. and <i>Calidithermus timidus</i> comb. nov., respectively, and emended description of the genus <i>Meiothermus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1060-1069.	1.7	28
2685	<i>Aggregatilinea zenta</i> gen. nov., sp. nov., a slow-growing, facultatively anaerobic bacterium isolated from subseafloor sediment, and proposal of the new order <i>Aggregatilineales</i> ord. nov. within the class <i>Anaerolineae</i> of the phylum <i>Chloroflexi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1185-1194.	1.7	32
2686	Mycoparasitism illuminated by genome and transcriptome sequencing of <i>Coniothyrium minitans</i> , an important biocontrol fungus of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>Microbial Genomics</i> , 2020, 6, .	2.0	15
2687	Enhanced functionalisation of major facilitator superfamily transporters via fusion of C-terminal protein domains is both extensive and varied in bacteria. <i>Microbiology (United Kingdom)</i> , 2019, 165, 419-424.	1.8	7
2817	<i>SIMBAD</i>: a sequence-independent molecular-replacement pipeline. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 595-605.	2.3	25
2818	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. <i>Environmental Microbiology</i> , 2018, 20, 385-401.	3.8	21

#	ARTICLE	IF	CITATIONS
2819	Retention of a chromosomal inversion from an anadromous ancestor provides the genetic basis for alternative freshwater ecotypes in rainbow trout. <i>Molecular Ecology</i> , 2019, 28, 1412-1427.	3.9	58
2820	Characterization of imine reductases in reductive amination for the exploration of structure-activity relationships. <i>Science Advances</i> , 2020, 6, eaay9320.	10.3	48
2821	Protein interaction networks revealed by proteome coevolution. <i>Science</i> , 2019, 365, 185-189.	12.6	208
2822	The PGRS Domain of Mycobacterium tuberculosis PE_PGRS Protein Rv0297 Is Involved in Endoplasmic Reticulum Stress-Mediated Apoptosis through Toll-Like Receptor 4. <i>MBio</i> , 2018, 9, .	4.1	67
2823	Metabolic Modeling of Streptococcus mutans Reveals Complex Nutrient Requirements of an Oral Pathogen. <i>MSystems</i> , 2019, 4, .	3.8	20
2824	Integration of Heterogeneous Experimental Data Improves Global Map of Human Protein Complexes. , 2019, 2019, 144-153.		1
2825	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	156	132
2826	LGR4 deficiency results in delayed puberty through impaired Wnt/ β -catenin signaling. <i>JCI Insight</i> , 2020, 5, .	5.0	25
2827	CDKN2B upregulation prevents teratoma formation in multipotent fibromodulin-reprogrammed cells. <i>Journal of Clinical Investigation</i> , 2019, 129, 3236-3251.	8.2	16
2828	Insulin resistance causes inflammation in adipose tissue. <i>Journal of Clinical Investigation</i> , 2018, 128, 1538-1550.	8.2	303
2829	Pulmonary alveolar microlithiasis: no longer in the stone age. <i>ERJ Open Research</i> , 2020, 6, 00289-2020.	2.6	12
2830	Association Between aquaporin-1 and Endurance Performance: A Systematic Review. <i>Sports Medicine - Open</i> , 2019, 5, 40.	3.1	9
2831	Last rolls of the yoyo: Assessing the human canonical protein count. <i>F1000Research</i> , 2017, 6, 448.	1.6	11
2832	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	1.6	6
2833	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	1.6	5
2834	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017, 6, 1845.	1.6	14
2835	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017, 6, 1845.	1.6	10
2836	Gene Annotation Easy Viewer (GAEV): Integrating KEGGâ€™s Gene Function Annotations and Associated Molecular Pathways. <i>F1000Research</i> , 0, 7, 416.	1.6	5

#	ARTICLE	IF	CITATIONS
2837	Gene Annotation Easy Viewer (GAEV): Integrating KEGG's Gene Function Annotations and Associated Molecular Pathways. F1000Research, 2018, 7, 416.	1.6	12
2838	drawProteins: a Bioconductor/R package for reproducible and programmatic generation of protein schematics. F1000Research, 2018, 7, 1105.	1.6	41
2839	Genome-wide CRISPR screening identifies new regulators of glycoprotein secretion. Wellcome Open Research, 0, 4, 119.	1.8	4
2840	A specialized MreB-dependent cell wall biosynthetic complex mediates the formation of stalk-specific peptidoglycan in <i>Caulobacter crescentus</i> . PLoS Genetics, 2019, 15, e1007897.	3.5	31
2841	Genome-scale metabolic models highlight stage-specific differences in essential metabolic pathways in <i>Trypanosoma cruzi</i> . PLoS Neglected Tropical Diseases, 2020, 14, e0008728.	3.0	8
2842	Identification of chironomid species as natural reservoirs of toxigenic <i>Vibrio cholerae</i> strains with pandemic potential. PLoS Neglected Tropical Diseases, 2020, 14, e0008959.	3.0	9
2843	Molecular mechanics of <i>Staphylococcus aureus</i> adhesin, CNA, and the inhibition of bacterial adhesion by stretching collagen. PLoS ONE, 2017, 12, e0179601.	2.5	37
2844	RNA-seq analysis identifies cytoskeletal structural genes and pathways for meat quality in beef. PLoS ONE, 2020, 15, e0240895.	2.5	9
2845	Genotype and transcriptome effects on somatic embryogenesis in <i>Cryptomeria japonica</i> . PLoS ONE, 2020, 15, e0244634.	2.5	12
2846	An enumeration of natural products from microbial, marine and terrestrial sources. Physical Sciences Reviews, 2020, 5, .	0.8	13
2847	Modulation of Toxin-Antitoxin System Rnl AB Type II in Phage-Resistant Gammaproteobacteria Surviving Photodynamic Treatment. Journal of Lasers in Medical Sciences, 2019, 10, 21-28.	1.2	5
2848	Microtubule number and length determine cellular shape and function in <i>Plasmodium</i> . EMBO Journal, 2019, 38, e100984.	7.8	59
2849	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
2850	Gene Ontology: A Resource for Analysis and Interpretation of Alzheimer's Disease Data. , 0, , 23-36.		9
2851	Valine biosynthesis in <i>Saccharomyces cerevisiae</i> is regulated by the mitochondrial branched-chain amino acid aminotransferase Bat1. Microbial Cell, 2018, 5, 293-299.	3.2	18
2852	Successful aging: insights from proteome analyses of healthy centenarians. Aging, 2020, 12, 3502-3515.	3.1	31
2853	ZNF139/circZNF139 promotes cell proliferation, migration and invasion via activation of PI3K/AKT pathway in bladder cancer. Aging, 2020, 12, 9915-9934.	3.1	17
2854	Phosphoproteome profiling reveals critical role of JAK-STAT signaling in maintaining chemoresistance in breast cancer. Oncotarget, 2017, 8, 114756-114768.	1.8	16

#	ARTICLE	IF	CITATIONS
2855	PAF1 complex interactions with SETDB1 mediate promoter H3K9 methylation and transcriptional repression of <i>Hoxa9</i> and <i>Meis1</i> in acute myeloid leukemia. <i>Oncotarget</i> , 2018, 9, 22123-22136.	1.8	22
2856	Enhanced proteasomal activity is essential for long term survival and recurrence of innately radiation resistant residual glioblastoma cells. <i>Oncotarget</i> , 2018, 9, 27667-27681.	1.8	9
2857	Integrative landscape of dysregulated signaling pathways of clinically distinct pancreatic cancer subtypes. <i>Oncotarget</i> , 2018, 9, 29123-29139.	1.8	15
2858	Imbalanced sphingolipid signaling is maintained as a core proponent of a cancerous phenotype in spite of metabolic pressure and epigenetic drift. <i>Oncotarget</i> , 2019, 10, 449-479.	1.8	6
2859	Genotify: Fast, lightweight gene lookup and summarization. <i>Journal of Open Source Software</i> , 2018, 3, 885.	4.6	3
2860	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. <i>SSRN Electronic Journal</i> , 0, , .	0.4	8
2861	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. <i>Protein and Peptide Letters</i> , 2020, 27, 259-264.	0.9	12
2862	The In Silico Drug Discovery Toolbox: Applications in Lead Discovery and Optimization. <i>Current Medicinal Chemistry</i> , 2019, 26, 3838-3873.	2.4	47
2863	Sam Domains in Multiple Diseases. <i>Current Medicinal Chemistry</i> , 2020, 27, 450-476.	2.4	12
2864	Unlocking the Potential of HK2 in Cancer Metabolism and Therapeutics. <i>Current Medicinal Chemistry</i> , 2020, 26, 7285-7322.	2.4	122
2865	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. <i>Current Genomics</i> , 2019, 20, 389-399.	1.6	11
2866	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. <i>Current Protein and Peptide Science</i> , 2017, 19, 200-210.	1.4	7
2867	Understanding Membrane Protein Drug Targets in Computational Perspective. <i>Current Drug Targets</i> , 2019, 20, 551-564.	2.1	45
2868	Design, Synthesis, Molecular Docking Study and Anti-Hepatocellular Carcinoma Evaluation of New Bis-Triazolothiadiazines. <i>Mini-Reviews in Medicinal Chemistry</i> , 2020, 20, 788-800.	2.4	13
2869	Autophagy and Apoptosis Specific Knowledgebases-guided Systems Pharmacology Drug Research. <i>Current Cancer Drug Targets</i> , 2019, 19, 716-728.	1.6	2
2870	Cell Penetrating Peptide: Sequence-Based Computational Prediction for Intercellular Delivery of Arginine Deiminase. <i>Current Proteomics</i> , 2020, 17, 117-131.	0.3	10
2871	Application of Machine Learning Methods in Predicting Nuclear Receptors and their Families. <i>Medicinal Chemistry</i> , 2020, 16, 594-604.	1.5	5
2872	Elucidating the Functional Role of Predicted miRNAs in Post- Transcriptional Gene Regulation Along with Symbiosis in <i>Medicago truncatula</i> . <i>Current Bioinformatics</i> , 2020, 15, 108-120.	1.5	11

#	ARTICLE	IF	CITATIONS
2873	Inter-Pathogen Peptide Sharing and the Original Antigenic Sin: Solving a Paradox. The Open Immunology Journal, 2018, 08, 16-27.	1.5	24
2874	Bafilomycin-A1 and ML9 Exert Different Lysosomal Actions to Induce Cell Death. Current Molecular Pharmacology, 2019, 12, 261-271.	1.5	15
2875	Genetic diversity and structure of Oriental and European beech populations from Iran and Europe. Silvae Genetica, 2020, 69, 55-62.	0.8	7
2876	Waardenburg Syndrome Expression and Penetrance. Journal of Rare Diseases Research & Treatment, 2017, 2, 31-40.	1.1	5
2877	Investigating the natural resistance of blackfoot p-a%%KERN_ERR%%ua Haliotis iris to abalone viral ganglioneuritis using whole transcriptome analysis. Diseases of Aquatic Organisms, 2019, 135, 107-119.	1.0	7
2878	Proteomic Analysis of Peroxynitrite-Induced Protein Nitration in Isolated Beef Heart Mitochondria. Physiological Research, 2018, , 239-250.	0.9	3
2879	Proteomic Analysis of Peroxynitrite-Induced Protein Nitration in Isolated Beef Heart Mitochondria. Physiological Research, 2018, 67, 239-250.	0.9	10
2880	Identification of Critical Genes and Proteins for Stent Restenosis Induced by Esophageal Benign Hyperplasia in Esophageal Cancer. Frontiers in Genetics, 2020, 11, 563954.	2.3	6
2881	Silent Witness: Dual-Species Transcriptomics Reveals Epithelial Immunological Quiescence to Helminth Larval Encounter and Fostered Larval Development. Frontiers in Immunology, 2018, 9, 1868.	4.8	13
2882	Multipath: An R Package to Generate Integrated Reproducible Pathway Models. Biology, 2020, 9, 483.	2.8	3
2883	A Reference Genome of Bursaphelenchus mucronatus Provides New Resources for Revealing Its Displacement by Pinewood Nematode. Genes, 2020, 11, 570.	2.4	10
2884	Allosteric Binding Sites On Nuclear Receptors: Focus On Drug Efficacy and Selectivity. International Journal of Molecular Sciences, 2020, 21, 534.	4.1	11
2885	Principal component analysis on LCâ€MS/MS and 2DEâ€MALDIâ€TOF in glioblastoma cell lines reveals that mitochondria act as organelle sensors of the metabolic state in glioblastoma. Oncology Reports, 2020, 44, 661-673.	2.6	8
2886	Long nonâ€coding RNA MEG3 suppresses epithelialâ€toâ€mesenchymal transition by inhibiting the PSAT1â€dependent GSKâ€3Î²/Snail signaling pathway in esophageal squamous cell carcinoma. Oncology Reports, 2020, 44, 2130-2142.	2.6	14
2887	Native and introduced Argentine ant populations are characterised by distinct transcriptomic signatures associated with behaviour and immunity. NeoBiota, 0, 49, 105-126.	1.0	9
2888	Antisoma Application: A Fully Integrated V-Like Antibodies Platform. AIMS Medical Science, 2017, 4, 784-797.	0.4	4
2889	A Review of Software Applications and Databases for the Interpretation of Glycopeptide Data. Trends in Glycoscience and Glycotechnology, 2017, 29, E51-E62.	0.1	9
2890	Exploration of Mutation and DNA Methylation of Polo-Like Kinase 1 (PLK1) in Colorectal Cancer. Open Journal of Pathology, 2017, 07, 45-57.	0.2	1

#	ARTICLE	IF	CITATIONS
2891	Mesenchymal stem cells secretome: The cornerstone of cell-free regenerative medicine. World Journal of Stem Cells, 2020, 12, 1529-1552.	2.8	72
2892	Homology Modeling and Molecular Docking of hABCC3/MRP3 with Chemotherapeutic Agents in Acute Leukemia. Jundishapur Journal of Natural Pharmaceutical Products, 2020, 15, .	0.6	3
2893	Insights from the Molecular modeling, docking analysis of illicit drugs and Bomb Compounds with Honey Bee Odorant Binding Proteins (OBPs). Bioinformation, 2018, 14, 219-231.	0.5	9
2894	Expression and purification of full-length Alanyl-tRNA-synthetase from Thermus thermophilus HB27. Biopolymers and Cell, 2018, 34, 435-444.	0.4	1
2895	Cdc48-like protein of actinobacteria (Cpa) is a novel proteasome interactor in mycobacteria and related organisms. ELife, 2018, 7, .	6.0	17
2896	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. ELife, 2018, 7, .	6.0	62
2897	Gating mechanisms during actin filament elongation by formins. ELife, 2018, 7, .	6.0	25
2898	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. ELife, 2018, 7, .	6.0	73
2899	Selective agonist of TRPML2 reveals direct role in chemokine release from innate immune cells. ELife, 2018, 7, .	6.0	71
2900	A dedicated diribonuclease resolves a key bottleneck for the terminal step of RNA degradation. ELife, 2019, 8, .	6.0	21
2901	Genetic interactions of G-quadruplexes in humans. ELife, 2019, 8, .	6.0	91
2902	The C-terminal tail of the bacterial translocation ATPase SecA modulates its activity. ELife, 2019, 8, .	6.0	9
2903	Common activation mechanism of class A GPCRs. ELife, 2019, 8, .	6.0	339
2904	Structure-based discovery of potent and selective melatonin receptor agonists. ELife, 2020, 9, .	6.0	28
2905	Genomic and phenotypic evolution of Escherichia coli in a novel citrate-only resource environment. ELife, 2020, 9, .	6.0	26
2906	Database limitations for studying the human gut microbiome. PeerJ Computer Science, 2020, 6, e289.	4.5	11
2907	Analysis of drug binding pockets and repurposing opportunities for twelve essential enzymes of ESKAPE pathogens. PeerJ, 2017, 5, e3765.	2.0	5
2908	Biotea: semantics for Pubmed Central. PeerJ, 2018, 6, e4201.	2.0	5

#	ARTICLE	IF	CITATIONS
2909	Peptide presentation by HLA-DQ molecules is associated with the development of immune tolerance. PeerJ, 2018, 6, e5118.	2.0	11
2910	Single mutations in the $\hat{\mu}$ subunit from thermophilic <i>Bacillus</i> PS3 generate a high binding affinity site for ATP. PeerJ, 2018, 6, e5505.	2.0	3
2911	SLiM-Enrich: computational assessment of protein-protein interaction data as a source of domain-motif interactions. PeerJ, 2018, 6, e5858.	2.0	11
2912	MLPA is a practical and complementary alternative to CMA for diagnostic testing in patients with autism spectrum disorders and identifying new candidate CNVs associated with autism. PeerJ, 2019, 6, e6183.	2.0	8
2913	TGF-beta signalling in bovine mammary gland involution and a comparative assessment of MAC-T and BME-UV1 cells as in vitro models for its study. PeerJ, 2019, 6, e6210.	2.0	8
2914	Lightweight data management with dtool. PeerJ, 2019, 7, e6562.	2.0	5
2915	Genome skimming is a low-cost and robust strategy to assemble complete mitochondrial genomes from ethanol preserved specimens in biodiversity studies. PeerJ, 2019, 7, e7543.	2.0	52
2916	Whole genome sequencing of a novel, dichloromethane-fermenting <i>Peptococcaceae</i> from an enrichment culture. PeerJ, 2019, 7, e7775.	2.0	14
2917	Global transcriptome analysis of alfalfa reveals six key biological processes of senescent leaves. PeerJ, 2020, 8, e8426.	2.0	9
2918	Co-expression clustering across flower development identifies modules for diverse floral forms in <i>Achimenes</i> (Gesneriaceae). PeerJ, 2020, 8, e8778.	2.0	8
2919	ECMPride: prediction of human extracellular matrix proteins based on the ideal dataset using hybrid features with domain evidence. PeerJ, 2020, 8, e9066.	2.0	5
2920	VIRdb: a comprehensive database for interactive analysis of genes/proteins involved in the pathogenesis of vitiligo. PeerJ, 2020, 8, e9119.	2.0	3
2921	Post-Translational Modifications of PCNA in Control of DNA Synthesis and DNA Damage Tolerance-the Implications in Carcinogenesis. International Journal of Biological Sciences, 2021, 17, 4047-4059.	6.4	16
2922	The carbohydrate-active enzyme database: functions and literature. Nucleic Acids Research, 2022, 50, D571-D577.	14.5	813
2923	OUP accepted manuscript. Nucleic Acids Research, 2022, 50, D402-D412.	14.5	12
2924	scEnhancer: a single-cell enhancer resource with annotation across hundreds of tissue/cell types in three species. Nucleic Acids Research, 2022, 50, D371-D379.	14.5	16
2925	Enolase 1, a Moonlighting Protein, as a Potential Target for Cancer Treatment. International Journal of Biological Sciences, 2021, 17, 3981-3992.	6.4	40
2926	Immunoglobulin A Glycosylation and Its Role in Disease. Experientia Supplementum (2012), 2021, 112, 433-477.	0.9	7

#	ARTICLE	IF	CITATIONS
2927	Ensemble of Template-Free and Template-Based Classifiers for Protein Secondary Structure Prediction. International Journal of Molecular Sciences, 2021, 22, 11449.	4.1	1
2928	De novo transcriptome analysis provides insights into the salt tolerance of <i>Podocarpus macrophyllus</i> under salinity stress. BMC Plant Biology, 2021, 21, 489.	3.6	9
2929	Network Pharmacology-Based and Molecular Docking-Based Analysis of Suanzaoren Decoction for the Treatment of Parkinson's Disease with Sleep Disorder. BioMed Research International, 2021, 2021, 1-12.	1.9	21
2931	Plastic-Degrading Potential across the Global Microbiome Correlates with Recent Pollution Trends. MBio, 2021, 12, e0215521.	4.1	51
2932	Distribution of bacteriocin genes in the lineages of <i>Lactiplantibacillus plantarum</i> . Scientific Reports, 2021, 11, 20063.	3.3	15
2933	Exploring the Freedoms in Data Mining: Why the Trustworthiness and Integrity of the Findings are the Casualties, and How to Resolve These?. Lecture Notes in Networks and Systems, 2022, , 616-635.	0.7	1
2934	The V2475F CPVT1 mutation yields distinct RyR2 channel populations that differ in their responses to cytosolic Ca ²⁺ and Mg ²⁺ . Journal of Physiology, 2021, 599, 5179-5201.	2.9	2
2935	Mass Dynamics 1.0: A Streamlined, Web-Based Environment for Analyzing, Sharing, and Integrating Label-Free Data. Journal of Proteome Research, 2021, 20, 5180-5188.	3.7	4
2936	Transcriptomic and rRNA:rDNA Signatures of Environmental versus Enteric <i>Enterococcus faecalis</i> Isolates under Oligotrophic Freshwater Conditions. Microbiology Spectrum, 2021, 9, e0081721.	3.0	0
2937	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. Molecular Systems Biology, 2021, 17, e10427.	7.2	17
2938	Study on the mechanism of treating COVID-19 with Shenqi Wan based on network pharmacology. Drug Development and Industrial Pharmacy, 2021, , 1-11.	2.0	8
2942	High-quality reference genome of <i>Fasciola gigantica</i> : Insights into the genomic signatures of transposon-mediated evolution and specific parasitic adaption in tropical regions. PLoS Neglected Tropical Diseases, 2021, 15, e0009750.	3.0	12
2943	Predictive regulatory and metabolic network models for systems analysis of <i>Clostridioides difficile</i> . Cell Host and Microbe, 2021, 29, 1709-1723.e5.	11.0	12
2944	Delineating infection strategies of <i>Leishmania donovani</i> secretory proteins in Human through host-pathogen protein Interactome prediction. Pathogens and Disease, 2021, 79, .	2.0	2
2945	Network Pharmacology-Based Study of the Underlying Mechanisms of Huangqi Sijunzi Decoction for Alzheimer's Disease. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-13.	1.2	5
2947	In Silico Prediction, Computational Physico Chemical Analysis in Gymnemic Acids. International Journal of Pharma and Bio Sciences, 2021, 11, .	0.1	0
2948	Identifying the beta-site amyloid precursor protein cleaving enzyme 1 interactome through the proximity-dependent biotin identification assay. Neuroscience Letters, 2021, , 136302.	2.1	1
2949	Design, synthesis, biological evaluation, and molecular modeling studies of pyrazole-benzofuran hybrids as new α -glucosidase inhibitor. Scientific Reports, 2021, 11, 20776.	3.3	15

#	ARTICLE	IF	CITATIONS
2950	Machine Learning for Prediction of Drug Targets in Microbe Associated Cardiovascular Diseases by Incorporating Host-Pathogen Interaction Network Parameters. <i>Molecular Informatics</i> , 2022, 41, e2100115.	2.5	7
2951	Molecular insight into the affinity, specificity and cross-reactivity of systematic hepatocellular carcinoma RALT interaction profile with human receptor tyrosine kinases. <i>Amino Acids</i> , 2021, 53, 1715-1728.	2.7	2
2953	Investigating Alzheimer's Disease Candidate Genes Based on Combined Network Using Subnetwork Extraction Algorithms. <i>Lecture Notes in Computer Science</i> , 2017, , 559-565.	1.3	0
2972	Approaches to <i>ab initio</i> molecular replacement of α -helical transmembrane proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 985-996.	2.3	6
2977	Molecular Docking Studies of Phytocompounds from Aloe vera (L.) Burm.f. having Anticancer Property, against an Antiapoptotic Bcl-2 Protein. <i>Biosciences, Biotechnology Research Asia</i> , 2017, 14, 1449-1456.	0.5	2
2981	SNPViz - Visualization of SNPs in proteins. <i>Genomics and Computational Biology</i> , 2017, 4, 100048.	0.7	1
2982	Gene-environment interactions as the basis of health formation. <i>Ecological Genetics</i> , 2017, 15, 19-32.	0.5	1
2984	Representation of Proteins with Posttranslational Modifications in the HL7 SPL Standard. <i>Methods in Pharmacology and Toxicology</i> , 2018, , 1.	0.2	1
2986	Application of Bioinformatics to Asthma. <i>Translational Bioinformatics</i> , 2018, , 349-359.	0.0	0
2987	Proteomic Data. , 2018, , 227-250.		0
2993	A Centipede Toxin Family Defines a New Ancient Class of CSSS Defensins. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3002	Structural analyses of putative porcine cluster of differentiation (CD) 24 gene. <i>Journal of Biomedical Translational Research</i> , 2018, 19, 1-9.	0.1	0
3005	Gene Annotation Easy Viewer (GAEV): Integrating KEGG's Gene Function Annotations and Associated Molecular Pathways. <i>F1000Research</i> , 2018, 7, 416.	1.6	5
3024	BED: a Biological Entity Dictionary based on a graph data model. <i>F1000Research</i> , 2018, 7, 195.	1.6	1
3046	Automatic Human-like Mining and Constructing Reliable Genetic Association Database with Deep Reinforcement Learning. , 2018, , .		4
3049	Peptide Sharing between Parvovirus B19 and DNA Methylating/ Histone Modifying Enzymes. A Potential Link to Childhood Acute Lymphoblastic Leukemia. <i>International Journal of Pediatrics and Child Health</i> , 0, 5, 29-39.	0.1	4
3051	Function Prediction of Human Proteins Using Machine Learning Algorithms. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3052	An Approach for Semantic Data Integration in Cancer Studies. <i>Lecture Notes in Computer Science</i> , 2019, , 60-73.	1.3	2

#	ARTICLE	IF	CITATIONS
3054	Amyloid-Like Assembly During Embryogenesis Activates Herzog, a Novel Prion-Like Phosphatase. SSRN Electronic Journal, 0, , .	0.4	0
3055	Protein Secondary Structure Prediction in 2018. , 2019, , 1-9.		0
3056	Systems Biology: Generating and Understanding Big Data. Success in Academic Surgery, 2019, , 233-243.	0.1	0
3097	Use and application of bioinformatics for the characterization of plant proteomes. Journal-Agrarian and Natural Resource Economics, 0, , 11-18.	0.0	0
3102	In silico Defining the Repeat-containing Proteins in the Acinetobacter baumannii Proteome, a Great Reservoir of Templates for Synthetic Biology. Current Chemical Biology, 2019, 13, 149-158.	0.5	0
3103	Identification of Novel Key Biomarkers in Simpson-Golabi-Behmel Syndrome (SGBS). International Annals of Science, 2019, 8, 1-11.	0.4	1
3118	Review of Issues and Solutions to Data Analysis Reproducibility and Data Quality in Clinical Proteomics. Methods in Molecular Biology, 2020, 2051, 345-371.	0.9	3
3126	Fundamentals of Drug Metabolism and Pharmacogenomics Within a Learning Healthcare System Workflow Perspective. Computers in Health Care, 2020, , 59-80.	0.3	0
3129	Oligopeptides for Immunotherapy Approaches in Ovarian Cancer Treatment. Current Drug Discovery Technologies, 2019, 16, 285-289.	1.2	4
3132	Proteome Bioinformatics Methods for Studying Histidine Phosphorylation. Methods in Molecular Biology, 2020, 2077, 237-250.	0.9	0
3138	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
3139	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
3143	Osteoking improves OP rat by enhancing HSP90 α 2 expression. International Journal of Molecular Medicine, 2020, 45, 1543-1553.	4.0	4
3145	Post-translational modifications and stress adaptation: the paradigm of FKBP51. Biochemical Society Transactions, 2020, 48, 441-449.	3.4	10
3152	Kinetics and Computational Evaluation of Eugenol and Vanillic Acid on Inhibition of a Potential Enzyme of a Nosocomial Pathogen that Promotes Struvite Formation. Current Enzyme Inhibition, 2020, 16, 162-171.	0.4	1
3159	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. Medicinal Chemistry, 2020, 16, 605-619.	1.5	2
3161	Comprehensive functional network analysis and screening of deleterious pathogenic variants in non-syndromic hearing loss causative genes. Bioscience Reports, 2021, 41, .	2.4	0
3163	Capsicumicine, a New Bioinspired Peptide from Red Peppers Prevents Staphylococcal Biofilm In Vitro and In Vivo via a Matrix Anti-Assembly Mechanism of Action. Microbiology Spectrum, 2021, 9, e0047121.	3.0	2

#	ARTICLE	IF	CITATIONS
3164	Proteomics Profiling with SWATH-MS Quantitative Analysis of Changes in the Human Brain with HIV Infection Reveals a Differential Impact on the Frontal and Temporal Lobes. Brain Sciences, 2021, 11, 1438.	2.3	1
3166	Conserved Trigger Loop Histidine of RNA Polymerase II Functions as a Positional Catalyst Primarily through Steric Effects. Biochemistry, 2021, 60, 3323-3336.	2.5	4
3167	Proteomic Database Search Engine for Two-Dimensional Partial Covariance Mass Spectrometry. Analytical Chemistry, 2021, 93, 14946-14954.	6.5	3
3168	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	0
3169	Complete chloroplast genome comparisons for Pityopsis (Asteraceae). PLoS ONE, 2020, 15, e0241391.	2.5	7
3170	Alteration in the Culex pipiens transcriptome reveals diverse mechanisms of the mosquito immune system implicated upon Rift Valley fever phlebovirus exposure. PLoS Neglected Tropical Diseases, 2020, 14, e0008870.	3.0	4
3175	The Multiple Representation of Protein Sequence Motifs Using Sequence Binary Decision Diagrams. Journal of Computer Chemistry Japan, 2020, 19, 8-17.	0.1	1
3178	The Role of Nrf2 in the Cardiovascular System and Atherosclerosis. Agents and Actions Supplements, 2020, , 97-127.	0.2	0
3179	Building Knowledge Graph Across Different Subdomains Using Interlinking Ontology for Biomedical Concepts. Communications in Computer and Information Science, 2020, , 182-190.	0.5	0
3180	Species Assignment for Gene Normalization Through Exploring the Structure of Full Length Article. Lecture Notes in Computer Science, 2020, , 285-290.	1.3	0
3181	Sequence Alignment Using Machine Learning for Accurate Template-based Protein Structure Prediction. Bio-protocol, 2020, 10, e3600.	0.4	2
3182	Genome-wide CRISPR screening identifies new regulators of glycoprotein secretion. Wellcome Open Research, 2019, 4, 119.	1.8	3
3183	The Genetic Basis of Flower Color Differences in Nicotiana tabacum. Compendium of Plant Genomes, 2020, , 175-193.	0.5	1
3184	In Silico T Cell Epitope Identification for SARS-CoV-2: Progress and Perspectives. SSRN Electronic Journal, 0, , .	0.4	1
3185	Computational Approaches for Elucidating Protein-Protein Interactions in Cation Channel Signaling. Current Drug Targets, 2020, 21, 179-192.	2.1	0
3187	A Systems Biology Driven Approach to Map the EP300 Interactors Using Comprehensive Protein Interaction Network. Lecture Notes in Computer Science, 2020, , 204-214.	1.3	0
3188	Experiencing DfAnalyzer for Runtime Analysis of Phylogenomic Dataflows. Lecture Notes in Computer Science, 2020, , 105-116.	1.3	0
3189	9 Fungal Genomics. , 2020, , 207-224.		0

#	ARTICLE	IF	CITATIONS
3201	Comparative transcriptomics characterized the distinct biosynthetic abilities of terpenoid and paeoniflorin biosynthesis in herbaceous peony strains. PeerJ, 2020, 8, e8895.	2.0	4
3202	New tale on LianHuaQingWen: IL6R/IL6/IL6ST complex is a potential target for COVID-19 treatment. Aging, 2021, 13, 23913-23935.	3.1	5
3203	Adaptation of Phytophthora nicotianae to multiple sources of partial-resistance in tobacco.. Plant Disease, 2021,, .	1.4	1
3204	Potential roles of imprinted genes in the teratogenic effects of alcohol on the placenta, somatic growth, and the developing brain. Experimental Neurology, 2022, 347, 113919.	4.1	7
3205	Explainable machine learning predictions of dual-target compounds reveal characteristic structural features. Scientific Reports, 2021, 11, 21594.	3.3	11
3206	MPS1 is involved in the HPV16-E7-mediated centrosomes amplification. Cell Division, 2021, 16, 6.	2.4	1
3207	Structure-Aware Mycobacterium tuberculosis Functional Annotation Uncloaks Resistance, Metabolic, and Virulence Genes. MSystems, 2021, , e0067321.	3.8	4
3210	Updated functional annotation of the Mycobacterium bovis AF2122/97 reference genome. Access Microbiology, 2020, 2, acmi000129.	0.5	4
3217	Antigen Discovery in Bacterial Panproteomes. Methods in Molecular Biology, 2021, 2183, 43-62.	0.9	6
3218	Elucidation of an essential function of the unique charged domain of <i>Plasmodium</i> topoisomerase III. Biochemical Journal, 2020, 477, 4745-4767.	3.7	6
3220	Construction of Protein Expression Network. Methods in Molecular Biology, 2021, 2189, 119-132.	0.9	1
3221	Three Co-expression Pattern Types across Microbial Transcriptional Networks of Plankton in Two Oceanic Waters. , 2020, , .		1
3222	Excavating the functionally crucial active-site residues of the DXS protein of Bacillus subtilis by exploring its closest homologues. Journal of Genetic Engineering and Biotechnology, 2020, 18, 76.	3.3	3
3223	Potential Therapeutic Approaches to Alzheimer's Disease By Bioinformatics, Cheminformatics And Predicted Adme-Tox Tools. Current Neuropharmacology, 2020, 18, 696-719.	2.9	10
3224	Waardenburg Syndrome Expression and Penetrance. , 2017, 2, 31-40.		3
3225	Automatic Human-like Mining and Constructing Reliable Genetic Association Database with Deep Reinforcement Learning. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 112-123.	0.7	1
3226	Bioinformatics analysis of various signal peptides for periplasmic expression of parathyroid hormone in. Journal of Medicine and Life, 2019, 12, 184-191.	1.3	0
3227	Systems biology and big data analytics. , 2022, , 425-442.		0

#	ARTICLE	IF	CITATIONS
3228	Transcriptomic profiling of the floral fragrance biosynthesis pathway of <i>Liriodendron</i> and functional characterization of the <i>LtuDXR</i> gene. <i>Plant Science</i> , 2022, 314, 111124.	3.6	6
3229	The male and female gonad transcriptome of the edible sea urchin, <i>Paracentrotus lividus</i> : Identification of sex-related and lipid biosynthesis genes. <i>Aquaculture Reports</i> , 2022, 22, 100936.	1.7	6
3230	In-Silico Tool for Predicting, Scanning, and Designing Defensins. <i>Frontiers in Immunology</i> , 2021, 12, 780610.	4.8	5
3231	A ubiquitous disordered protein interaction module orchestrates transcription elongation. <i>Science</i> , 2021, 374, 1113-1121.	12.6	34
3232	Scalable Enrichment of Immunomodulatory Human Acute Myeloid Leukemia Cell Line-Derived Extracellular Vesicles. <i>Cells</i> , 2021, 10, 3321.	4.1	3
3233	Genomic expansion of <i>Aldh1a1</i> protects beavers against high metabolic aldehydes from lipid oxidation. <i>Cell Reports</i> , 2021, 37, 109965.	6.4	7
3234	Exploring the predictive capability of advanced machine learning in identifying severe disease phenotype in <i>Salmonella enterica</i> . <i>Food Research International</i> , 2022, 151, 110817.	6.2	10
3235	Identification of cerebrospinal fluid biomarkers for parkinsonism using a proteomics approach. <i>Npj Parkinson's Disease</i> , 2021, 7, 107.	5.3	11
3237	The Identification of the Biomarkers of Sheng-Ji Hua-Yu Formula Treated Diabetic Wound Healing Using Modular Pharmacology. <i>Frontiers in Pharmacology</i> , 2021, 12, 726158.	3.5	4
3238	Inhibition of the renin-angiotensin system causes concentric hypertrophy of renal arterioles in mice and humans. <i>JCI Insight</i> , 2021, 6, .	5.0	16
3239	High-resolution epitope mapping and characterization of SARS-CoV-2 antibodies in large cohorts of subjects with COVID-19. <i>Communications Biology</i> , 2021, 4, 1317.	4.4	27
3240	A Standardized Brain Molecular Atlas: A Resource for Systems Modeling and Simulation. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 604559.	2.9	3
3242	Designing of a Multi-epitope Vaccine against the Structural Proteins of Marburg Virus Exploiting the Immunoinformatics Approach. <i>ACS Omega</i> , 2021, 6, 32043-32071.	3.5	43
3243	Transcriptomic responses to drought stress in <i>Polygonatum kingianum</i> tuber. <i>BMC Plant Biology</i> , 2021, 21, 537.	3.6	7
3244	Enantioselectivity of Chiral Derivatives of Xanthenes in Virulence Effects of Resistant Bacteria. <i>Pharmaceuticals</i> , 2021, 14, 1141.	3.8	5
3245	Novel Neurotoxic Activity in <i>Calliophis intestinalis</i> Venom. <i>Neurotoxicity Research</i> , 2022, 40, 173-178.	2.7	3
3246	Potential Mechanism of Dingji Fumai Decoction Against Atrial Fibrillation Based on Network Pharmacology, Molecular Docking, and Experimental Verification Integration Strategy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 712398.	2.4	13
3247	Mechanistically Diverse Pathways for Sulfoquinovose Degradation in Bacteria. <i>ACS Catalysis</i> , 2021, 11, 14740-14750.	11.2	21

#	ARTICLE	IF	CITATIONS
3248	Development of SSR Markers for <i>Psammochloa villosa</i> (Trin.) Bor (Poaceae), a Dominant Species in the Inner Mongolian Plateau. <i>Cytology and Genetics</i> , 2021, 55, 576-582.	0.5	0
3249	The possible mechanism of <i>Hippophae fructus</i> oil applied in tympanic membrane repair identified based on network pharmacology and molecular docking. <i>Journal of Clinical Laboratory Analysis</i> , 2021, , e24157.	2.1	4
3251	The GeneCards Suite. , 2021, , 27-56.		182
3252	Biclique extension as an effective approach to identify missing links in metabolic compoundâ€“protein interaction networks. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	5
3253	Elaborate the Mechanism of Ancient Classic Prescriptions (Erzhi Formula) in Reversing GIOP by Network Pharmacology Coupled with Zebrafish Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-17.	1.2	7
3254	Immobilization of <i>Thermomyces lanuginosus</i> lipase via ionic adsorption on superparamagnetic iron oxide nanoparticles: Facile synthesis and improved catalytic performance. <i>Chemical Engineering Journal</i> , 2022, 431, 134128.	12.7	5
3255	Identification of damaging SNPs and their effects on Alzheimerâ€™s disease-associated PSEN1 protein: Computational analysis. <i>AdÃ±yaman University Journal of Science</i> , 0, , .	0.0	0
3256	Metabolic properties, gene functions, and biosafety analysis reveal the action of three rhizospheric plant growth-promoting bacteria of <i>Jujuncao</i> (<i>Pennisetum giganteum</i>). <i>Environmental Science and Pollution Research</i> , 2022, 29, 38435-38449.	5.3	4
3257	AgroLD: A Knowledge Graph Database for Plant Functional Genomics. <i>Methods in Molecular Biology</i> , 2022, 2443, 527-540.	0.9	2
3258	Comparative Transcriptome Analysis in <i>Taraxacum koksaghyz</i> to Identify Genes that Determine Root Volume and Root Length. <i>Frontiers in Genetics</i> , 2021, 12, 784883.	2.3	1
3259	Barcode fusion genetics-protein-fragment complementation assay (BFG-PCA): tools and resources that expand the potential for binary protein interaction discovery. <i>Nucleic Acids Research</i> , 2022, 50, e54-e54.	14.5	4
3260	The <i>Bacteroidetes</i> <i>Aequorivita</i> sp. and <i>Kaistella jeonii</i> Produce Promiscuous Esterases With PET-Hydrolyzing Activity. <i>Frontiers in Microbiology</i> , 2021, 12, 803896.	3.5	21
3261	PlantGF: an analysis and annotation platform for plant gene families. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
3263	UbE3-APA: a bioinformatic strategy to elucidate ubiquitin E3 ligase activities in quantitative proteomics study. <i>Bioinformatics</i> , 2022, 38, 2211-2218.	4.1	1
3264	Variants in Mitochondrial <sc>ATP</sc> Synthase Cause Variable Neurologic Phenotypes. <i>Annals of Neurology</i> , 2022, 91, 225-237.	5.3	12
3266	Computational prediction of protein functional sitesâ€“Applications in biotechnology and biomedicine. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 39-57.	2.3	2
3267	Regulation of heat shock proteins 70 and their role in plant immunity. <i>Journal of Experimental Botany</i> , 2022, 73, 1894-1909.	4.8	44
3268	Multiomic Metabolic Enrichment Network Analysis Reveals Metaboliteâ€“Protein Physical Interaction Subnetworks Altered in Cancer. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100189.	3.8	4

#	ARTICLE	IF	CITATIONS
3269	Bacterial low-abundant taxa are key determinants of a healthy airway metagenome in the early years of human life. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 175-186.	4.1	16
3270	Prediction of the Mechanisms by Which Quercetin Enhances Cisplatin Action in Cervical Cancer: A Network Pharmacology Study and Experimental Validation. <i>Frontiers in Oncology</i> , 2021, 11, 780387.	2.8	9
3271	Recent Developments in Clinical Plasma Proteomics Applied to Cardiovascular Research. <i>Biomedicines</i> , 2022, 10, 162.	3.2	17
3272	Network Pharmacology- and Molecular Docking-Based Identification of Potential Phytocompounds from <i>Argyrea capitiformis</i> in the Treatment of Inflammation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-22.	1.2	10
3273	A Workflow of Integrated Resources to Catalyze Network Pharmacology Driven COVID-19 Research. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 718-729.	5.4	2
3274	Using metagenomic data to boost protein structure prediction and discovery. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 434-442.	4.1	3
3275	The crystal structure of the varicella-zoster Orf24-Orf27 nuclear egress complex spotlights multiple determinants of herpesvirus subfamily specificity. <i>Journal of Biological Chemistry</i> , 2022, 298, 101625.	3.4	8
3276	Genome-Scale Modeling Specifies the Metabolic Capabilities of <i>Rhizophagus irregularis</i> . <i>MSystems</i> , 2022, 7, e0121621.	3.8	7
3277	The P5-type ATPase ATP13A1 modulates major histocompatibility complex I-related protein 1 (MR1)-mediated antigen presentation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101542.	3.4	7
3278	Kinetic and Stoichiometric Modeling-Based Analysis of Docosahexaenoic Acid (DHA) Production Potential by <i>Cryptocodium cohnii</i> from Glycerol, Glucose and Ethanol. <i>Marine Drugs</i> , 2022, 20, 115.	4.6	6
3279	DisintegrinDB: The first integrated database resource of disintegrins from snake venoms. <i>Biochemical and Biophysical Research Communications</i> , 2022, 597, 77-82.	2.1	0
3280	A common TMPRSS2 variant has a protective effect against severe COVID-19. <i>Current Research in Translational Medicine</i> , 2022, 70, 103333.	1.8	30
3281	Disrupted Circadian Rest-Activity Cycles in Inflammatory Bowel Disease Are Associated With Aggressive Disease Phenotype, Subclinical Inflammation, and Dysbiosis. <i>Frontiers in Medicine</i> , 2021, 8, 770491.	2.6	7
3282	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer. <i>JCO Clinical Cancer Informatics</i> , 2022, 6, e2100144.	2.1	4
3283	Tousled-like kinase 2 targets ASF1 histone chaperones through client mimicry. <i>Nature Communications</i> , 2022, 13, 749.	12.8	9
3284	Lung cancer prediction using multi-gene genetic programming by selecting automatic features from amino acid sequences. <i>Computational Biology and Chemistry</i> , 2022, 98, 107638.	2.3	6
3286	Identification and Validation of Ikaros (IKZF1) as a Cancer Driver Gene for Marek's Disease Virus-Induced Lymphomas. <i>Microorganisms</i> , 2022, 10, 401.	3.6	4
3287	Prediction of the Active Components and Possible Targets of <i>Xanthii Fructus</i> Based on Network Pharmacology for Use in Chronic Rhinosinusitis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-15.	1.2	4

#	ARTICLE	IF	CITATIONS
3288	Predicting lncRNA-Protein Interactions by Heterogeneous Network Embedding. <i>Frontiers in Genetics</i> , 2021, 12, 814073.	2.3	5
3289	Evolution of the albumin protein family in reptiles. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107435.	2.7	1
3290	Simultaneously Identifying and Distinguishing Glycoproteins with O-GlcNAc and O-GalNAc (the Tn) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	8.5	10
3291	Interaction between Rag genes results in a unique synergistic transcriptional response that enhances soybean resistance to soybean aphids. <i>BMC Genomics</i> , 2021, 22, 887.	2.8	1
3292	From Drug Molecules to Thermoset Shape Memory Polymers: A Machine Learning Approach. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 60508-60521.	8.0	15
3293	Spike Protein and the Various Cell-Surface Carbohydrates: An Interaction Study. <i>ACS Chemical Biology</i> , 2022, 17, 103-117.	3.4	3
3294	Guided assembly of cellular network models from knowledge in literature. , 2021, 2021, 4458-4464.		1
3295	Insights into the evolution of extracellular leucine-rich repeats in metazoans with special reference to Toll-like receptor 4. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	1
3296	Phosphorylation mapping of Laminin Î²1-chain: Kinases in association with active sites. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	0
3297	Mining histone methyltransferases and demethylases from whole genome sequence. <i>Journal of Biosciences</i> , 2020, 45, .	1.1	1
3298	Study on Mechanism of <i>Caulis spatholobi</i> on Knee Osteoarthritis Based on Network Pharmacology. <i>Pharmacy Information</i> , 2022, 11, 66-76.	0.0	0
3299	Diseases 2.0: a weekly updated database of disease-gene associations from text mining and data integration. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	30
3300	Deciphering the structure of Arabidopsis thaliana 5-enol-pyruvyl-shikimate-3-phosphate synthase: An essential step toward the discovery of novel inhibitors to supersede glyphosate. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1494-1505.	4.1	2
3301	Whole-Exome Sequencing Reveals a Missense Variant c.1612C>T (p.Arg538Cys) in the BTG Gene Leading to Neuromyelitis Optica Spectrum Disorder in Saudi Families. <i>Frontiers in Pediatrics</i> , 2021, 9, 829251.	1.9	4
3302	Development, validation, and utility of species-specific diagnostic markers for detection of <i>Peronospora belbahrii</i>. <i>Phytopathology</i> , 2022, , .	2.2	1
3303	Functional Classification and Characterization of the Fungal Glycoside Hydrolase 28 Protein Family. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 217.	3.5	6
3304	Post-translational modification: a strategic response to high temperature in plants. <i>ABIOTECH</i> , 2022, 3, 49-64.	3.9	15
3305	Using deep learning to annotate the protein universe. <i>Nature Biotechnology</i> , 2022, 40, 932-937.	17.5	133

#	ARTICLE	IF	CITATIONS
3306	Phylogenetic inference of changes in amino acid propensities with single-position resolution. PLoS Computational Biology, 2022, 18, e1009878.	3.2	0
3307	Cultivating Lentinula edodes on Substrate Containing Composted Sawdust Affects the Expression of Carbohydrate and Aromatic Amino Acid Metabolism-Related Genes. MSystems, 2022, 7, e0082721.	3.8	5
3310	Structure of a cereal purple acid phytase provides new insights to phytate degradation in plants. Plant Communications, 2022, 3, 100305.	7.7	5
3311	Mass spectrometry, data re-analysis, and homology modelling predict posttranslational modifications of leucine-rich alpha-2-glycoprotein as a marker of myelodysplastic syndrome. Cancer Biomarkers, 2022, , 1-8.	1.7	0
3312	Intrinsic disorder in proteins associated with oxidative stress-induced JNK signaling. Cellular and Molecular Life Sciences, 2022, 79, 202.	5.4	9
3313	Next-Generation Molecular Discovery: From Bottom-Up In Vivo and In Vitro Approaches to In Silico Top-Down Approaches for Therapeutics Neogenesis. Life, 2022, 12, 363.	2.4	1
3314	Pangenome Analysis of the Soilborne Fungal Phytopathogen Rhizoctonia solani and Development of a Comprehensive Web Resource: RsolaniDB. Frontiers in Microbiology, 2022, 13, 839524.	3.5	14
3315	High Resistance to Quinlorac in Multiple-Resistant Echinochloa colona Associated with Elevated Stress Tolerance Gene Expression and Enriched Xenobiotic Detoxification Pathway. Genes, 2022, 13, 515.	2.4	9
3317	Systematic analysis and molecular profiling of EGFR allosteric inhibitor cross-reactivity across the proto-oncogenic ErbB family kinases by integrating dynamics simulation, energetics calculation and biochemical assay. European Biophysics Journal, 2022, , 1.	2.2	0
3318	Phage-encoded ribosomal protein S21 expression is linked to late-stage phage replication. ISME Communications, 2022, 2, .	4.2	10
3319	Celsr family genes are dynamically expressed in embryonic and juvenile zebrafish. Developmental Neurobiology, 2022, 82, 192-213.	3.0	3
3320	Exploring Active Compounds and Mechanisms of Angong Niu Huang Wan on Ischemic Stroke Based on Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-13.	1.2	2
3322	Noncanonical Function of AGO2 Augments T-cell Receptor Signaling in T-cell Prolymphocytic Leukemia. Cancer Research, 2022, 82, 1818-1831.	0.9	9
3323	Compoundâ€“protein interaction prediction by deep learning: Databases, descriptors and models. Drug Discovery Today, 2022, 27, 1350-1366.	6.4	23
3324	Molecular Modeling is an Enabling Approach to Complement and Enhance Channelopathy Research. , 2022, 12, 3141-3166.		0
3325	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. Communications Biology, 2022, 5, 247.	4.4	3
3326	The Function, Structure, and Origins of the ER Membrane Protein Complex. Annual Review of Biochemistry, 2022, 91, 651-678.	11.1	27
3327	Draft genomes assembly and annotation of Carex parvula and Carex kokanica reveals stress-specific genes. Scientific Reports, 2022, 12, 4970.	3.3	7

#	ARTICLE	IF	CITATIONS
3328	Deciphering Genomes: Genetic Signatures of Plant-Associated Micromonospora. <i>Frontiers in Plant Science</i> , 2022, 13, 872356.	3.6	3
3329	Transcriptomic Analysis of Liver Indicates Novel Vaccine to Porcine Reproductive and Respiratory Virus Promotes Homeostasis in T-Cell and Inflammatory Immune Responses Compared to a Commercial Vaccine in Pigs. <i>Frontiers in Veterinary Science</i> , 2022, 9, 791034.	2.2	0
3330	Cupuassu (<i>Theobroma grandiflorum</i> [Willd. ex Sprengel] Schumann) Fruit Development: Key Genes Involved in Primary Metabolism and Stress Response. <i>Agronomy</i> , 2022, 12, 763.	3.0	1
3331	Intrinsically disordered signaling proteins: Essential hub players in the control of stress responses in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2022, 17, e0265422.	2.5	3
3333	Protein design via deep learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	33
3335	Heterotrimeric G Protein β -Subunits - Structures, Peptide-Derived Inhibitors, and Mechanisms. <i>Current Medicinal Chemistry</i> , 2022, 29, 6359-6378.	2.4	7
3336	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
3337	Transcriptome analysis of Pacific white shrimp (<i>Litopenaeus vannamei</i>) hepatopancreas challenged by <i>Vibrio alginolyticus</i> reveals lipid metabolic disturbance. <i>Fish and Shellfish Immunology</i> , 2022, 123, 238-247.	3.6	21
3338	UPIMAPI, reCOGnizer and KEGGCharter: Bioinformatics tools for functional annotation and visualization of (meta)-omics datasets. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1798-1810.	4.1	14
3339	Maternal Sodium β -Perfluorooctanesulfonate Exposure Disturbed Lipid Metabolism and Induced an Imbalance in Tyrosine Metabolism in the F1 Generation of Mice. <i>Chemical Research in Toxicology</i> , 2022, 35, 651-662.	3.3	9
3340	Novel ZNF414 activity characterized by integrative analysis of ChIP-exo, ATAC-seq and RNA-seq data. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194811.	1.9	1
3341	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications. <i>PeerJ</i> , 2022, 10, e13061.	2.0	6
3342	Spatial proteomics reveals subcellular reorganization in human keratinocytes exposed to UVA light. <i>IScience</i> , 2022, 25, 104093.	4.1	4
3343	Encapsulating Cas9 into extracellular vesicles by protein myristoylation. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12196.	12.2	22
3344	Subtractive proteomics assisted therapeutic targets mining and designing ensemble vaccine against <i>Candida auris</i> for immune response induction. <i>Computers in Biology and Medicine</i> , 2022, 145, 105462.	7.0	10
3345	RdsA Is a Global Regulator That Controls Cell Shape and Division in <i>Rhizobium etli</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 858440.	3.5	0
3346	Pregnane-based steroids are novel positive NMDA receptor modulators that may compensate for the effect of loss of α -function disease-associated α GRIN mutations. <i>British Journal of Pharmacology</i> , 2022, 179, 3970-3990.	5.4	6
3347	A network pharmacology technique used to investigate the potential mechanism of Ligustilide's effect on atherosclerosis. <i>Journal of Food Biochemistry</i> , 2022, 46, e14146.	2.9	2

#	ARTICLE	IF	CITATIONS
3348	Proteome dataset of sea bass (<i>Dicentrarchus labrax</i>) skin-scales exposed to fluoxetine and estradiol. Data in Brief, 2022, 41, 107971.	1.0	0
3349	Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae. Molecular Ecology, 2022, 31, 2898-2919.	3.9	8
3350	Protecting effect of emodin in experimental autoimmune encephalomyelitis mice by inhibiting microglia activation and inflammation via Myd88/PI3K/Akt/NF- κ B signalling pathway. Bioengineered, 2022, 13, 9322-9344.	3.2	16
3351	Features, modulation and analysis of glycosylation patterns of therapeutic recombinant immunoglobulin A. Biotechnology and Genetic Engineering Reviews, 2022, 38, 247-269.	6.2	4
3352	Genomic evolution of the Coronaviridae family. Virology, 2022, 570, 123-133.	2.4	13
3353	Statistical and machine learning methods to study human CD4+ T cell proteome profiles. Immunology Letters, 2022, 245, 8-17.	2.5	3
3354	Proteome based mapping and reverse vaccinology techniques to contrive multi-epitope based subunit vaccine (MEBSV) against <i>Streptococcus pyogenes</i> . Infection, Genetics and Evolution, 2022, 100, 105259.	2.3	7
3355	An extensive computational study to identify potential inhibitors of Acyl-homoserine-lactone synthase from <i>Acinetobacter baumannii</i> (strain AYE). Journal of Molecular Graphics and Modelling, 2022, 114, 108168.	2.4	8
3356	Network Pharmacology Study on Molecular Mechanisms of Zhishi Xiebai Guizhi Decoction in the Treatment of Coronary Heart Disease. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-10.	1.2	5
3357	Redirected Stress Responses in a Genome-Minimized <i>Bacillus</i> ™ Strain with Enhanced Capacity for Protein Secretion. MSystems, 2021, 6, e0065521.	3.8	5
3359	Systematic profiling and identification of the peptide-mediated interactions between human Yes-associated protein and its partners in esophageal cancer. Journal of Molecular Recognition, 2022, 35, e2947.	2.1	2
3360	Long-term <i>in vivo</i> survival of 3D-bioprinted human lipoaspirate-derived adipose tissue: proteomic signature and cellular content. Adipocyte, 2022, 11, 34-46.	2.8	8
3361	In-silico analysis reveals druggable single nucleotide polymorphisms in angiotensin 1 converting enzyme involved in the onset of blood pressure. BMC Research Notes, 2021, 14, 457.	1.4	2
3362	Purification, Characterization, and Structural Studies of a Sulfatase from <i>Pedobacter yulinensis</i> . Molecules, 2022, 27, 87.	3.8	1
3364	Systems biology and machine learning approaches identify drug targets in diabetic nephropathy. Scientific Reports, 2021, 11, 23452.	3.3	6
3365	Computational modeling of human-nCoV protein-protein interaction network. Methods, 2022, 203, 488-497.	3.8	5
3366	Storage protein composition during germination and its association with physiological seed quality in common bean. Acta Scientiarum - Agronomy, 0, 44, e53434.	0.6	3
3367	In silico investigation of the interactions of certain drugs proposed for the treatment of Covid-19 with the paraoxonase-1. Journal of Biomolecular Structure and Dynamics, 2021, , 1-13.	3.5	0

#	ARTICLE	IF	CITATIONS
3368	Common Features in lncRNA Annotation and Classification: A Survey. <i>Non-coding RNA</i> , 2021, 7, 77.	2.6	13
3369	FAIRifying the exposome journal: Templates for chemical structures and transformations. <i>Exposome</i> , 2022, 2, .	2.8	10
3370	Multi-omic Approaches to Identify Genetic Factors in Metabolic Syndrome. , 2021, 12, 3045-3084.		4
3372	A Conserved Allosteric Site on Drug-Metabolizing CYPs: A Systematic Computational Assessment. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13215.	4.1	9
3373	DeepLoc 2.0: multi-label subcellular localization prediction using protein language models. <i>Nucleic Acids Research</i> , 2022, 50, W228-W234.	14.5	180
3374	Computational structural assessment of BRCA1 susceptibility protein (BRCA1) and BRCA1-Associated Ring Domain protein 1 (BARD1) mutations on the protein-protein interface. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 375-397.	2.3	4
3375	Comprehensive analysis of miRNA-mRNA interactions in ovaries of aged mice. <i>Animal Science Journal</i> , 2022, 93, e13721.	1.4	3
3376	Promises of eukaryotic ribonucleases for cancer treatment: a systematic review. <i>Translational Medicine Communications</i> , 2022, 7, .	1.4	1
3377	A functional corona around extracellular vesicles enhances angiogenesis, skin regeneration and immunomodulation. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12207.	12.2	70
3378	Whole genome sequencing of spotted stem borer, <i>Chilo partellus</i> , reveals multiple genes encoding enzymes for detoxification of insecticides. <i>Functional and Integrative Genomics</i> , 2022, , 1.	3.5	0
3380	Response of the Anaerobic Methanotrophic Archaeon <i>Candidatus Methanoperedens nitroreducens</i> to the Long-Term Ferrihydrite Amendment. <i>Frontiers in Microbiology</i> , 2022, 13, 799859.	3.5	5
3382	A Network Pharmacology Approach for Uncovering the Antitumor Effects and Potential Mechanisms of the Sijunzi Decoction for the Treatment of Gastric Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	1.2	7
3383	An E3 Ubiquitin Ligase Scaffolding Protein Is Proviral during Chikungunya Virus Infection in <i>Aedes aegypti</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0059522.	3.0	6
3385	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	27.8	239
3386	Exploring synergies between plant metabolic modelling and machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1885-1900.	4.1	7
3387	Impaired phosphate transport in SLC34A2 variants in patients with pulmonary alveolar microlithiasis. <i>Human Genomics</i> , 2022, 16, 13.	2.9	3
3729	Bioinformatics analysis of various signal peptides for periplasmic expression of parathyroid hormone in <i>E.coli</i> . <i>Journal of Medicine and Life</i> , 2019, 12, 184-191.	1.3	2
3731	Homozygotes NAT2*5B slow acetylators are highly associated with hepatotoxicity induced by anti-tuberculosis drugs. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2022, 117, e210328.	1.6	0

#	ARTICLE	IF	CITATIONS
3732	Proteomics as a tool to understand the biology of agricultural crops. , 2022, , 107-122.		0
3733	Low Complexity Regions in Mammalian Proteins are Associated with Low Protein Abundance and High Transcript Abundance. Molecular Biology and Evolution, 2022, 39, .	8.9	5
3734	Wuzi Yanzong pill attenuates MPTP-induced Parkinsonâ€™s Disease via PI3K/Akt signaling pathway. Metabolic Brain Disease, 2022, 37, 1435-1450.	2.9	7
3735	Integrated Network Pharmacology and Comprehensive Bioinformatics Identifying the Mechanisms and Molecular Targets of Yizhiqingxin Formula for Treatment of Comorbidity With Alzheimerâ€™s Disease and Depression. Frontiers in Pharmacology, 2022, 13, 853375.	3.5	7
3736	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis. Frontiers in Genetics, 2022, 13, 855739.	2.3	0
3737	Rate-limiting transport of positively charged arginine residues through the Sec-machinery is integral to the mechanism of protein secretion. ELife, 2022, 11, .	6.0	13
3738	ImitateDB: A database for domain and motif mimicry incorporating host and pathogen protein interactions. Amino Acids, 2022, 54, 923-934.	2.7	9
3739	Membranome 3.0: Database of singleâ€pass membrane proteins with <scp>AlphaFold</scp> models. Protein Science, 2022, 31, e4318.	7.6	20
3741	Kinome-wide polypharmacology profiling of small molecules by multi-task graph isomorphism network approach. Acta Pharmaceutica Sinica B, 2023, 13, 54-67.	12.0	9
3742	In silico study predicts a key role of <scp>RNA</scp>â€™binding domains 3 and 4 in <scp>nucleolinâ€™miRNA</scp> interactions. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1837-1850.	2.6	1
3743	Subtilisin of Leishmania amazonensis as Potential Druggable Target: Subcellular Localization, In Vitro Leishmanicidal Activity and Molecular Docking of PF-429242, a Subtilisin Inhibitor. Current Issues in Molecular Biology, 2022, 44, 2089-2106.	2.4	2
3744	ProtPathDB: A Web-based Resource of Parasite Proteases. Current Bioinformatics, 2022, 17, 710-722.	1.5	0
3745	Spatially resolved cell tagging and surfaceome labeling via targeted photocatalytic decaging. Chem, 2022, 8, 2179-2191.	11.7	19
3746	Functional annotation of creeping bentgrass protein sequences based on convolutional neural network. BMC Plant Biology, 2022, 22, 227.	3.6	0
3747	Network Pharmacology Approach for Medicinal Plants: Review and Assessment. Pharmaceuticals, 2022, 15, 572.	3.8	99
3748	Predicting protein intrinsically disordered regions by applying natural language processing practices. Soft Computing, 0, , 1.	3.6	0
3749	Evidence of multiple genome duplication events in Mytilus evolution. BMC Genomics, 2022, 23, 340.	2.8	12
3750	BDDE-Inspired Chalcone Derivatives to Fight Bacterial and Fungal Infections. Marine Drugs, 2022, 20, 315.	4.6	6

3752	Bioinformatic Analysis of the Perilymph Proteome to Generate a Human Protein Atlas. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 847157.	3.7	2
3753	Structural Mapping of BMP Conformational Epitopes and Bioengineering Design of Osteogenic Peptides to Specifically Target the Epitope-Binding Sites. <i>Cellular and Molecular Bioengineering</i> , 2022, 15, 341-352.	2.1	3
3754	Molecular dynamic assisted investigation on impact of mutations in deazaflavin dependent nitroreductase against pretomanid: a computational study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 4421-4443.	3.5	1
3755	Network pharmacology and bioinformatics analysis identified essential genes of Jingulian in the treatment of rheumatoid arthritis and COVID-19. <i>Annals of Translational Medicine</i> , 2022, 10, 635-635.	1.7	2
3756	<scp>HMSâ€Šâ€Š</scp>: A tool for the identification of Sulphur metabolismâ€related genes and analysis of operon structures in genome and metagenome assemblies. <i>Molecular Ecology Resources</i> , 2022, 22, 2758-2774.	4.8	8
3757	Sensitive Plant N-Terminome Profiling with HUNTER. <i>Methods in Molecular Biology</i> , 2022, 2447, 139-158.	0.9	2
3758	Profiling Sequence Specificity of Proteolytic Activities Using Proteome-Derived Peptide Libraries. <i>Methods in Molecular Biology</i> , 2022, 2447, 159-174.	0.9	0
3759	A User Guide to Validation, Annotation, and Evaluation of N-Terminome Datasets with MANTI. <i>Methods in Molecular Biology</i> , 2022, 2447, 271-283.	0.9	1
3760	Visual barcodes for clonal-multiplexing of live microscopy-based assays. <i>Nature Communications</i> , 2022, 13, 2725.	12.8	7
3761	Predicting epitopes for vaccine development using bioinformatics tools. , 2022, 10, 251513552211002.	2.3	6
3763	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle <i>Peltogaster reticulata</i> (Crustacea: Rhizocephala). <i>F1000Research</i> , 0, 11, 583.	1.6	4
3764	Pontocerebellar Hypoplasia Type 9: A New Case with a Novel Mutation and Review of Literature. <i>Journal of Pediatric Genetics</i> , 0, , .	0.7	0
3765	Protein language-model embeddings for fast, accurate, and alignment-free protein structure prediction. <i>Structure</i> , 2022, 30, 1169-1177.e4.	3.3	52
3766	Improving recombinant protein production by yeast through genome-scale modeling using proteome constraints. <i>Nature Communications</i> , 2022, 13, .	12.8	18
3767	BIAPSS: A Comprehensive Physicochemical Analyzer of Proteins Undergoing Liquidâ€Liquid Phase Separation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6204.	4.1	9
3769	Representation of polysaccharide molecules by SNFG and 3D-SNFG methodsâ€”Take <i>Potentilla anserina</i> L polysaccharide molecule as an example. <i>Biochemical and Biophysical Research Communications</i> , 2022, 617, 7-10.	2.1	1
3770	Cancerâ€related somatic mutations alter adenosine A₁ receptor pharmacologyâ€A focus on mutations in the loops and Câ€™terminus. <i>FASEB Journal</i> , 2022, 36, .	0.5	3

#	ARTICLE	IF	CITATIONS
3771	Next-Generation Sequencing Reveals Novel Homozygous Missense Variant c.934T > C in POLR1C Gene Causing Leukodystrophy and Hypomyelinating Disease. <i>Frontiers in Pediatrics</i> , 2022, 10, .	1.9	1
3772	A Molecular Docking Study of Human STEAP2 for the Discovery of New Potential Anti-Prostate Cancer Chemotherapeutic Candidates. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	0
3773	In silico analyses of acetylcholinesterase (AChE) and its genetic variants in interaction with the anti-Alzheimer drug Rivastigmine. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 1259-1277.	2.6	5
3774	InflamNat: web-based database and predictor of anti-inflammatory natural products. <i>Journal of Cheminformatics</i> , 2022, 14, .	6.1	4
3775	Universal protein misfolding intermediates can bypass the proteostasis network and remain soluble and less functional. <i>Nature Communications</i> , 2022, 13, .	12.8	24
3776	Artificial neural networks enable genome-scale simulations of intracellular signaling. <i>Nature Communications</i> , 2022, 13, .	12.8	17
3778	Drug repositioning for cancer in the era of AI, big omics, and real-world data. <i>Critical Reviews in Oncology/Hematology</i> , 2022, 175, 103730.	4.4	10
3780	Applications of omics in life detection beyond Earth. , 2022, , 193-219.		0
3783	Machine learning and comparative genomics approaches for the discovery of xylose transporters in yeast. , 2022, 15, .		4
3785	Cancer-Related Somatic Mutations in Transmembrane Helices Alter Adenosine A1 Receptor Pharmacology. <i>Molecules</i> , 2022, 27, 3742.	3.8	1
3787	Study the Mechanism of Gualou Niubang Decoction in Treating Plasma Cell Mastitis Based on Network Pharmacology and Molecular Docking. <i>BioMed Research International</i> , 2022, 2022, 1-21.	1.9	6
3788	iKcr_CNN: A novel computational tool for imbalance classification of human nonhistone crotonylation sites based on convolutional neural networks with focal loss. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3268-3279.	4.1	5
3789	The 3D mutational constraint on amino acid sites in the human proteome. <i>Nature Communications</i> , 2022, 13, .	12.8	15
3790	Omicron (BA.1) and subvariants (BA.1.1, BA.2, and BA.3) of SARS-CoV-2 spike infectivity and pathogenicity: A comparative sequence and structural-based computational assessment. <i>Journal of Medical Virology</i> , 2022, 94, 4780-4791.	5.0	133
3791	Development of Multi-epitope Based Subunit Vaccine Against Crimean-Congo Hemorrhagic Fever Virus Using Reverse Vaccinology Approach. <i>International Journal of Peptide Research and Therapeutics</i> , 2022, 28, .	1.9	2
3792	Ribosome profiling reveals multiple roles of SecA in cotranslational protein export. <i>Nature Communications</i> , 2022, 13, .	12.8	9
3793	Network Pharmacology-Based Strategy to Investigate the Pharmacologic Mechanisms of Coptidis Rhizoma for the Treatment of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	3.4	16
3794	Carbohydrate Structure Database and Other Glycan Databases as an Important Element of Glycoinformatics. <i>Russian Journal of Bioorganic Chemistry</i> , 2022, 48, 457-466.	1.0	1

#	ARTICLE	IF	CITATIONS
3795	Investigation on the potential targets of Astragaloside IV against intracerebral hemorrhage based on network pharmacology and experimental validation. <i>Bioorganic Chemistry</i> , 2022, 127, 105975.	4.1	6
3796	An accurate prediction model of digenic interaction for estimating pathogenic gene pairs of human diseases. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3639-3652.	4.1	4
3797	Pharmacological analysis of Empagliflozin: Acting through the CaMKII pathway in type 2 diabetes and acute cardiovascular events. <i>PLoS ONE</i> , 2022, 17, e0270152.	2.5	1
3798	Anti-hepatic carcinoma mechanisms of calycosin through targeting of ferroptosis. <i>Intelligent Medicine</i> , 2022, , .	3.1	0
3799	Deep learning-based kcat prediction enables improved enzyme-constrained model reconstruction. <i>Nature Catalysis</i> , 2022, 5, 662-672.	34.4	98
3800	The Landscape of Virus-Host Protein-Protein Interaction Databases. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
3801	Mechanisms of Action of Semen Ziziphi spinosae in the Treatment of Tourette Syndrome. <i>Degenerative Neurological and Neuromuscular Disease</i> , 0, Volume 12, 85-96.	1.3	0
3802	Artificial intelligence and machine-learning approaches in structure and ligand-based discovery of drugs affecting central nervous system. <i>Molecular Diversity</i> , 2023, 27, 959-985.	3.9	11
3803	Exaggerated trans-membrane charge of ammonium transporters in nutrient-poor marine environments. <i>Open Biology</i> , 2022, 12, .	3.6	1
3805	Arginine methylation of MTHFD1 by PRMT5 enhances anoikis resistance and cancer metastasis. <i>Oncogene</i> , 2022, 41, 3912-3924.	5.9	14
3806	LGCA-VHPPI: A local-global residue context aware viral-host protein-protein interaction predictor. <i>PLoS ONE</i> , 2022, 17, e0270275.	2.5	5
3807	Deciphering the pharmacological mechanisms of <i>Chaenomeles Fructus</i> against rheumatoid arthritis by integrating network pharmacology and experimental validation. <i>Food Science and Nutrition</i> , 2022, 10, 3380-3394.	3.4	2
3808	Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing. <i>Nature Methods</i> , 2022, 19, 823-826.	19.0	152
3809	Role of <i>Staphylococcus agnetis</i> and <i>Staphylococcus hyicus</i> in the Pathogenesis of Buffalo Fly Skin Lesions in Cattle. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
3811	In Silico Identification of lncRNAs Regulating Sperm Motility in the Turkey (<i>Meleagris gallopavo</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7642.	4.1	2
3813	Profiling 26,000 <i>Aplysia californica</i> neurons by single cell mass spectrometry reveals neuronal populations with distinct neuropeptide profiles. <i>Journal of Biological Chemistry</i> , 2022, 298, 102254.	3.4	12
3814	Panzootic chytrid fungus exploits diverse amphibian host environments through plastic infection strategies. <i>Molecular Ecology</i> , 2022, 31, 4558-4570.	3.9	6
3815	System-wide analyses reveal essential roles of N-terminal protein modification in bacterial membrane integrity. <i>IScience</i> , 2022, 25, 104756.	4.1	3

#	ARTICLE	IF	CITATIONS
3816	Identification and dipeptidyl peptidase IV (DPP-IV) inhibitory activity verification of peptides from mouse lymphocytes. Food Science and Human Wellness, 2022, 11, 1515-1526.	4.9	0
3817	Transcriptome Analysis and HPLC Profiling of Flavonoid Biosynthesis in Citrus aurantium L. during Its Key Developmental Stages. Biology, 2022, 11, 1078.	2.8	1
3818	Effects of 6-Hydroxykaempferol: A Potential Natural Product for Amelioration of Tendon Impairment. Frontiers in Pharmacology, 0, 13, .	3.5	1
3819	Proteomic Analysis of Methanococcus voltae Grown in the Presence of Mineral and Nonmineral Sources of Iron and Sulfur. Microbiology Spectrum, 2022, 10, .	3.0	1
3820	Reduction of multiple reaction monitoring protein target list using correlation analysis. Journal of Dairy Science, 2022, 105, 7216-7229.	3.4	1
3822	Comparative physiological and transcriptome analysis reveals the potential mechanism of selenium accumulation and tolerance to selenate toxicity of <i>Broussonetia papyrifera</i> . Tree Physiology, 2022, 42, 2578-2595.	3.1	2
3824	Principles and correction of 5â€™-splice site selection. RNA Biology, 2022, 19, 943-960.	3.1	9
3825	The genome of the mustard hill coral, <i>Porites astreoides</i> . GigaByte, 0, 2022, 1-12.	0.0	4
3826	Investigating anticancer potency of in vitro propagated endemic <i>Thymus cilicicus</i> Boiss. & Bal. extract on human lung, breast, and prostate cancer cell lines. , 2022, 77, 3229-3239.		1
3827	Mechanism of Danhong Injection in the Treatment of Arrhythmia Based on Network Pharmacology, Molecular Docking, and In Vitro Experiments. BioMed Research International, 2022, 2022, 1-14.	1.9	3
3828	DES-Amyloidoses ðœ Amyloidoses through the looking-glassâ€ A knowledgebase developed for exploring and linking information related to human amyloid-related diseases. PLoS ONE, 2022, 17, e0271737.	2.5	0
3829	Follistatin-like 1 and its paralogs in heart development and cardiovascular disease. Heart Failure Reviews, 2022, 27, 2251-2265.	3.9	6
3830	First study on the effect of transforming growth factor beta 1 and insulin-like growth factor 1 on the chondrogenesis of elephant articular chondrocytes in a scaffold-based 3D culture model. Veterinary World, 0, , 1869-1879.	1.7	0
3831	Pharmacological activation of the C5a receptor leads to stimulation of the Î²2-adrenergic receptor and alleviates cognitive impairment in a murine model of familial Alzheimerâ€™s disease. Frontiers in Immunology, 0, 13, .	4.8	2
3832	Effects of in ovo injection of nicotinamide riboside on high-yield broiler myogenesis. Journal of Animal Science, 2022, 100, .	0.5	1
3833	Subgroup-Enriched Pathways and Kinase Signatures in Medulloblastoma Patient-Derived Xenografts. Journal of Proteome Research, 2022, 21, 2124-2136.	3.7	3
3834	The gill transcriptome of threatened European freshwater mussels. Scientific Data, 2022, 9, .	5.3	10
3835	Calpains in cyanobacteria and the origin of calpains. Scientific Reports, 2022, 12, .	3.3	0

#	ARTICLE	IF	CITATIONS
3836	Eukaryotic initiation factor 5A2 mediates hypoxia-induced autophagy and cisplatin resistance. <i>Cell Death and Disease</i> , 2022, 13, .	6.3	8
3838	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. <i>Microbiome</i> , 2022, 10, .	11.1	12
3839	<i>Escherichia coli</i> YigI is a Conserved Gammaproteobacterial Acyl-CoA Thioesterase Permitting Metabolism of Unusual Fatty Acid Substrates. <i>Journal of Bacteriology</i> , 2022, 204, .	2.2	2
3840	Computational design of a broad-spectrum multi-epitope vaccine candidate against seven strains of human coronaviruses. <i>3 Biotech</i> , 2022, 12, .	2.2	0
3841	Multilayered Networks of SalmoNet2 Enable Strain Comparisons of the Salmonella Genus on a Molecular Level. <i>MSystems</i> , 2022, 7, .	3.8	2
3842	Morphine and high-fat diet differentially alter the gut microbiota composition and metabolic function in lean versus obese mice. <i>ISME Communications</i> , 2022, 2, .	4.2	4
3843	Modular, cascade-like transcriptional program of regeneration in <i>Stentor</i> . <i>ELife</i> , 0, 11, .	6.0	9
3844	On solving an isotope dilution model for the partition of phenylalanine and tyrosine uptake by the liver of lactating dairy cows. <i>Journal of Agricultural Science</i> , 0, , 1-11.	1.3	0
3845	Improved Protein Real-Valued Distance Prediction Using Deep Residual Dense Network (DRDN). <i>Protein Journal</i> , 2022, 41, 468-476.	1.6	1
3846	Microglia contribute to the postnatal development of cortical somatostatin-positive inhibitory cells and to whisker-evoked cortical activity. <i>Cell Reports</i> , 2022, 40, 111209.	6.4	8
3847	Novel pyrazolo[3,4-d]pyrimidines as dual Src/Bcr-Abl kinase inhibitors: Synthesis and biological evaluation for chronic myeloid leukemia treatment. <i>Bioorganic Chemistry</i> , 2022, 128, 106071.	4.1	5
3848	Computational study of the conformational ensemble of CX3C chemokine receptor 1 (CX3CR1) and its interactions with antagonist and agonist ligands. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 117, 108278.	2.4	1
3849	Exploration of the core protein network under endometriosis symptomatology using a computational approach. <i>Frontiers in Endocrinology</i> , 0, 13, .	3.5	1
3852	A meta-summary and bioinformatic analysis identified interleukin 6 as a master regulator of COVID-19 severity biomarkers. <i>Cytokine</i> , 2022, 159, 156011.	3.2	10
3853	Protocol for gene annotation, prediction, and validation of genomic gene expansion. <i>STAR Protocols</i> , 2022, 3, 101692.	1.2	0
3854	A knowledge graph representation learning approach to predict novel kinase–substrate interactions. <i>Molecular Omics</i> , 2022, 18, 853-864.	2.8	3
3855	Strengthening Auto-Feature Engineering of Deep Learning Architecture in Protein–Protein Interaction Prediction. <i>Lecture Notes in Networks and Systems</i> , 2022, , 1205-1216.	0.7	1
3856	Prediction and validation of host-pathogen interactions by a versatile inference approach using <i>Aspergillus fumigatus</i> as a case study. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4225-4237.	4.1	1

#	ARTICLE	IF	CITATIONS
3857	Mechanism of Key Ingredient of Astragalus membranaceus on Lung Adenocarcinoma via PI3K/AKT Signaling Clarified by Utilizing Network Pharmacology Approach and Experimental Validation. Chinese Journal of Integrative Medicine, 0, , .	1.6	0
3859	Absolute and relative quantitation of amylase/trypsin-inhibitors by LC-MS/MS from wheat lines obtained by CRISPR-Cas9 and RNAi. Frontiers in Plant Science, 0, 13, .	3.6	2
3860	Expression and prognosis analysis of PAQR5 in kidney cancer. Frontiers in Oncology, 0, 12, .	2.8	2
3861	Nitrogen deposition experiment mimicked with NH ₄ NO ₃ overestimates the effect on soil microbial community composition and functional potential in the Eurasian steppe. Environmental Microbiomes, 2022, 17, .	5.0	0
3862	Strain-specific impacts of probiotics are a significant driver of gut microbiome development in very preterm infants. Nature Microbiology, 2022, 7, 1525-1535.	13.3	48
3863	The Molecular Network behind Volatile Aroma Formation in Pear (Pyrus spp. Panguxiang) Revealed by Transcriptome Profiling via Fatty Acid Metabolic Pathways. Life, 2022, 12, 1494.	2.4	1
3864	Mismatches in Gene Deletions and Kidney-related Proteins as Candidates for Histocompatibility Factors in Kidney Transplantation. Kidney International Reports, 2022, 7, 2484-2494.	0.8	2
3865	Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. Current Biology, 2022, 32, 4607-4619.e7.	3.9	10
3867	Pain Interference in End Stage Kidney Disease is Associated with Changes in Gut Microbiome Features Before and After Kidney Transplantation. Pain Management Nursing, 2023, 24, 68-77.	0.9	2
3868	Whole genome analyses based on single, field collected spores of the arbuscular mycorrhizal fungus Funneliformis geosporum. Mycorrhiza, 2022, 32, 361-371.	2.8	6
3869	SILVI, an open-source pipeline for T-cell epitope selection. PLoS ONE, 2022, 17, e0273494.	2.5	0
3870	Target formation in muscle fibres indicates reinnervation “ A proteomic study in muscle samples from peripheral neuropathies. Neuropathology and Applied Neurobiology, 2023, 49, .	3.2	2
3871	Seasonal microbial dynamics in the ocean inferred from assembled and unassembled data: a view on the unknown biosphere. ISME Communications, 2022, 2, .	4.2	1
3872	MAIA, Fc receptor“like 3, supersedes JUNO as IZUMO1 receptor during human fertilization. Science Advances, 2022, 8, .	10.3	10
3873	Identification of candidate MYB transcription factors that influence CslF6 expression in barley grain. Frontiers in Plant Science, 0, 13, .	3.6	5
3874	Insight into molecular interaction between shrimp and white spot syndrome virus through MjstvCL-VP28 complex: an <i>in-silico</i> approach. Journal of Biomolecular Structure and Dynamics, 0, , 1-11.	3.5	0
3877	Noncoding RNAs responsive to nitric oxide and their protein-coding gene targets shed light on root hair formation in Arabidopsis thaliana. Frontiers in Genetics, 0, 13, .	2.3	1
3878	Deciphering microbial gene function using natural language processing. Nature Communications, 2022, 13, .	12.8	13

#	ARTICLE	IF	CITATIONS
3879	Disease resistance in coral is mediated by distinct adaptive and plastic gene expression profiles. <i>Science Advances</i> , 2022, 8, .	10.3	8
3880	Function and structure of bradykinin receptor 2 for drug discovery. <i>Acta Pharmacologica Sinica</i> , 2023, 44, 489-498.	6.1	8
3881	Quantitative Cell Proteomic Atlas: Pathway-Scale Targeted Mass Spectrometry for High-Resolution Functional Profiling of Cell Signaling. <i>Journal of Proteome Research</i> , 2022, 21, 2535-2544.	3.7	0
3882	From Bowen disease to cutaneous squamous cell carcinoma: eight markers were verified from transcriptomic and proteomic analyses. <i>Journal of Translational Medicine</i> , 2022, 20, .	4.4	5
3883	A novel strategy for developing vaccine candidate against Jaagsiekte sheep retrovirus from the envelope and gag proteins: an in-silico approach. <i>BMC Veterinary Research</i> , 2022, 18, .	1.9	3
3884	Direct capture, inhibition and crystal structure of <scp>HsaD</scp> (Rv3569c) from <i>M.â€™tuberculosis</i>. <i>FEBS Journal</i> , 2023, 290, 1563-1582.	4.7	2
3885	A novel deep learning-assisted hybrid network for plasmodium falciparum parasite mitochondrial proteins classification. <i>PLoS ONE</i> , 2022, 17, e0275195.	2.5	0
3886	Physiological and transcriptomic analysis uncovers salinity stress mechanisms in a facultative crassulacean acid metabolism plant <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3887	Cross-attention PHV: Prediction of human and virus protein-protein interactions using cross-attentionâ€™based neural networks. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5564-5573.	4.1	3
3889	Experimental Clarification of PRPS-1 Structural Essentials. <i>Cell Biochemistry and Biophysics</i> , 2022, 80, 699-709.	1.8	1
3890	Novel active compounds and the anti-diabetic mechanism of mulberry leaves. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	8
3891	Efficiency of Protein Renewal Is Limited by Feed Intake and Not by Protein Lifetime in Aging <i>Caenorhabditis elegans</i>. <i>Journal of Proteome Research</i> , 0, , .	3.7	0
3892	REDDA: Integrating multiple biological relations to heterogeneous graph neural network for drug-disease association prediction. <i>Computers in Biology and Medicine</i> , 2022, 150, 106127.	7.0	20
3893	Epitranscriptome Analysis of Oxidative Stressed Retinal Epithelial Cells Depicted a Possible RNA Editing Landscape of Retinal Degeneration. <i>Antioxidants</i> , 2022, 11, 1967.	5.1	30
3894	Discovery and In Vivo Efficacy of Trace Amine-Associated Receptor 1 (TAAR1) Agonist 4-(2-Aminoethyl)-N-(3,5-dimethylphenyl)piperidine-1-carboxamide Hydrochloride (AP163) for the Treatment of Psychotic Disorders. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11579.	4.1	1
3895	ML-DTD: Machine Learning-Based Drug Target Discovery for the Potential Treatment of COVID-19. <i>Vaccines</i> , 2022, 10, 1643.	4.4	5
3896	A combined polygenic score of 21,293 rare and 22 common variants improves diabetes diagnosis based on hemoglobin A1C levels. <i>Nature Genetics</i> , 2022, 54, 1609-1614.	21.4	20
3897	Study on saltiness sensing during oral processing of dry-cured pork base on salivary proteomics. , 2022, 1, 100127.		1

#	ARTICLE	IF	CITATIONS
3898	Molecular modeling, molecular dynamics simulation, and essential dynamics analysis of grancalcin: An upregulated biomarker in experimental autoimmune encephalomyelitis mice. <i>Heliyon</i> , 2022, 8, e11232.	3.2	5
3899	Tn6553, a Tn7-family transposon encoding putative iron uptake functions found in <i>Acinetobacter</i> . <i>Archives of Microbiology</i> , 2022, 204, .	2.2	1
3900	CNNArginineMe: A CNN structure for training models for predicting arginine methylation sites based on the One-Hot encoding of peptide sequence. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
3901	A survey of continuous subgraph matching for dynamic graphs. <i>Knowledge and Information Systems</i> , 2023, 65, 945-989.	3.2	4
3902	Uncovering the antimalarial potential of toad venoms through a bioassay-guided fractionation process. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2022, 20, 97-107.	3.4	1
3903	Characterization of the interactome profiling of <i>Mycoplasma fermentans</i> DnaK in cancer cells reveals interference with key cellular pathways. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
3904	Network Pharmacology and Molecular Docking of Shiwei Qingwen Decoction Reveal TNF as a Potential Target for Alleviating Mild COVID-19 Symptoms. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211250.	0.5	1
3905	The NAD Interactome, Identification of Putative New NAD-Binding Proteins. <i>Lecture Notes in Networks and Systems</i> , 2023, , 43-54.	0.7	1
3906	Network Pharmacology Was Used to Predict the Active Components and Prospective Targets of <i>Paeoniae Radix Alba</i> for Treatment in Endometriosis. <i>Reproductive Sciences</i> , 2023, 30, 1103-1117.	2.5	1
3907	Clinical variant interpretation and biologically relevant reference transcripts. <i>Npj Genomic Medicine</i> , 2022, 7, .	3.8	2
3908	Does Oxidative DNA Damage Trigger Histotoxic Hypoxia via PARP1/AMP-Driven Mitochondrial ADP Depletion-Induced ATP Synthase Inhibition in Alzheimer's Disease?. <i>Mitochondrion</i> , 2022, , .	3.4	1
3909	Direct Identification of Proteolytic Cleavages on Living Cells Using a Glycan-Tethered Peptide Ligase. <i>ACS Central Science</i> , 2022, 8, 1447-1456.	11.3	9
3910	Impact of different oral treatments on the composition of the supragingival plaque microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, .	2.7	3
3911	A contiguous <i>de novo</i> genome assembly of sugar beet EL10 (<i>Beta vulgaris</i> L.). <i>DNA Research</i> , 2023, 30, .	3.4	15
3912	An automatic hypothesis generation for plausible linkage between xanthium and diabetes. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
3913	AHoJ: rapid, tailored search and retrieval of apo and holo protein structures for user-defined ligands. <i>Bioinformatics</i> , 0, , .	4.1	1
3914	IntEnzyDB: an Integrated Structure-Kinetics Enzymology Database. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 5841-5848.	5.4	6
3915	Towards rational computational peptide design. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	11

#	ARTICLE	IF	CITATIONS
3916	Identification of defactinib derivatives targeting focal adhesion kinase using ensemble docking, molecular dynamics simulations and binding free energy calculations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 8654-8670.	3.5	2
3917	Molecular Docking and Molecular Dynamics Studies Reveal Secretory Proteins as Novel Targets of Temozolomide in Glioblastoma Multiforme. <i>Molecules</i> , 2022, 27, 7198.	3.8	14
3918	Passenger Pathogens on Physicians. <i>American Journal of Infection Control</i> , 2022, , .	2.3	0
3919	In-Depth Metaproteomics Analysis of Oral Microbiome for Lung Cancer. <i>Research</i> , 2022, 2022, .	5.7	6
3920	In-silico approach of identifying novel therapeutic targets against <i>Yersinia pestis</i> using pan and subtractive genomic analysis. <i>Computational Biology and Chemistry</i> , 2022, 101, 107784.	2.3	2
3921	Dose-related shifts in proteome and function of extracellular vesicles secreted by fetal neural stem cells following chronic alcohol exposure. <i>Heliyon</i> , 2022, , e11348.	3.2	6
3922	Genomic and Phenotypic Trait Variation of the Opportunistic Human Pathogen <i>Aspergillus flavus</i> and Its Close Relatives. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	9
3924	Mechanism investigation of fermented egg-milk peptides on colonic inflammatory diseases: based on <i>in vivo</i> and <i>in silico</i> research. <i>Food and Function</i> , 2022, 13, 12707-12720.	4.6	2
3925	Overview and considerations in bottom-up proteomics. <i>Analyst</i> , The, 2023, 148, 475-486.	3.5	21
3926	Prostate cancer resistance leads to a global deregulation of translation factors and unconventional translation. <i>NAR Cancer</i> , 2022, 4, .	3.1	2
3927	Total optimization potential (TOP) approach based constrained design of isoprene and cis-abienol production in <i>A. thaliana</i> . <i>Biochemical Engineering Journal</i> , 2023, 190, 108723.	3.6	1
3928	Discovery of Trace Amine-Associated Receptor 1 (TAAR1) Agonist 2-(5-(4-Chloro-[1,1'-biphenyl]-4-yl)-4H-1,2,4-triazol-3-yl)ethan-1-amine (LK00764) for the Treatment of Psychotic Disorders. <i>Biomolecules</i> , 2022, 12, 1650.	4.0	2
3929	Nearest neighbor search on embeddings rapidly identifies distant protein relations. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	13
3930	NT-proBNP and stem cell factor plasma concentrations are independently associated with cardiovascular outcomes in end-stage renal disease hemodialysis patients. <i>European Heart Journal Open</i> , 2022, 2, .	2.3	1
3931	The alternative proteome in neurobiology. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	3.7	3
3932	Single Nucleotide Polymorphisms in Insulin-like Growth Factor 2 (IGF2) gene and their associations with body weight and growth rate traits in indigenous guinea fowls (<i>Numida meleagris</i>) of northern Ghana. <i>Animal Gene</i> , 2023, 27, 200139.	0.7	0
3933	New Chalcone-Triazole Hybrids with Promising Antimicrobial Activity in Multidrug Resistance Strains. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14291.	4.1	6
3934	Identification of Potential Indicators for Survival in Patients with Thyroid Cancer Based on Expressions of FAM3 Members. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2022, , .	0.9	0

#	ARTICLE	IF	CITATIONS
3935	Parallel Exchange of Randomized SubGraphs for Optimization of Network Alignment: PERSONA. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, , 1-14.	3.0	0
3936	Molecular evolution and structural analyses of proteins involved in metabolic pathways of volatile organic compounds in <i>Petunia hybrida</i> (Solanaceae). Genetics and Molecular Biology, 2023, 46, .	1.3	0
3937	Accurate protein stability predictions from homology models. Computational and Structural Biotechnology Journal, 2023, 21, 66-73.	4.1	12
3938	Comparative transcriptome and proteome analysis of lily clones inoculated with <i>Fusarium oxysporum</i> f. sp. <i>lilii</i> . Ornamental Plant Research, 2022, 2, 1-10.	0.9	0
3939	High-throughput proteomics of nanogram-scale samples with Zeno SWATH MS. ELife, 0, 11, .	6.0	26
3940	Derivatives of Trimethoxybenzoic Acid and Gallic Acid as Potential Efflux Pump Inhibitors: In Silico and In Vitro Studies. International Journal of Molecular Sciences, 2022, 23, 14468.	4.1	0
3941	Prediction of protein-protein interactions between anti-CRISPR and CRISPR-Cas using machine learning technique. Journal of Plant Biochemistry and Biotechnology, 2023, 32, 818-830.	1.7	1
3942	Integration of network pharmacology and intestinal flora to investigate the mechanism of action of Chinese herbal <i>Cichorium intybus</i> formula in attenuating adenine and ethambutol hydrochloride-induced hyperuricemic nephropathy in rats. Pharmaceutical Biology, 2022, 60, 2338-2354.	2.9	4
3943	Functional analysis of germline <i>RAD51C</i> missense variants highlight the role of RAD51C in replication fork protection. Human Molecular Genetics, 0, , .	2.9	2
3944	Extracting and characterizing protein-free megabase-pair DNA for in vitro experiments. Cell Reports Methods, 2022, 2, 100366.	2.9	0
3945	Asperosaponin VI induces osteogenic differentiation of human umbilical cord mesenchymal stem cells via the estrogen signaling pathway. Medicine (United States), 2022, 101, e32344.	1.0	1
3946	Diminazene aceturate uses different pathways to induce relaxation in healthy and atherogenic blood vessels. Biochemical Pharmacology, 2023, 208, 115397.	4.4	2
3947	Analysis of carbohydrates and glycoconjugates by matrix-assisted laser desorption/ionization mass spectrometry: An update for 2019-2020. Mass Spectrometry Reviews, 2023, 42, 1984-2206.	5.4	6
3948	Interference with orco gene expression affects host recognition in <i>Diorhabda tarsalis</i> . Frontiers in Physiology, 0, 13, .	2.8	1
3950	DrugCentral 2023 extends human clinical data and integrates veterinary drugs. Nucleic Acids Research, 2023, 51, D1276-D1287.	14.5	18
3951	Conformation and energy investigation of microtubule longitudinal dynamic instability induced by natural products. Chemical Biology and Drug Design, 0, , .	3.2	0
3953	Parallel evolution of reduced cancer risk and tumor suppressor duplications in <i>Xenarthra</i> . ELife, 0, 11, .	6.0	2
3954	Scanning aldoxime dehydratase sequence space and characterization of a new aldoxime dehydratase from <i>Fusarium vanettenii</i> . Enzyme and Microbial Technology, 2023, 164, 110187.	3.2	8

#	ARTICLE	IF	CITATIONS
3955	Identification of Genetic Markers for the Detection of <i>Bacillus thuringiensis</i> Strains of Interest for Food Safety. <i>Foods</i> , 2022, 11, 3924.	4.3	1
3956	Targeting Ligand Independent Tropism of siRNA@LNP by Small Molecules for Directed Therapy of Liver or Myeloid Immune Cells. <i>Advanced Healthcare Materials</i> , 0, , .	7.6	7
3957	Emerging TACnology: Heterobifunctional Small Molecule Inducers of Targeted Posttranslational Protein Modifications. <i>Molecules</i> , 2023, 28, 690.	3.8	5
3958	Preterm birth is associated with xenobiotics and predicted by the vaginal metabolome. <i>Nature Microbiology</i> , 2023, 8, 246-259.	13.3	23
3959	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle <i>Peltogaster reticulata</i> (Crustacea: Rhizocephala). <i>F1000Research</i> , 0, 11, 583.	1.6	0
3960	Identifying the Mechanisms and Molecular Targets of Guchang Zhixie Pills on Ulcerative Colitis: Coupling Network Pharmacology with GEO Database and experiment verification. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, .	1.1	0
3961	Papyrus: a large-scale curated dataset aimed at bioactivity predictions. <i>Journal of Cheminformatics</i> , 2023, 15, .	6.1	13
3962	Distance geometry for word representations and applications. <i>Journal of Computational Mathematics and Data Science</i> , 2023, 6, 100073.	2.3	1
3963	MetaFunc: Taxonomic and Functional Analyses of High Throughput Sequencing for Microbiomes. <i>Gut Microbiome</i> , 0, , 1-41.	3.2	2
3964	Comparative Proteomics of Outer Membrane Vesicles from Polymyxin-Susceptible and Extremely Drug-Resistant <i>Klebsiella pneumoniae</i> . <i>MSphere</i> , 0, , .	2.9	3
3965	Unraveling the Secrets of a Double-Life Fungus by Genomics: <i>Ophiocordyceps australis</i> CCMB661 Displays Molecular Machinery for Both Parasitic and Endophytic Lifestyles. <i>Journal of Fungi (Basel)</i> , Tj ETQq0 0 0 rg815/Overlook 10 Tf 50	3.5	4
3966	Applications of deep learning in understanding gene regulation. <i>Cell Reports Methods</i> , 2023, 3, 100384.	2.9	13
3967	-Omics Technologies and Big Data. <i>Translational Bioinformatics</i> , 2023, , 33-54.	0.0	0
3968	Oral microbiome and risk of incident head and neck cancer: A nested case-control study. <i>Oral Oncology</i> , 2023, 137, 106305.	1.5	2
3969	In silico engineering a CD80 variant with increased affinity to CTLA-4 and decreased affinity to CD28 for optimized cancer immunotherapy. <i>Journal of Immunological Methods</i> , 2023, 513, 113425.	1.4	4
3970	Potent ClpP agonists with anticancer properties bind with improved structural complementarity and alter the mitochondrial N-terminome. <i>Structure</i> , 2023, 31, 185-200.e10.	3.3	8
3971	Genomic Epidemiology of the SARS-CoV-2 Epidemic in Cyprus from November 2020 to October 2021: The Passage of Waves of Alpha and Delta Variants of Concern. <i>Viruses</i> , 2023, 15, 108.	3.3	3
3972	Imaging of GÎ±q Proteins in Mouse and Human Organs and Tissues. <i>Pharmaceutics</i> , 2023, 15, 57.	4.5	0

#	ARTICLE	IF	CITATIONS
3973	BSR and Full-Length Transcriptome Approaches Identified Candidate Genes for High Seed Ratio in <i>Camellia vietnamensis</i> . <i>Current Issues in Molecular Biology</i> , 2023, 45, 311-326.	2.4	0
3974	Antimicrobial resistance in <i>Klebsiella pneumoniae</i> : identification of bacterial DNA adenine methyltransferase as a novel drug target from hypothetical proteins using subtractive genomics. <i>Genomics and Informatics</i> , 2022, 20, e47.	0.8	3
3975	Characterization of the TBR1 interactome: variants associated with neurodevelopmental disorders disrupt novel protein interactions. <i>Human Molecular Genetics</i> , 2023, 32, 1497-1510.	2.9	3
3976	Introductory Bioinformatics. , 2019, , 139-160.		0
3977	Molecular Mimicry between Respiratory Syncytial Virus F Antigen and the Human Proteome. <i>Global Medical Genetics</i> , 2023, 10, 19-21.	0.9	1
3978	A major locus confers triclabendazole resistance in <i>Fasciola hepatica</i> and shows dominant inheritance. <i>PLoS Pathogens</i> , 2023, 19, e1011081.	4.7	8
3979	Detection of Circulating SARS-CoV-2 Variants of Concern (VOCs) Using a Multiallelic Spectral Genotyping Assay. <i>Life</i> , 2023, 13, 304.	2.4	3
3980	Machine learning in computational modelling of membrane protein sequences and structures: From methodologies to applications. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 1205-1226.	4.1	3
3982	The Effective Components, Core Targets, and Key Pathways of Ginseng against Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-12.	1.2	8
3983	Medical Knowledge Graph: Data Sources, Construction, Reasoning, and Applications. <i>Big Data Mining and Analytics</i> , 2023, 6, 201-217.	8.9	16
3984	Isl1 promotes gene transcription through physical interaction with Set1/Mll complexes. <i>European Journal of Cell Biology</i> , 2023, 102, 151295.	3.6	1
3985	Introduction to Bioinformatics. , 2021, , 318-333.		0
3990	Key ingredients in <i>Verbena officinalis</i> and determination of their anti-atherosclerotic effect using a computer-aided drug design approach. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3991	CIPDB: A biological structure databank for studying cation and π interactions. <i>Drug Discovery Today</i> , 2023, 28, 103546.	6.4	2
3992	Is BF.7 more infectious than other Omicron subtypes: Insights from structural and simulation studies of BF.7 spike RBD variant. <i>International Journal of Biological Macromolecules</i> , 2023, 238, 124154.	7.5	4
3993	Lysine long-chain fatty acylation regulates the TEAD transcription factor. <i>Cell Reports</i> , 2023, 42, 112388.	6.4	3
3995	MetaProD: A Highly-Configurable Mass Spectrometry Analyzer for Multiplexed Proteomic and Metaproteomic Data. <i>Journal of Proteome Research</i> , 2023, 22, 442-453.	3.7	0
3996	CusProSe: a customizable protein annotation software with an application to the prediction of fungal secondary metabolism genes. <i>Scientific Reports</i> , 2023, 13, .	3.3	4

#	ARTICLE	IF	CITATIONS
3997	Tanshinone IIA Inhibits Triple-Negative Breast Cancer Cells MDA-MB-231 via G Protein-Coupled Estrogen Receptor- (GPER-) Dependent Signaling Pathway. <i>Disease Markers</i> , 2023, 2023, 1-14.	1.3	1
3998	Genome editing with natural and engineered CjCas9 orthologs. <i>Molecular Therapy</i> , 2023, 31, 1177-1187.	8.2	2
3999	Plant Growth Promotion, Phytohormone Production and Genomics of the Rhizosphere-Associated Microalga, <i>Micractinium rhizosphaerae</i> sp. nov.. <i>Plants</i> , 2023, 12, 651.	3.5	4
4000	An Efficient Feature Selection Algorithm for Gene Families Using NMF and ReliefF. <i>Genes</i> , 2023, 14, 421.	2.4	3
4001	Mechanisms of Protein Trafficking and Quality Control in the Kidney and Beyond. <i>Annual Review of Physiology</i> , 2023, 85, 407-423.	13.1	1
4002	Insights into the substrate specificity, structure, and dynamics of plant histidinol-phosphate aminotransferase (HISN6). <i>Plant Physiology and Biochemistry</i> , 2023, 196, 759-773.	5.8	1
4003	Transfer learning: The key to functionally annotate the protein universe. <i>Patterns</i> , 2023, 4, 100691.	5.9	0
4004	Machine Learning Advances in Predicting Peptide/Protein-Protein Interactions Based on Sequence Information for Lead Peptides Discovery. <i>Advanced Biology</i> , 2023, 7, .	2.5	5
4005	N-Glycoprofiling of SLC35A2-CDG: Patient with a Novel Hemizygous Variant. <i>Biomedicines</i> , 2023, 11, 580.	3.2	1
4006	Staying below the Radar: Unraveling a New Family of Ubiquitous “Cryptic” Non-Tailed Temperate Vibriophages and Implications for Their Bacterial Hosts. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3937.	4.1	1
4008	Ultra-small bacteria and archaea exhibit genetic flexibility towards groundwater oxygen content, and adaptations for attached or planktonic lifestyles. <i>ISME Communications</i> , 2023, 3, .	4.2	3
4009	Protein domains provide a new layer of information for classifying human variations in rare diseases. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	2
4010	Mechanism of Jiawei Zhengqi Powder in the Treatment of Ulcerative Colitis Based on Network Pharmacology and Molecular Docking. <i>BioMed Research International</i> , 2023, 2023, 1-18.	1.9	0
4011	Comparative transcriptome analysis of adult worker bees under short-term heat stress. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	2.2	0
4014	Whole-genome resequencing provides key genomic insights in farmed Arctic charr (<i>Salvelinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Applications, 0, , .	3.1	0
4015	Data-driven design of orthogonal protein-protein interactions. <i>Science Signaling</i> , 2023, 16, .	3.6	0
4017	The Gene Ontology knowledgebase in 2023. <i>Genetics</i> , 2023, 224, .	2.9	253
4019	Draft Genome Sequence of <i>Aspergillus ochraceus</i> Strain DY1, a Lignin-Degrading Fungus Isolated from Wood Rot. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	1

#	ARTICLE	IF	CITATIONS
4020	Study of NAD-interacting proteins highlights the extent of NAD regulatory roles in the cell and its potential as a therapeutic target. <i>Journal of Integrative Bioinformatics</i> , 2023, .	1.5	0
4021	Online protein digestion in membranes between capillary electrophoresis and mass spectrometry. <i>Analyst</i> , The, 2023, 148, 1611-1619.	3.5	1
4022	Higher-order modular regulation of the human proteome. <i>Molecular Systems Biology</i> , 2023, 19, .	7.2	4
4023	Molecular cloning and production of recombinant Pcal_0672, a family GH57 glycoside hydrolase from <i>Pyrobaculum caldifontis</i> . , 0, , .		1
4024	Proteomic and Bioinformatic Tools to Identify Potential Hub Proteins in the Audiogenic Seizure-Prone Hamster GASH/Sal. <i>Diagnostics</i> , 2023, 13, 1048.	2.6	1
4025	Quorum Quenchers from <i>Reynoutria japonica</i> in the Battle against Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA). <i>Molecules</i> , 2023, 28, 2635.	3.8	2
4027	Molecular mechanisms of Huanglian Jiedu decoction in treating Alzheimer's disease by regulating microbiome via network pharmacology and molecular docking analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	2
4028	A human cell orthogonal enzyme β -galacturonidase for sensitive detection of antigen proteins. <i>Analyst</i> , The, 0, , .	3.5	0
4029	Functional and Proteomic Insights into Aculeata Venoms. <i>Toxins</i> , 2023, 15, 224.	3.4	2
4030	Pangenome profiling of novel drug target against vancomycin-resistant <i>Enterococcus faecium</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 15647-15660.	3.5	2
4032	Multi-Targeted Prediction of the Antiviral Effect of <i>Momordica charantia</i> extract based on Network Pharmacology. <i>Journal of Natural Remedies</i> , 0, , 169-183.	0.3	0
4033	Study of FOXO1-interacting proteins using TurboID-based proximity labeling technology. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
4034	Plasma ApoE4 Levels Are Lower than ApoE2 and ApoE3 Levels, and Not Associated with Plasma A β 40/42 Ratio as a Biomarker of Amyloid- β Amyloidosis in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2023, , 1-16.	2.6	0
4035	Integrated bioinformatic analysis and cell line experiments reveal the significant role of the novel immune checkpoint TIGIT in kidney renal clear cell carcinoma. <i>Frontiers in Oncology</i> , 0, 13, .	2.8	1
4037	Transcriptomics Reveals the Molecular Basis for Methyl Jasmonate to Promote the Synthesis of Monoterpenoids in <i>Schizonepeta tenuifolia</i> Briq.. <i>Current Issues in Molecular Biology</i> , 2023, 45, 2738-2756.	2.4	1
4038	<i>Saccharopolyspora</i> sp. NFXS83 in Marine Biotechnological Applications: From Microalgae Growth Promotion to the Production of Secondary Metabolites. <i>Microorganisms</i> , 2023, 11, 902.	3.6	0
4039	Prognostic biomarkers and molecular pathways mediating <i>Helicobacter pylori</i> -induced gastric cancer: a network-biology approach. <i>Genomics and Informatics</i> , 2023, 21, e8.	0.8	1
4040	Antibiotic resistance in <i>Neisseria gonorrhoeae</i> : broad-spectrum drug target identification using subtractive genomics. <i>Genomics and Informatics</i> , 2023, 21, e5.	0.8	1

#	ARTICLE	IF	CITATIONS
4042	Calcium-dependent activation of CPK12 facilitates its cytoplasm-to-nucleus translocation to potentiate plant hypoxia sensing by phosphorylating ERF-VII transcription factors. <i>Molecular Plant</i> , 2023, 16, 979-998.	8.3	21
4043	O ₂ partitioning of sulfur oxidizing bacteria drives acidity and thiosulfate distributions in mining waters. <i>Nature Communications</i> , 2023, 14, .	12.8	2
4044	Clinical Phenotype in Individuals With Birk-Landau-Perez Syndrome Associated With Biallelic SLC30A9 Pathogenic Variants. <i>Neurology</i> , 2023, Publish Ahead of Print, .	1.1	0
4045	Foundation models for generalist medical artificial intelligence. <i>Nature</i> , 2023, 616, 259-265.	27.8	208
4046	Interactions between curcumin and human salt-induced kinase 3 elucidated from computational tools and experimental methods. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	0
4047	Does AlphaFold2 model proteinsâ€™ intracellular conformations? An experimental test using cross-linking mass spectrometry of endogenous ciliary proteins. <i>Communications Biology</i> , 2023, 6, .	4.4	7
4048	The proteomic landscape of genome-wide genetic perturbations. <i>Cell</i> , 2023, 186, 2018-2034.e21.	28.9	12
4050	The Metal-binding Protein Atlas (MbPA): An Integrated Database for Curating Metalloproteins in All Aspects. <i>Journal of Molecular Biology</i> , 2023, 435, 168117.	4.2	5
4051	Genomic and Secretomic Analyses of the Newly Isolated Fungus <i>Perenniporia fraxinea</i> SS3 Identified CAZymes Potentially Related to a Serious Pathogenesis of Hardwood Trees. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	0
4052	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode <i>Brugia malayi</i> . <i>Scientific Reports</i> , 2023, 13, .	3.3	0
4053	The clinical and molecular spectrum of the KDM6B-related neurodevelopmental disorder. <i>American Journal of Human Genetics</i> , 2023, 110, 963-978.	6.2	3
4054	Design, synthesis and biological evaluation of antiparasitic dinitroaniline-ether phospholipid hybrids. <i>Bioorganic Chemistry</i> , 2023, 138, 106615.	4.1	1
4055	Unlocking the mystery associated with infertility and prostate cancer: an update. , 2023, 40, .		5
4056	A correlation coefficient-based feature selection approach for virus-host protein-protein interaction prediction. <i>PLoS ONE</i> , 2023, 18, e0285168.	2.5	0
4057	Rational identification of a catalytically promiscuous nitrilase by predicting a unique catalytic triad motif feature through an <i>in silico</i> strategy. <i>Catalysis Science and Technology</i> , 0, , .	4.1	0
4058	In silico structure prediction and molecular docking analyses to reveal potential binding domain of Hepatitis B virus genotype A2. <i>Biomedical Letters</i> , 2023, 9, 25-30.	0.3	0
4059	Introduction to biological databases. , 2023, , 19-42.		0
4060	Integration of network pharmacology, transcriptomics and molecular docking reveals two novel hypoglycemic components in snow chrysanthemum. <i>Biomedicine and Pharmacotherapy</i> , 2023, 163, 114818.	5.6	2

#	ARTICLE	IF	CITATIONS
4061	De Novo Design of Anti-COVID Drugs Using Machine Learning-Based Equivariant Diffusion Model Targeting the Spike Protein. <i>Current Issues in Molecular Biology</i> , 2023, 45, 4261-4284.	2.4	3
4062	FTSH PROTEASE 3 facilitates Complex I degradation through a direct interaction with the Complex I subunit PSST. <i>Plant Cell</i> , 0, , .	6.6	1
4063	Deep self-supervised learning for biosynthetic gene cluster detection and product classification. <i>PLoS Computational Biology</i> , 2023, 19, e1011162.	3.2	3
4064	On the Unknown Proteins of Eukaryotic Proteomes. <i>Journal of Molecular Evolution</i> , 2023, 91, 492-501.	1.8	1
4065	Targeting multi-drug-resistant <i>Acinetobacter baumannii</i> : a structure-based approach to identify the promising lead candidates against glutamate racemase. <i>Journal of Molecular Modeling</i> , 2023, 29, .	1.8	2
4066	AI-Assisted chemical probe discovery for the understudied Calcium-Calmodulin Dependent Kinase, PNCK. <i>PLoS Computational Biology</i> , 2023, 19, e1010263.	3.2	1
4067	Elucidating the Mesocarp Drupe Transcriptome of Açaí (<i>Euterpe oleracea</i> Mart.): An Amazonian Tree Palm Producer of Bioactive Compounds. <i>International Journal of Molecular Sciences</i> , 2023, 24, 9315.	4.1	0
4069	Chromosome-length genome assembly and karyotype of the endangered black-footed ferret (<i>Mustela nigripes</i>). <i>Journal of Heredity</i> , 2023, 114, 539-548.	2.4	4
4070	New insights in the genetic variant spectrum of SLC34A2 in pulmonary alveolar microlithiasis; a systematic review. <i>Orphanet Journal of Rare Diseases</i> , 2023, 18, .	2.7	2
4071	Mechanism analysis and improved molecular modification: Design of high efficiency and environmentally friendly triazole fungicide substitutes. <i>Chemosphere</i> , 2023, 336, 139150.	8.2	1
4072	StandEnA: A customizable workflow for standardized annotation and generating a presence-absence matrix of proteins. <i>Bioinformatics Advances</i> , 0, , .	2.4	0
4073	Identification of novel p-cresol inhibitors that reduce <i>Clostridioides difficile</i> 's ability to compete with species of the gut microbiome. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
4074	Unraveling the glycosylated immunopeptidome with HLA-Glyco. <i>Nature Communications</i> , 2023, 14, .	12.8	2
4077	Molecular Dynamics of Mismatch Detection – How MutS Uses Indirect Readout to Find Errors in DNA. <i>Biophysical Journal</i> , 2023, , .	0.5	0
4078	The diagnostic significance of the ZNF gene family in pancreatic cancer: a bioinformatics and experimental study. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
4079	Variants in ACTC1 underlie distal arthrogryposis accompanied by congenital heart defects. <i>Human Genetics and Genomics Advances</i> , 2023, 4, 100213.	1.7	2
4080	Identifying promising sequences for protein engineering using a deep transformer protein language model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 1471-1486.	2.6	1
4081	Molecular defense responses to natural enemies determine seedling survival in a subtropical forest. <i>Forest Ecology and Management</i> , 2023, 544, 121191.	3.2	0

#	ARTICLE	IF	CITATIONS
4082	Aquaporin 9 is involved in CRC metastasis through DVL2-dependent Wnt/ β^2 -catenin signaling activation. Gastroenterology Report, 2022, 11, .	1.3	0
4084	<i>Vitis vinifera</i> leaf extract liposomal Carbopol gel preparation's potential wound healing and antibacterial benefits: <i>in vivo</i> , phytochemical, and computational investigation. Food and Function, 2023, 14, 7156-7175.	4.6	2
4085	Cell-type specific defects in <i>PTEN</i> -mutant cortical organoids converge on abnormal circuit activity. Human Molecular Genetics, 0, , .	2.9	0
4086	Identification, classification, and functional characterization of novel sponge-associated acidimicrobiial species. Systematic and Applied Microbiology, 2023, 46, 126426.	2.8	0
4087	Autophagy dark genes: Can we find them with machine learning?. Natural Sciences, 2023, 3, .	2.1	1
4089	Effect of Indole-Containing Pyrazino[2,1-b]quinazoline-3,6-diones in the Virulence of Resistant Bacteria. Antibiotics, 2023, 12, 922.	3.7	0
4090	Potential thyroid hormone disorder risks of tire antioxidants to aquatic food chain organisms after absorbing free radicals in marine and freshwater environments. Aquatic Toxicology, 2023, 260, 106587.	4.0	2
4091	Genomic, functional and structural analyses elucidate evolutionary innovation within the sea anemone 8 toxin family. BMC Biology, 2023, 21, .	3.8	5
4094	Protein abundance in the midgut of wild tsetse flies (<i>Glossina palpalis palpalis</i>) naturally infected by <i>Trypanosoma congolense</i> s.l. Medical and Veterinary Entomology, 0, , .	1.5	0
4095	In Silico Functional Characterization of a Hypothetical Protein From <i>Pasteurella Multocida</i> Reveals a Novel <i>S</i> -Adenosylmethionine-Dependent Methyltransferase Activity. Bioinformatics and Biology Insights, 2023, 17, .	2.0	0
4096	Evolutionary history of an Alpine Archaeognath (<i>Machilis pallida</i>): Insights from different variant. Ecology and Evolution, 2023, 13, .	1.9	0
4097	Investigating the Binding Efficacy of Snake Venom Proteins as GLP-1 Analogs for Diabetes mellitus Management: An In silico Study. Oriental Journal of Chemistry, 2023, 39, 581-591.	0.3	0
4099	Functional viromic screens uncover regulatory RNA elements. Cell, 2023, 186, 3291-3306.e21.	28.9	5
4100	MSFP: undergraduate â€œcollaborate-from-homeâ€™ research in macromolecular structure and function. Bioinformatics Advances, 2023, 3, .	2.4	0
4101	Role of molecular mimicry in the SARS-CoV-2-human interactome for pathogenesis of cardiovascular diseases: An update to ImitateDB. Computational Biology and Chemistry, 2023, 106, 107919.	2.3	0
4102	<i>Paenibacillus polymyxa</i> YLC1: a promising antagonistic strain for biocontrol of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> , causing kiwifruit bacterial canker. Pest Management Science, 2023, 79, 4357-4366.	3.4	1
4105	N6AMT1 is a novel potential diagnostic, prognostic and immunotherapy response biomarker in pan-cancer. Aging, 2023, 15, 6526-6544.	3.1	2
4106	Microplastics in cultivated soil environment: Construction of toxicity grading evaluation system, development of priority control checklist, and toxicity mechanism analysis. Journal of Hazardous Materials, 2023, 459, 132046.	12.4	1

#	ARTICLE	IF	CITATIONS
4107	Patterns of transcription factor binding and epigenome at promoters allow interpretable predictability of multiple functions of non-coding and coding genes. Computational and Structural Biotechnology Journal, 2023, 21, 3590-3603.	4.1	0
4108	Machine Learning Methods for Virus-Host Protein-Protein Interaction Prediction. Methods in Molecular Biology, 2023, , 401-417.	0.9	0
4109	Jingfang granule alleviates Pseudomonas aeruginosa-induced acute lung inflammation through suppression of STAT3/IL-17/NF- κ B pathway based on network pharmacology analysis and experimental validation. Journal of Ethnopharmacology, 2024, 318, 116899.	4.1	1
4110	RecJ3/4-aRNase J form a Ubl-associated nuclease complex functioning in survival against DNA damage in <i>Haloferax volcanii</i> . MBio, 0, , .	4.1	0
4111	Coptidis rhizoma and evodiae fructus against lipid droplet deposition in nonalcoholic fatty liver disease-related liver cancer by Akt . Chemical Biology and Drug Design, 2023, 102, 828-842.	3.2	1
4112	Resisting Radiation Through Tardigrade DSUP. Microscopy and Microanalysis, 2023, 29, 2053-2054.	0.4	0
4113	Elucidation of the anti-lung cancer mechanism of Juan-Liu-San-Jie prescription based on network pharmacology and experimental validation. Heliyon, 2023, 9, e18298.	3.2	0
4114	Screening eco-friendliness tire antioxidants alternatives: functional 2,2,4-trimethyl-1,2-dihydroquinoline derivatives design and toxicity evaluation. Environmental Science and Pollution Research, 0, , .	5.3	0
4116	Integrating Omics Data in Genome-Scale Metabolic Modeling: A Methodological Perspective for Precision Medicine. Metabolites, 2023, 13, 855.	2.9	2
4119	The metagenome-derived esterase PET40 is highly promiscuous and hydrolyses polyethylene terephthalate (PET). FEBS Journal, 2024, 291, 70-91.	4.7	3
4120	Machine learning for drug repositioning: Recent advances and challenges. Current Research in Chemical Biology, 2023, 3, 100042.	2.9	2
4121	Qi-Po-Sheng-Mai granule ameliorates Ach-CaCl ₂ -induced atrial fibrillation by regulating calcium homeostasis in cardiomyocytes. Phytomedicine, 2023, 119, 155017.	5.3	1
4123	Mosaic TP53 Mutation on Tumour Development in Pigs: A Case Study. Veterinary Medicine International, 2023, 2023, 1-6.	1.5	0
4124	Understanding the Molecular Regulation of Serotonin Receptor 5-HT _{1B} -Arrestin1 Complex in Stress and Anxiety Disorders. Journal of Molecular Neuroscience, 2023, 73, 664-677.	2.3	2
4125	Data sets of human and mouse protein kinase inhibitors with curated activity data including covalent inhibitors. Future Science OA, 0, , .	1.9	0
4126	Proteomic Profiling and Tumor Microenvironment Characterization Reveal Molecular and Immunological Hallmarks of Left-Sided and Right-Sided Colon Cancer Tumorigenesis. Journal of Proteome Research, 2023, 22, 2973-2984.	3.7	0
4127	Quantitative and functional characterisation of extracellular vesicles after passive loading with hydrophobic or cholesterol-tagged small molecules. Journal of Controlled Release, 2023, 361, 694-716.	9.9	2
4128	Hypomyelination, hypodontia and craniofacial abnormalities in a <i>Polr3b</i> mouse model of leukodystrophy. Brain, 2023, 146, 5070-5085.	7.6	3

#	ARTICLE	IF	CITATIONS
4130	Unraveling the Dynamics of Omicron (BA.1, BA.2, and BA.5) Waves and Emergence of the Deltacron Variant: Genomic Epidemiology of the SARS-CoV-2 Epidemic in Cyprus (Oct 2021–Oct 2022). <i>Viruses</i> , 2023, 15, 1933.	3.3	1
4131	Multiplexed Assessment of Promiscuous Non-Canonical Amino Acid Synthase Activity in a Pyridoxal Phosphate-Dependent Protein Family. <i>ACS Catalysis</i> , 2023, 13, 11644-11655.	11.2	0
4132	Multivariate Genome-Wide Association Study of Concentrations of Seven Elements in Seeds Reveals Four New Loci in Russian Wheat Lines. <i>Plants</i> , 2023, 12, 3019.	3.5	0
4133	Linking extreme seasonality and gene expression in Arctic marine protists. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
4134	Atomic visualization of flipped-back conformations of high mannose glycans interacting with cargo lectins: An MD simulation perspective. <i>Proteins: Structure, Function and Bioinformatics</i> , 0, .	2.6	0
4135	Data-driven large-scale genomic analysis reveals an intricate phylogenetic and functional landscape in J-domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	7
4136	NCSML-HDTD: Network Centrality and Sequence-Based Machine Learning Methodology for Human Drug Targets Discovery of COVID-19. <i>Lecture Notes in Networks and Systems</i> , 2023, , 515-523.	0.7	0
4137	Prebiotic inulin enhances gut microbial metabolism and anti-inflammation in apolipoprotein E4 mice with sex-specific implications. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
4138	GeNetOntology: identifying affected gene ontology terms via grouping, scoring, and modeling of gene expression data utilizing biological knowledge-based machine learning. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	3
4139	Identification and characterization of putative biomarkers and therapeutic axis in Glioblastoma multiforme microenvironment. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	1
4140	Enabling Broader Adoption of Biocatalysis in Organic Chemistry. <i>Jacs Au</i> , 2023, 3, 2073-2085.	7.9	4
4141	A pathway model of glucose-stimulated insulin secretion in the pancreatic Î²-cell. <i>Frontiers in Endocrinology</i> , 0, 14, .	3.5	2
4142	Mass-produced gram-negative bacterial outer membrane vesicles activate cancer antigen-specific stem-like CD8 ⁺ T cells which enables an effective combination immunotherapy with anti-PD-1. <i>Journal of Extracellular Vesicles</i> , 2023, 12, .	12.2	3
4143	Theoretical 3D Modeling of NLRP3 Inflammasome Complex. <i>Methods in Molecular Biology</i> , 2023, , 269-280.	0.9	0
4144	Human Triosephosphate Isomerase Is a Potential Target in Cancer Due to Commonly Occurring Post-Translational Modifications. <i>Molecules</i> , 2023, 28, 6163.	3.8	0
4145	Monte Carlo Thompson sampling-guided design for antibody engineering. <i>MAbs</i> , 2023, 15, .	5.2	0
4146	Pulmonary alveolar microlithiasis: a rare case report from Syria. <i>Annals of Medicine and Surgery</i> , 2023, 85, 4566-4569.	1.1	0
4147	Data Engineering Challenges in AI automation. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
4148	Genomic-driven nutritional interventions for radiotherapy-resistant rectal cancer patient. Scientific Reports, 2023, 13, .	3.3	0
4149	Characterization of Proteoform Post-Translational Modifications by Top-Down and Bottom-Up Mass Spectrometry in Conjunction with Annotations. Journal of Proteome Research, 2023, 22, 3178-3189.	3.7	1
4150	Docetaxel radiosensitizes castration-resistant prostate cancer by downregulating CAV-1. International Journal of Radiation Biology, 2024, 100, 256-267.	1.8	0
4151	Artificial Intelligence Generative Chemistry Design of Target-Specific Scaffold-Focused Small Molecule Drug Libraries. , 2023, , 503-521.		0
4152	pAtbP-EnC: Identifying Anti-Tubercular Peptides Using Multi-Feature Representation and Genetic Algorithm-Based Deep Ensemble Model. IEEE Access, 2023, 11, 137099-137114.	4.2	6
4153	AcrTransAct: Pre-trained Protein Transformer Models for the Detection of Type I Anti-CRISPR Activities. , 2023, , .		0
4156	Identifying genetic variation associated with environmental gradients and drought tolerance phenotypes in ponderosa pine. Ecology and Evolution, 2023, 13, .	1.9	0
4159	Machine learning-based antioxidant protein identification model: Progress and evaluation. Journal of Cellular Biochemistry, 2023, 124, 1825-1834.	2.6	0
4160	Exploring the action mechanism of Jinxin oral liquid on asthma by network pharmacology, molecular docking, and microRNA recognition. Medicine (United States), 2023, 102, e35438.	1.0	0
4161	The DNA-binding induced (de)AMPylation activity of a Coxiella burnetii Fic enzyme targets Histone H3. Communications Biology, 2023, 6, .	4.4	0
4162	Data-Driven Drug Repurposing in Diabetes Mellitus through an Enhanced Knowledge Graph. , 0, , .		0
4163	Interactome profiling of Crimean-Congo hemorrhagic fever virus glycoproteins. Nature Communications, 2023, 14, .	12.8	0
4164	Dissection of the antitumor mechanism of tetrandrine based on metabolite profiling and network pharmacology. Rapid Communications in Mass Spectrometry, 2024, 38, .	1.5	0
4165	In silico designing of an epitope-based peptide vaccine cocktail against Nipah virus: an Indian population-based epidemiological study. Archives of Microbiology, 2023, 205, .	2.2	0
4166	Computational prediction of protein-protein interactions network in Arabidopsis thaliana. Acta Physiologiae Plantarum, 2023, 45, .	2.1	0
4167	EMC rectifies the topology of multipass membrane proteins. Nature Structural and Molecular Biology, 0, , .	8.2	1
4168	Stemness signature and targeted therapeutic drugs identification for Triple Negative Breast Cancer. Scientific Data, 2023, 10, .	5.3	0
4169	Antibody landscape of C57BL/6 mice cured of B78 melanoma via a combined radiation and immunocytokine immunotherapy regimen. Frontiers in Immunology, 0, 14, .	4.8	0

#	ARTICLE	IF	CITATIONS
4170	Taxonomic and environmental distribution of bacterial amino acid auxotrophies. <i>Nature Communications</i> , 2023, 14, .	12.8	3
4171	Genome-Wide Identification of Selenium-Responsive MicroRNAs in Tea Plant (<i>Camellia sinensis</i> L. O.) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	1
4172	A new paradigm for molecular dynamics databases: the COVID-19 database, the legacy of a titanic community effort. <i>Nucleic Acids Research</i> , 2024, 52, D393-D403.	14.5	2
4175	Camphene and ginsamide: dynamics of potential interactions with the influenza virus M2 channel. <i>Russian Chemical Bulletin</i> , 2023, 72, 2548-2558.	1.5	0
4176	The Nucleic Acid Knowledgebase: a new portal for 3D structural information about nucleic acids. <i>Nucleic Acids Research</i> , 0, , .	14.5	2
4178	Complementarity of two proteomic data analysis tools in the identification of drug-metabolising enzymes and transporters in human liver. <i>Molecular Omics</i> , 2024, 20, 115-127.	2.8	0
4180	Chromosome-level genome assembly of Przevalskiâ€™s partridge (<i>Alectoris magna</i>). <i>Scientific Data</i> , 2023, 10, .	5.3	0
4181	Boosting knowledge and harmonisation in the mycotoxin field through sustainable scientific alliances â€œ MYCOBOOST. EFSA Supporting Publications, 2023, 20, .	0.7	0
4182	A large-scale genomically predicted protein mass database enables rapid and broad-spectrum identification of bacterial and archaeal isolates by mass spectrometry. <i>Genome Biology</i> , 2023, 24, .	8.8	0
4184	The OREGANO knowledge graph for computational drug repurposing. <i>Scientific Data</i> , 2023, 10, .	5.3	1
4185	Comprehensive Representation ofÂVariation Interpretation Data viaÂConceptual Modeling. <i>Lecture Notes in Computer Science</i> , 2023, , 25-34.	1.3	0
4186	From Proteins to Ligands: Decoding Deep Learning Methods for Binding Affinity Prediction. <i>Journal of Chemical Information and Modeling</i> , 0, , .	5.4	2
4189	Decoding the alpha-amylase inhibitory activity of <i>Garcinia indica</i> Choisy by computational and experimental studies. <i>South African Journal of Botany</i> , 2024, 165, 14-29.	2.5	0
4191	Sequence-based identification of amyloidogenic Î²-hairpins reveals a prostatic acid phosphatase fragment promoting semen amyloid formation. <i>Computational and Structural Biotechnology Journal</i> , 2024, 23, 417-430.	4.1	0
4193	Draft genome sequence and comparative genomic analysis of <i>Penicillium pancosmium</i> MUM 23.27 isolated from raw honey. <i>Archives of Microbiology</i> , 2024, 206, .	2.2	0
4194	Unusual weak and delayed GTPase activity of FtsZ from human pathogenic bacteria <i>Helicobacter pylori</i>. <i>Journal of Biochemistry</i> , 0, , .	1.7	0
4195	The Extent of Edgetic Perturbations in the Human Interactome Caused by Population-Specific Mutations. <i>Biomolecules</i> , 2024, 14, 40.	4.0	0
4196	Discovery of Kinetin in inhibiting colorectal cancer progression via enhancing PSMB1-mediated RAB34 degradation. <i>Cancer Letters</i> , 2024, 584, 216600.	7.2	0

#	ARTICLE	IF	CITATIONS
4197	High-altitude adaptation is accompanied by strong signatures of purifying selection in the mitochondrial genomes of three Andean waterfowl. <i>PLoS ONE</i> , 2024, 19, e0294842.	2.5	1
4198	In silico study on the catalytic activity of lipase from <i>Fusarium oxysporum</i> f. sp. <i>tracheiphilum</i> in the bioconversion of Annonalide and its acylated derivatives. <i>Molecular Catalysis</i> , 2023, 547, 113385.	2.0	0
4199	AG1Â® Induces a Favorable Impact on Gut Microbial Structure and Functionality in the Simulator of Human Intestinal Microbial EcosystemÂ® Model. <i>Current Issues in Molecular Biology</i> , 2024, 46, 557-569.	2.4	0
4200	SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. <i>International Journal of Molecular Sciences</i> , 2024, 25, 1183.	4.1	0
4201	Translatability of findings from cynomolgus monkey to human suggests a mechanistic role for IL-21 in promoting immunogenicity to an anti-PD-1/IL-21 mutein fusion protein. <i>Frontiers in Immunology</i> , 0, 15, .	4.8	0
4202	LipidSIM: Inferring mechanistic lipid biosynthesis perturbations from lipidomics with a flexible, low-parameter, Markov modeling framework. <i>Metabolic Engineering</i> , 2024, 82, 110-122.	7.0	0
4203	M-Ionic: prediction of metal-ion-binding sites from sequence using residue embeddings. <i>Bioinformatics</i> , 2024, 40, .	4.1	0
4204	Metabolite-sensing GPCRs in rheumatoid arthritis. <i>Trends in Pharmacological Sciences</i> , 2024, 45, 118-133.	8.7	0
4207	Exploring the potential mechanism of Simiao Yongan decoction in the treatment of diabetic peripheral vascular disease based on network pharmacology and molecular docking technology. <i>Medicine (United States)</i> , 2023, 102, e36762.	1.0	0
4209	Genomic insights into the evolution and adaptation of secondary metabolite gene clusters in fungicolous species <i>Cladobotryum mycophilum</i> ATHUM6906. <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
4210	Leveraging inter-individual transcriptional correlation structure to infer discrete signaling mechanisms across metabolic tissues. <i>ELife</i> , 0, 12, .	6.0	0
4211	PandoGen: Generating complete instances of future SARS-CoV-2 sequences using Deep Learning. <i>PLoS Computational Biology</i> , 2024, 20, e1011790.	3.2	1
4212	Type IV collagen. , 2024, , 37-53.		0
4214	Proteomics Research on Features of Life Activity of Parasitic Worms. <i>Biology Bulletin Reviews</i> , 2023, 13, S155-S171.	0.9	0
4215	Comparative interactome analysis of ð±-arrestin families in human and <i>Drosophila</i> . <i>ELife</i> , 0, 12, .	6.0	0
4216	Proteomics for heart failure risk stratification: a systematic review. <i>BMC Medicine</i> , 2024, 22, .	5.5	0
4217	Dynamic profiles of lncRNAs reveal a functional natural antisense RNA that regulates the development of <i>Schistosoma japonicum</i> . <i>PLoS Pathogens</i> , 2024, 20, e1011949.	4.7	0
4218	Oxidative Stress Promotes Liver Cancer Metastasis via RNF25â€Mediated Eâ€Cadherin Protein Degradation. <i>Advanced Science</i> , 2024, 11, .	11.2	0

#	ARTICLE	IF	CITATIONS
4220	An interdisciplinary course on computer-aided drug discovery to broaden student participation in original scientific research. <i>Biochemistry and Molecular Biology Education</i> , 0, , .	1.2	0
4221	Targeting with Structural Analogs of Natural Products the Purine Salvage Pathway in <i>Leishmania</i> (Leishmania) infantum by Computer-Aided Drug-Design Approaches. <i>Tropical Medicine and Infectious Disease</i> , 2024, 9, 41.	2.3	1
4222	Histological, chemical and gene expression differences between western redcedar seedlings resistant and susceptible to cedar leaf blight. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
4223	Microtubule-affinity regulating kinase family members distinctively affect tau phosphorylation and promote its toxicity in a <i>Drosophila</i> model. <i>Genes To Cells</i> , 2024, 29, 337-346.	1.2	0
4224	Development of a novel multi-epitope vaccine against the pathogenic human polyomavirus V6/7 using reverse vaccinology. <i>BMC Infectious Diseases</i> , 2024, 24, .	2.9	0
4225	Reconstructing the transcriptional regulatory network of probiotic <i>L. reuteri</i> is enabled by transcriptomics and machine learning. <i>MSystems</i> , 2024, 9, .	3.8	0
4226	C19ORF84 connects piRNA and DNA methylation machineries to defend the mammalian germ line. <i>Molecular Cell</i> , 2024, 84, 1021-1035.e11.	9.7	0
4227	Genome-wide identification, stress- and hormone-responsive expression characteristics, and regulatory pattern analysis of <i>Scutellaria baicalensis</i> SbSPLs. <i>Plant Molecular Biology</i> , 2024, 114, .	3.9	0
4228	Prediction of Drug-Target Interactions Using BERT for Protein Sequences and Drug Compound. , 2024, , .		0
4229	EncoMPASS: An encyclopedia of membrane proteins analyzed by structure and symmetry. <i>Structure</i> , 2024, 32, 492-504.e4.	3.3	0
4230	Weathered granites and soils harbour microbes with lanthanide-dependent methylotrophic enzymes. <i>BMC Biology</i> , 2024, 22, .	3.8	0
4231	An historical "wreck": A transcriptome assembly of the naval shipworm, <i>Teredo navalis</i> Linnaeus, 1778. <i>Marine Genomics</i> , 2024, 74, 101097.	1.1	0
4232	Lipid droplets in <i>Arabidopsis thaliana</i> leaves contain myosin-binding proteins and enzymes associated with furan-containing fatty acid biosynthesis. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
4233	Utilizing network pharmacology and experimental validation to investigate the underlying mechanism of Denglao Qingguan decoction against HCoV-229E. <i>Heliyon</i> , 2024, 10, e27829.	3.2	0
4234	Deciphering miRNA-lncRNA-mRNA interaction through experimental validation of miRNAs, lncRNAs, and miRNA targets on mRNAs in <i>Cajanus cajan</i> . <i>Plant Biology</i> , 0, , .	3.8	0
4235	EPI-SF: essential protein identification in protein interaction networks using sequence features. <i>PeerJ</i> , 0, 12, e17010.	2.0	0
4237	Comparison of In Silico Signal Sequence-Phospholipid Results with Described In Vitro and In Vivo Protein Translocation Studies Seems to Underscore the Significance of Phospholipids. , 2024, 1, 3-17.		0
4239	In silico Analysis of Structure and Function of Hypothetical Proteins in <i>Salmonella typhimurium</i> (SL1344). <i>Research Journal of Pharmacy and Technology</i> , 2024, , 643-650.	0.8	0

#	ARTICLE	IF	CITATIONS
4240	Integrative approach using network pharmacology, bioinformatics, and experimental methods to explore the mechanism of cantharidin in treating colorectal cancer. Naunyn-Schmiedeberg's Archives of Pharmacology, 0, , .	3.0	0