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Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Tools for protein science. <i>Protein Science</i> , 2018, 27, 6-9.	3.1	2
3	Homology Modelling and Molecular Docking Studies of Selected Substituted Lyase Receptor. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221986553.	1.0	35
4	Crystal structures of AztD provide mechanistic insights into direct zinc transfer between proteins. <i>Communications Biology</i> , 2019, 2, 308.	2.0	7
5	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	1.6	80
6	Prediction and validation of potent peptides against herpes simplex virus type 1 via immunoinformatic and systems biology approach. <i>Chemical Biology and Drug Design</i> , 2019, 94, 1868-1883.	1.5	26
7	Membrane organization of photosystem I complexes in the most abundant phototroph on Earth. <i>Nature Plants</i> , 2019, 5, 879-889.	4.7	22
8	Mitofusins modulate the increase in mitochondrial length, bioenergetics and secretory phenotype in therapy-induced senescent melanoma cells. <i>Biochemical Journal</i> , 2019, 476, 2463-2486.	1.7	17
9	Demethylated hopanoids in <i>Ca. Methylomirabilis oxyfera</i> ™ as biomarkers for environmental nitrite-dependent methane oxidation. <i>Organic Geochemistry</i> , 2019, 137, 103899.	0.9	7
10	RAFTS3G: an efficient and versatile clustering software to analyses in large protein datasets. <i>BMC Bioinformatics</i> , 2019, 20, 392.	1.2	3
11	Predicting Sequence Features, Function, and Structure of Proteins Using MESSA. <i>Current Protocols in Bioinformatics</i> , 2019, 67, e84.	25.8	0
12	Identification and Characterization of Preferred DNA-Binding Sites for the <i>Thermus thermophilus</i> HB8 Transcriptional Regulator TTHA0973. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3336.	1.8	7
13	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	1.6	15
14	Geno2proteo, a Tool for Batch Retrieval of DNA and Protein Sequences from Any Genomic or Protein Regions. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	0
15	Structural modeling of protein complexes: Current capabilities and challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1222-1232.	1.5	12
16	Underestimated Noncovalent Interactions in Protein Data Bank. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3389-3399.	2.5	25
17	An Asymmetric Reductase That Intercepts Acyclic Imino Acids Produced <i>in Situ</i> by a Partner Oxidase. <i>Journal of the American Chemical Society</i> , 2019, 141, 12258-12267.	6.6	5
18	Sleeping beauty genetic screen identifies miR-23b::BTBD7 gene interaction as crucial for colorectal cancer metastasis. <i>EBioMedicine</i> , 2019, 46, 79-93.	2.7	13
19	Alphabet Projection of Spectra. <i>Journal of Proteome Research</i> , 2019, 18, 3268-3281.	1.8	5

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20	Data-driven computational analysis of allosteric proteins by exploring protein dynamics, residue coevolution and residue interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, , .	1.1	17
21	Cell death and mitochondrial dysfunction induced by the dietary non-proteinogenic amino acid l-azetidine-2-carboxylic acid (Aze). <i>Amino Acids</i> , 2019, 51, 1221-1232.	1.2	10
22	Identification of the lipopolysaccharide Oâ€œantigen biosynthesis priming enzyme and the Oâ€œantigen ligase in <i>Myxococcus xanthus</i> : critical role of LPS Oâ€œantigen in motility and development. <i>Molecular Microbiology</i> , 2019, 112, 1178-1198.	1.2	17
23	N-terminal Î²-strand underpins biochemical specialization of an ATG8 isoform. <i>PLoS Biology</i> , 2019, 17, e3000373.	2.6	47
24	The Role of Iron and Copper on the Oligomerization Dynamics of DR_2577, the Main S-Layer Protein of <i>Deinococcus radiodurans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1450.	1.5	10
25	A tale of short tails, through thick and thin: investigating the sorting mechanisms of Golgi enzymes. <i>FEBS Letters</i> , 2019, 593, 2452-2465.	1.3	52
26	DR-SIP: protocols for higher order structure modeling with distance restraints- and cyclic symmetry-imposed packing. <i>Bioinformatics</i> , 2020, 36, 449-461.	1.8	1
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28	A Web Tool for Ranking Candidate Drugs Against a Selected Disease Based on a Combination of Functional and Structural Criteria. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 939-945.	1.9	10
29	Progressive changes in human follicular fluid composition over the course of ovulation: quantitative proteomic analyses. <i>Molecular and Cellular Endocrinology</i> , 2019, 495, 110522.	1.6	29
30	The Role of Protein Thermodynamics and Primary Structure in Fibrillogenesis of Variable Domains from Immunoglobulin Light Chains. <i>Journal of the American Chemical Society</i> , 2019, 141, 13562-13571.	6.6	24
32	In silico analysis of missense mutations in exons 1â€œ5 of the F9 gene that cause hemophilia B. <i>BMC Bioinformatics</i> , 2019, 20, 363.	1.2	9
33	Metagenomic analysis of bile salt biotransformation in the human gut microbiome. <i>BMC Genomics</i> , 2019, 20, 517.	1.2	44
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35	A structural model of the human serotonin transporter in an outward-occluded state. <i>PLoS ONE</i> , 2019, 14, e0217377.	1.1	17
36	CHNOSZ: Thermodynamic Calculations and Diagrams for Geochemistry. <i>Frontiers in Earth Science</i> , 2019, 7, .	0.8	62
37	HyperFoods: Machine intelligent mapping of cancer-beating molecules in foods. <i>Scientific Reports</i> , 2019, 9, 9237.	1.6	41
38	Determination of Ligand Profiles for <i>Pseudomonas aeruginosa</i> Solute Binding Proteins. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5156.	1.8	19

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39	Selection of sequence motifs and generative Hopfield-Potts models for protein families. <i>Physical Review E</i> , 2019, 100, 032128.	0.8	22
40	Integrated Bioinformatic Analyses and Immune Characterization of New <i>Neisseria gonorrhoeae</i> Vaccine Antigens Expressed during Natural Mucosal Infection. <i>Vaccines</i> , 2019, 7, 153.	2.1	14
41	motifer: An Integrated Web Software for Identification and Visualization of Protein Posttranslational Modification Motifs. <i>Proteomics</i> , 2019, 19, e1900245.	1.3	25
42	DNAproDB: an expanded database and web-based tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2019, 48, D277-D287.	6.5	41
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47	Targeting of copper-trafficking chaperones causes gene-specific systemic pathology in <i>Drosophila melanogaster</i> : prospective expansion of mutational landscapes that regulate tumor resistance to cisplatin. <i>Biology Open</i> , 2019, 8, .	0.6	6
48	Global gene expression analysis of <i>Escherichia coli</i> K-12 DH5 $\alpha$ after exposure to 2.4 GHz wireless fidelity radiation. <i>Scientific Reports</i> , 2019, 9, 14425.	1.6	15
49	The variability of SMCHD1 gene in FSHD patients: evidence of new mutations. <i>Human Molecular Genetics</i> , 2019, 28, 3912-3920.	1.4	9
50	Protein Preparation Automatic Protocol for High-Throughput Inverse Virtual Screening: Accelerating the Target Identification by Computational Methods. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4678-4690.	2.5	13
51	Human Papillomavirus Epitope Mimicry and Autoimmunity: The Molecular Truth of Peptide Sharing. <i>Pathobiology</i> , 2019, 86, 285-295.	1.9	24
52	Primary human chondrocytes respond to compression with phosphoproteomic signatures that include microtubule activation. <i>Journal of Biomechanics</i> , 2019, 97, 109367.	0.9	8
53	Local activity of comets: an indicator of non-uniform composition. <i>Monthly Notices of the Royal Astronomical Society</i> , 2019, 490, 2050-2055.	1.6	2
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58	CTCF-dependent chromatin boundaries formed by asymmetric nucleosome arrays with decreased linker length. <i>Nucleic Acids Research</i> , 2019, 47, 11181-11196.	6.5	44
59	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	6.5	126
60	Whole Genome Assembly of the Snout Otter Clam, <i>Lutraria rhynchaena</i> , Using Nanopore and Illumina Data, Benchmarked Against Bivalve Genome Assemblies. <i>Frontiers in Genetics</i> , 2019, 10, 1158.	1.1	16
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69	Characterization of Human Dosage-Sensitive Transcription Factor Genes. <i>Frontiers in Genetics</i> , 2019, 10, 1208.	1.1	8
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77	Yield of nextâ€”generation neuropathy gene panels in axonal neuropathies. <i>Journal of the Peripheral Nervous System</i> , 2019, 24, 324-329.	1.4	7
78	Analysis of Secondary Structure Biases in Naturally Presented HLA-I Ligands. <i>Frontiers in Immunology</i> , 2019, 10, 2731.	2.2	8
79	Effect of cysteine addition and heat treatment on the properties and microstructure of a calcium-induced whey protein cold-set gel. <i>Current Research in Food Science</i> , 2019, 1, 31-42.	2.7	15
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81	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
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89	Venom Diversity and Evolution in the Most Divergent Cone Snail Genus <i>Profundiconus</i> . <i>Toxins</i> , 2019, 11, 623.	1.5	16
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102	Transcriptomic analysis of <i>Macrobrachium rosenbergii</i> (giant fresh water prawn) post-larvae in response to <i>M. rosenbergii</i> nodavirus (MrNV) infection: de novo assembly and functional annotation. <i>BMC Genomics</i> , 2019, 20, 762.	1.2	23
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1867	AlnC: An extensive database of long non-coding RNAs in angiosperms. <i>PLoS ONE</i> , 2021, 16, e0247215.	1.1	16
1868	Analysis of temporal gene regulation of <i>Listeria monocytogenes</i> revealed distinct regulatory response modes after exposure to high pressure processing. <i>BMC Genomics</i> , 2021, 22, 266.	1.2	5
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1872	Web resources facilitate drug discovery in treatment of COVID-19. <i>Drug Discovery Today</i> , 2021, 26, 2358-2366.	3.2	4
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1879	Structural Determinants for the Mode of Action of Imidazopyridine DS2 at $\hat{\Gamma}$ -Containing $\hat{\Gamma}^3$ -Aminobutyric Acid Type A Receptors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4730-4743.	2.9	6
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1881	A community-supported metaproteomic pipeline for improving peptide identifications in hydrothermal vent microbiota. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
1882	A slowly cleaved viral signal peptide acts as a protein-integral immune evasion domain. <i>Nature Communications</i> , 2021, 12, 2061.	5.8	11
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1884	Dasatinib's SIK2 Binding Elucidated by Homology Modeling, Molecular Docking, and Dynamics Simulations. <i>ACS Omega</i> , 2021, 6, 11025-11038.	1.6	16
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1890	Label-free quantitative proteomics of <i>Sorghum bicolor</i> reveals the proteins strengthening plant defense against insect pest <i>Chilo partellus</i> . <i>Proteome Science</i> , 2021, 19, 6.	0.7	12
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1894	Master Blaster: an approach to sensitive identification of remotely related proteins. <i>Scientific Reports</i> , 2021, 11, 8746.	1.6	0
1900	Distinguishing Signal From Noise in Immunopeptidome Studies of Limiting-Abundance Biological Samples: Peptides Presented by I-Ab in C57BL/6 Mouse Thymus. <i>Frontiers in Immunology</i> , 2021, 12, 658601.	2.2	11

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1903	A data-driven, high-throughput methodology to determine tissue-specific differentially methylated regions able to discriminate body fluids. <i>Electrophoresis</i> , 2021, 42, 1168-1176.	1.3	4
1905	Bacteriophages against <i>Vibrio coralliilyticus</i> and <i>Vibrio tubiashii</i> : Isolation, Characterization, and Remediation of Larval Oyster Mortalities. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	13
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1908	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. <i>Nature Methods</i> , 2021, 18, 520-527.	9.0	32
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1910	Phylogenetic and Selection Analysis of an Expanded Family of Putatively Pore-Forming Jellyfish Toxins (Cnidaria: Medusozoa). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
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1915	Gene Expression Patterns for Proteins With Lectin Domains in Flax Stem Tissues Are Related to Deposition of Distinct Cell Wall Types. <i>Frontiers in Plant Science</i> , 2021, 12, 634594.	1.7	9
1916	Massive parallel sequencing in a family with rectal cancer. <i>Hereditary Cancer in Clinical Practice</i> , 2021, 19, 23.	0.6	3
1917	In silico validation of novel inhibitors of malarial aspartyl protease, plasmepsin V and antimalarial efficacy prediction. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 8352-8364.	2.0	1
1918	Mining Synergistic Microbial Interactions: A Roadmap on How to Integrate Multi-Omics Data. <i>Microorganisms</i> , 2021, 9, 840.	1.6	8
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1926	An Overview of Biological and Computational Methods for Designing Mechanism-Informed Anti-biofilm Agents. <i>Frontiers in Microbiology</i> , 2021, 12, 640787.	1.5	25
1927	Machine learning-based investigation of the cancer protein secretory pathway. <i>PLoS Computational Biology</i> , 2021, 17, e1008898.	1.5	7
1929	Proteome-Wide Analysis of Heat-Stress in <i>Pinus radiata</i> Somatic Embryos Reveals a Combined Response of Sugar Metabolism and Translational Regulation Mechanisms. <i>Frontiers in Plant Science</i> , 2021, 12, 631239.	1.7	15
1930	SH3BP4 promotes neuropilin-1 and $\beta$ 5-integrin endocytosis and is inhibited by Akt. <i>Developmental Cell</i> , 2021, 56, 1164-1181.e12.	3.1	7
1931	Nydomycin Inhibits both Fluoroquinolone-Sensitive and Fluoroquinolone-Resistant <i>Escherichia coli</i> DNA Gyrase. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	2
1932	Sputum Proteome Signatures of Mechanically Ventilated Intensive Care Unit Patients Distinguish Samples with or without Anti-pneumococcal Activity. <i>MSystems</i> , 2021, 6, .	1.7	4
1933	Cyanophage Diversity and Community Structure in Dead Zone Sediments. <i>MSphere</i> , 2021, 6, .	1.3	8
1934	Complete genome sequence of <i>Photobacterium ganghwense</i> C2.2: A new polyhydroxyalkanoate production candidate. <i>MicrobiologyOpen</i> , 2021, 10, e1182.	1.2	4
1935	Whole exome sequencing of a gut-associated lymphoid tissue neoplasm points to precursor or early form of sporadic colon carcinoma. <i>Pathology Research and Practice</i> , 2021, 220, 153406.	1.0	1
1937	Development of comprehensive two-dimensional low-flow liquid-chromatography setup coupled to high-resolution mass spectrometry for shotgun proteomics. <i>Analytica Chimica Acta</i> , 2021, 1156, 338349.	2.6	29
1938	A multi-targeting drug design strategy for identifying potent anti-SARS-CoV-2 inhibitors. <i>Acta Pharmacologica Sinica</i> , 2022, 43, 483-493.	2.8	43
1940	Integrating multi-scale neighbouring topologies and cross-modal similarities for drug-protein interaction prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
1941	Toward an Understanding of Pan-Assay Interference Compounds and Promiscuity: A Structural Perspective on Binding Modes. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2248-2262.	2.5	20
1942	Polymer-Protein Hybrid Network Involving Mucin: A Mineralized Biomimetic Template for Bone Tissue Engineering. <i>Macromolecular Bioscience</i> , 2021, 21, e2000381.	2.1	4
1943	Integrating site-specific peptide reporters and targeted mass spectrometry enables rapid substrate-specific kinase assay at the nanogram cell level. <i>Analytica Chimica Acta</i> , 2021, 1155, 338341.	2.6	2
1944	Familial Psychosis Associated With a Missense Mutation at MACF1 Gene Combined With the Rare Duplications DUP3p26.3 and DUP16q23.3, Affecting the CNTN6 and CDH13 Genes. <i>Frontiers in Genetics</i> , 2021, 12, 622886.	1.1	3

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1948	Detecting Protein Communities in Native Cell Extracts by Machine Learning: A Structural Biologist's Perspective. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 660542.	1.6	10
1950	Insights on the Evolutionary Genomics of the <i>Blautia</i> Genus: Potential New Species and Genetic Content Among Lineages. <i>Frontiers in Microbiology</i> , 2021, 12, 660920.	1.5	33
1951	Tissue-specific regulatory mechanism of lncRNAs and methylation in sheep adipose and muscle induced by <i>Allium mongolicum</i> Regel extracts. <i>Scientific Reports</i> , 2021, 11, 9186.	1.6	8
1952	Effects of pH on an IDP conformational ensemble explored by molecular dynamics simulation. <i>Biophysical Chemistry</i> , 2021, 271, 106552.	1.5	18
1953	A novel yeast hybrid modeling framework integrating Boolean and enzyme-constrained networks enables exploration of the interplay between signaling and metabolism. <i>PLoS Computational Biology</i> , 2021, 17, e1008891.	1.5	16
1954	HCN Channel Phosphorylation Sites Mapped by Mass Spectrometry in Human Epilepsy Patients and in an Animal Model of Temporal Lobe Epilepsy. <i>Neuroscience</i> , 2021, 460, 13-30.	1.1	9
1955	Obesity alters the ovarian proteomic response to zearalenone exposure. <i>Biology of Reproduction</i> , 2021, 105, 278-289.	1.2	14
1956	Characteristics of <i>fosA</i> -carrying plasmids in <i>E. coli</i> and <i>Klebsiella</i> spp. isolates originating from food and environmental samples. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2004-2011.	1.3	11
1957	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. <i>Biomolecules</i> , 2021, 11, 622.	1.8	18
1958	Summary Visualizations of Gene Ontology Terms With GO-Figure!. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	51
1959	Bacteria Make a Living Breathing the Nitroheterocyclic Insensitive Munitions Compound 3-Nitro-1,2,4-triazol-5-one (NTO). <i>Environmental Science &amp; Technology</i> , 2021, 55, 5806-5814.	4.6	12
1960	A combined RAD-Seq and WGS approach reveals the genomic basis of yellow color variation in bumble bee <i>Bombus terrestris</i> . <i>Scientific Reports</i> , 2021, 11, 7996.	1.6	7
1961	Substrate Selectivity of Coumarin Derivatives by Human CYP1 Enzymes: In Vitro Enzyme Kinetics and In Silico Modeling. <i>ACS Omega</i> , 2021, 6, 11286-11296.	1.6	8
1962	Revolutionizing enzyme engineering through artificial intelligence and machine learning. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 113-125.	1.1	21
1963	Coding and non-coding roles of MOCCI (C15ORF48) coordinate to regulate host inflammation and immunity. <i>Nature Communications</i> , 2021, 12, 2130.	5.8	56
1964	Comparative transcriptomics and network pharmacology analysis to identify the potential mechanism of celastrol against osteoarthritis. <i>Clinical Rheumatology</i> , 2021, 40, 4259-4268.	1.0	6
1965	The Human 2-Cys Peroxiredoxins form Widespread, Cysteine-Dependent- and Isoform-Specific Protein-Protein Interactions. <i>Antioxidants</i> , 2021, 10, 627.	2.2	22



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1967	Transcriptomic Profiles of CD47 in Breast Tumors Predict Outcome and Are Associated with Immune Activation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3836.	1.8	2
1968	Phylogenetic analysis of Harmonin homology domains. <i>BMC Bioinformatics</i> , 2021, 22, 190.	1.2	5
1969	Challenges of automation and scale: Bioinformatics and the evaluation of proteins to support genetically modified product safety assessments. <i>Journal of Invertebrate Pathology</i> , 2021, 186, 107587.	1.5	5
1970	Computer-Aided Drug Discovery Identifies Alkaloid Inhibitors of Parkinson's Disease Associated Protein, Prolyl Oligopeptidase. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-10.	0.5	3
1972	Copper mining bacteria: Converting toxic copper ions into a stable single-atom copper. <i>Science Advances</i> , 2021, 7, .	4.7	16
1973	Draft genome of a biparental beetle species, <i>Lethrus apterus</i> . <i>BMC Genomics</i> , 2021, 22, 301.	1.2	0
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1975	Biallelic variants in TMEM222 cause a new autosomal recessive neurodevelopmental disorder. <i>Genetics in Medicine</i> , 2021, 23, 1246-1254.	1.1	5
1977	Building Protein-Protein and Protein-Glycosaminoglycan Interaction Networks Using MatrixDB, the Extracellular Matrix Interaction Database. <i>Current Protocols</i> , 2021, 1, e47.	1.3	9
1979	DPP9: Comprehensive In Silico Analyses of Loss of Function Gene Variants and Associated Gene Expression Signatures in Human Hepatocellular Carcinoma. <i>Cancers</i> , 2021, 13, 1637.	1.7	9
1980	An extended catalogue of tandem alternative splice sites in human tissue transcriptomes. <i>PLoS Computational Biology</i> , 2021, 17, e1008329.	1.5	7
1981	Serpins in cartilage and osteoarthritis: what do we know?. <i>Biochemical Society Transactions</i> , 2021, 49, 1013-1026.	1.6	15
1982	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. <i>Journal of Molecular Biology</i> , 2021, 433, 166900.	2.0	8
1983	Retrospective Use of Whole-Genome Sequencing Expands the Multicountry Outbreak Cluster of <i>Listeria monocytogenes</i> ST1247. <i>International Journal of Genomics</i> , 2021, 2021, 1-5.	0.8	6
1984	Whole-exome sequencing with targeted analysis and epilepsy after acute symptomatic neonatal seizures. <i>Pediatric Research</i> , 2021, , .	1.1	6
1985	Proteome Regulation Patterns Determine <i>Escherichia coli</i> Wild-Type and Mutant Phenotypes. <i>MSystems</i> , 2021, 6, .	1.7	6
1986	Comparative analysis of <sup>13</sup> C chemical shifts of $\beta$ -sheet amyloid proteins and outer membrane proteins. <i>Journal of Biomolecular NMR</i> , 2021, 75, 151-166.	1.6	2

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1989	Mechanisms of Congenital Heart Disease Caused by NAA15 Haploinsufficiency. Circulation Research, 2021, 128, 1156-1169.	2.0	27
1992	Hypoxia exerts oxidative stress and changes in expression of antioxidant enzyme genes in gills of <i>Mytilus galloprovincialis</i> (Lamarck, 1819). Marine Biology Research, 2021, 17, 369-379.	0.3	6
1993	Cell Wall Layer Induced in Xylem Fibers of Flax Upon Gravistimulation Is Similar to Constitutively Formed Cell Walls of Bast Fibers. Frontiers in Plant Science, 2021, 12, 660375.	1.7	15
1994	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . Science, 2021, 372, .	6.0	91
1995	Abundance Imparts Evolutionary Constraints of Similar Magnitude on the Buried, Surface, and Disordered Regions of Proteins. Frontiers in Molecular Biosciences, 2021, 8, 626729.	1.6	4
1996	The dystrophin myotonia WD repeat-containing protein DMWD and WDR20 differentially regulate USP12 deubiquitinase. FEBS Journal, 2021, 288, 5943-5963.	2.2	1
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2000	Subcellular proteomics. Nature Reviews Methods Primers, 2021, 1, .	11.8	159
2003	CladeOScope: functional interactions through the prism of clade-wise co-evolution. NAR Genomics and Bioinformatics, 2021, 3, lqab024.	1.5	19
2004	Transcriptome of weeping pinyon pine, <i>Pinus pinceana</i> , shows differences across heterogeneous habitats. Trees - Structure and Function, 2021, 35, 1351-1365.	0.9	4
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2007	The evaluation of the antidiabetic effects of red wine polyphenols with the view of in silico prediction methods. Food Bioscience, 2021, 40, 100920.	2.0	6
2008	MolluscDB: a genome and transcriptome database for molluscs. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200157.	1.8	17
2009	Identifying potential drug targets and candidate drugs for COVID-19: biological networks and structural modeling approaches. F1000Research, 0, 10, 127.	0.8	10
2010	Data set of competitive and allosteric protein kinase inhibitors confirmed by X-ray crystallography. Data in Brief, 2021, 35, 106816.	0.5	4

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2012	Identification of a Chlorovirus PBCV-1 Protein Involved in Degrading the Host Cell Wall during Virus Infection. <i>Viruses</i> , 2021, 13, 782.	1.5	10
2013	Meta-analysis of QTLome for grain zinc and iron contents in wheat ( <i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2021, 217, 1.	0.6	25
2014	Resourcing, annotating, and analysing synthetic peptides of SARS-CoV-2 for immunopeptidomics and other immunological studies. <i>Proteomics</i> , 2021, 21, e2100036.	1.3	7
2015	Next generation sequencing approaches to evaluate water and wastewater quality. <i>Water Research</i> , 2021, 194, 116907.	5.3	62
2016	Expasy, the Swiss Bioinformatics Resource Portal, as designed by its users. <i>Nucleic Acids Research</i> , 2021, 49, W216-W227.	6.5	333
2018	Characterization of Extracellular Vesicles Secreted in Lentiviral Producing HEK293SF Cell Cultures. <i>Viruses</i> , 2021, 13, 797.	1.5	9
2020	Structural Profiling of Bacterial Effectors Reveals Enrichment of Host-Interacting Domains and Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 626600.	1.6	4
2021	ProteoSushi: A Software Tool to Biologically Annotate and Quantify Modification-Specific, Peptide-Centric Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 3621-3628.	1.8	6
2022	Based on Network Pharmacology and Molecular Docking to Explore the Underlying Mechanism of Huangqi Gegen Decoction for Treating Diabetic Nephropathy. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-14.	0.5	9
2023	BetAware-Deep: An Accurate Web Server for Discrimination and Topology Prediction of Prokaryotic Transmembrane $\beta$ -barrel Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 166729.	2.0	13
2024	Using an Ensemble to Identify and Classify Macroalgae Antimicrobial Peptides. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 321-333.	2.2	4
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2026	Proline codon pair selection determines ribosome pausing strength and translation efficiency in bacteria. <i>Communications Biology</i> , 2021, 4, 589.	2.0	13
2027	Skeletal and molecular findings in 51 Cleidocranial dysplasia patients from Turkey. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 2488-2495.	0.7	8
2028	Insulin-induced conformational changes in the full-length insulin receptor: structural insights gained from molecular modeling analyses. <i>Acta Biochimica Et Biophysica Sinica</i> , 2021, 53, 848-869.	0.9	2
2030	Pretraining model for biological sequence data. <i>Briefings in Functional Genomics</i> , 2021, 20, 181-195.	1.3	16
2031	Characterization of the Cerebrospinal Fluid Proteome in Patients with Fragile X-Associated Tremor/Ataxia Syndrome. <i>Cerebellum</i> , 2022, 21, 86-98.	1.4	5

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2033	Transcriptome of different fruiting stages in the cultivated mushroom <i>Cyclocybe aegerita</i> suggests a complex regulation of fruiting and reveals enzymes putatively involved in fungal oxylipin biosynthesis. <i>BMC Genomics</i> , 2021, 22, 324.	1.2	21
2034	Systems Pharmacology and In Silico Docking Analysis Uncover Association of CA2, PPARC, RXRA, and VDR with the Mechanisms Underlying the Shi Zhen Tea Formula Effect on Eczema. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	1
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