OMIM.org: Online Mendelian Inheritance in Man (OMIM genes and genetic disorders

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Citation Report

#	Article	IF	Citations
1	Genomic Imprinting and Human Reproduction. , 2014, , .		0
2	Emerging novel concept of chaperone therapies for protein misfolding diseases. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2014, 90, 145-162.	1.6	55
3	PhenomeCentral: A Portal for Phenotypic and Genotypic Matchmaking of Patients with Rare Genetic Diseases. Human Mutation, 2015, 36, 931-940.	1.1	107
4	The Genomic Birthday Paradox: How Much Is Enough?. Human Mutation, 2015, 36, 989-997.	1.1	13
5	Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. Human Mutation, 2015, 36, 979-984.	1.1	36
6	The mouse gene expression database: New features and how to use them effectively. Genesis, 2015, 53, 510-522.	0.8	14
7	Evidence of Mitochondrial Dysfunction within the Complex Genetic Etiology of Schizophrenia. Molecular Neuropsychiatry, 2015, 1, 201-219.	3.0	74
8	A functional module-based exploration between inflammation and cancer in esophagus. Scientific Reports, 2015, 5, 15340.	1.6	3
9	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. Scientific Reports, 2015, 5, 17201.	1.6	43
10	FlyNet: a versatile network prioritization server for theDrosophilacommunity. Nucleic Acids Research, 2015, 43, W91-W97.	6.5	18
11	Functional and Structural Consequence of Rare Exonic Single Nucleotide Polymorphisms: One Story, Two Tales. Genome Biology and Evolution, 2015, 7, 2929-2940.	1.1	12
12	Dintor: functional annotation of genomic and proteomic data. BMC Genomics, 2015, 16, 1081.	1.2	10
13	Phenotype-driven strategies for exome prioritization of human Mendelian disease genes. Genome Medicine, 2015, 7, 81.	3.6	97
14	DDA: A Novel Network-Based Scoring Method to Identify Disease-Disease Associations. Bioinformatics and Biology Insights, 2015, 9, BBI.S35237.	1.0	27
15	Using Gene Essentiality and Synthetic Lethality Information to Correct Yeast and CHO Cell Genome-Scale Models. Metabolites, 2015, 5, 536-570.	1.3	31
16	Dissecting the Genetic Basis of a Complex cis-Regulatory Adaptation. PLoS Genetics, 2015, 11, e1005751.	1.5	30
17	How to Use SNP_TATA_Comparator to Find a Significant Change in Gene Expression Caused by the Regulatory SNP of This Geneâ€™s Promoter via a Change in Affinity of the TATA-Binding Protein for This Promoter. BioMed Research International, 2015, 2015, 1-17.	0.9	34
18	Human Genes Encoding Transcription Factors and Chromatin-Modifying Proteins Have Low Levels of Promoter Polymorphism: A Study of 1000 Genomes Project Data. International Journal of Genomics, 2015, 2015, 1-15.	0.8	13

#	Article	IF	Citations
19	Transgenerational inheritance of metabolic disease. Seminars in Cell and Developmental Biology, 2015, 43, 131-140.	2.3	51
20	Integrating ontologies of rare diseases and radiological diagnosis. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1164-1168.	2.2	8
21	The 2015 Nucleic Acids Research Database Issue and Molecular Biology Database Collection. Nucleic Acids Research, 2015, 43, D1-D5.	6.5	79
22	Facilitating Collaboration in Rare Genetic Disorders Through Effective Matchmaking in DECIPHER. Human Mutation, 2015, 36, 941-949.	1.1	38
23	Capturing phenotypes for precision medicine. Journal of Physical Education and Sports Management, 2015, 1, a000372.	0.5	32
24	Next-generation diagnostics and disease-gene discovery with the Exomiser. Nature Protocols, 2015, 10, 2004-2015.	5.5	296
25	A Call for Systematic Research on Solute Carriers. Cell, 2015, 162, 478-487.	13.5	457
26	Formation and Malformation of Cardiac Trabeculae: Biological Basis, Clinical Significance, and Special Yield of Magnetic Resonance Imaging in Assessment. Canadian Journal of Cardiology, 2015, 31, 1325-1337.	0.8	28
27	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
28	Receptor tyrosine kinase mutations in developmental syndromes and cancer: two sides of the same coin. Human Molecular Genetics, 2015, 24, R60-R66.	1.4	70
29	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. American Journal of Human Genetics, 2015, 97, 199-215.	2.6	574
30	Vinculin networkâ€“mediated cytoskeletal remodeling regulates contractile function in the aging heart. Science Translational Medicine, 2015, 7, 292ra99.	5.8	81
31	Principles for the organization of gene-sets. Computational Biology and Chemistry, 2015, 59, 139-149.	1.1	10
32	Mechanical Properties and Failure of Biopolymers: Atomistic Reactions to Macroscale Response. Topics in Current Chemistry, 2015, 369, 317-343.	4.0	14
33	Emerging molecular networks common in ionizing radiation, immune and inflammatory responses by employing bioinformatics approaches. Cancer Letters, 2015, 368, 164-172.	3.2	60
34	A look behind the scenes: the risk and pathogenesis of primary osteoporosis. Nature Reviews Rheumatology, 2015, 11, 462-474.	3.5	204
35	Rare diseases in ICD11: making rare diseases visible in health information systems through appropriate coding. Orphanet Journal of Rare Diseases, 2015, 10, 35.	1.2	95
36	Whole-exome sequencing as a diagnostic tool: current challenges and future opportunities. Expert Review of Molecular Diagnostics, 2015, 15, 749-760.	1.5	62

#	Article	IF	Citations
37	GXD: a community resource of mouse Gene Expression Data. Mammalian Genome, 2015, 26, 314-324.	1.0	23
38	Biological Databases for Human Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 55-63.	3.0	84
39	Neuroimaging experience in pediatric Horner syndrome. Pediatric Radiology, 2015, 45, 1535-1543.	1.1	19
40	The Disease Ontology: fostering interoperability between biological and clinical human disease-related data. Mammalian Genome, 2015, 26, 584-589.	1.0	60
41	Disease insights through cross-species phenotype comparisons. Mammalian Genome, 2015, 26, 548-555.	1.0	19
42	The 2015 IUIS Phenotypic Classification for Primary Immunodeficiencies. Journal of Clinical Immunology, 2015, 35, 727-738.	2.0	199
43	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2015, 43, W128-W133.	6.5	60
44	Bioinformatic resources for the investigation of proteins and proteomes. Peptidomics, 2016, 2, .	0.3	1
45	HEDD: the human epigenetic drug database. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw159.	1.4	44
46	A network pharmacology approach to discover active compounds and action mechanisms of San-Cao Granule for treatment of liver fibrosis. Drug Design, Development and Therapy, 2016, 10, 733.	2.0	27
47	Candidate SNP Markers of Chronopathologies Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. BioMed Research International, 2016, 2016, 1-21.	0.9	21
48	Integrated Approaches to Drug Discovery for Oxidative Stress-Related Retinal Diseases. Oxidative Medicine and Cellular Longevity, 2016, 2016, 1-9.	1.9	12
49	Candidate SNP Markers of Gender-Biased Autoimmune Complications of Monogenic Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Immunology, 2016, 7, 130.	2.2	17
50	Cross-Species Integrative Functional Genomics in GeneWeaver Reveals a Role for Pafah1b1 in Altered Response to Alcohol. Frontiers in Behavioral Neuroscience, 2016, 10, 1.	1.0	123
52	Fusing literature and full network data improves disease similarity computation. BMC Bioinformatics, 2016, 17, 326.	1.2	16
53	A Multi-scale Computational Platform to Mechanistically Assess the Effect of Genetic Variation on Drug Responses in Human Erythrocyte Metabolism. PLoS Computational Biology, 2016, 12, e1005039.	1.5	12
54	Text Mining Genotype-Phenotype Relationships from Biomedical Literature for Database Curation and Precision Medicine. PLoS Computational Biology, 2016, 12, e1005017.	1.5	81
55	BLAT2DOLite: An Online System for Identifying Significant Relationships between Genetic Sequences and Diseases. PLoS ONE, 2016, 11, e0157274.	1.1	2

#	Article	IF	Citations
56	LSDBs and How They Have Evolved. Human Mutation, 2016, 37, 532-539.	1.1	6
57	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	3.8	89
58	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
59	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	6.5	308
60	Rapid Communication: Cholesterol deficiencyâ€“associated APOB mutation impacts lipid metabolism in Holstein calves and breeding bulls1. Journal of Animal Science, 2016, 94, 1761-1766.	0.2	18
61	A compendium of human genes regulating feeding behavior and body weight, its functional characterization and identification of GWAS genes involved in brain-specific PPI network. BMC Genetics, 2016, 17, 158.	2.7	15
62	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. BMC Bioinformatics, 2016, 17, 441.	1.2	20
63	Exploring FlyBase Data Using QuickSearch. Current Protocols in Bioinformatics, 2016, 56, 1.31.1-1.31.23.	25.8	6
64	Alternate-locus aware variant calling in whole genome sequencing. Genome Medicine, 2016, 8, 130.	3.6	16
65	Identification of critical paralog groups with indispensable roles in the regulation of signaling flow. Scientific Reports, 2016, 6, 38588.	1.6	8
66	Toward the next step in G protein-coupled receptor research: a knowledge-driven analysis for the next potential targets in drug discovery. Journal of Structural and Functional Genomics, 2016, 17, 111-133.	1.2	4
67	Robust Inductive Matrix Completion strategy to explore associations between lincRNAs and human disease phenotypes. , 2016, , .		0
68	UMDâ€Predictor: A Highâ€Throughput Sequencing Compliant System for Pathogenicity Prediction of any Human cDNA Substitution. Human Mutation, 2016, 37, 439-446.	1.1	104
69	Target-enrichment sequencing and copy number evaluation in inherited polyneuropathy. Neurology, 2016, 86, 1762-1771.	1.5	52
70	A flexible method for estimating the fraction of fitness influencing mutations from large sequencing data sets. Genome Research, 2016, 26, 834-843.	2.4	10
71	Copa Syndrome: a Novel Autosomal Dominant Immune Dysregulatory Disease. Journal of Clinical Immunology, 2016, 36, 377-387.	2.0	141
72	MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. Nucleic Acids Research, 2016, 44, D848-D854.	6.5	40
73	Prediction of key genes in ovarian cancer treated with decitabine based on network strategy. Oncology Reports, 2016, 35, 3548-3558.	1.2	5

#	Article	IF	Citations
74	A Clinicianâ€™s perspective on clinical exome sequencing. Human Genetics, 2016, 135, 643-654.	1.8	33
75	How to Identify Pathogenic Mutations among All Those Variations: Variant Annotation and Filtration in the Genome Sequencing Era. Human Mutation, 2016, 37, 1272-1282.	1.1	28
76	Optimization of cell lines as tumour models by integrating multi-omics data. Briefings in Bioinformatics, 2016, 18, bbw082.	3.2	14
77	Function-driven discovery of disease genes in zebrafish using an integrated genomics big data resource. Nucleic Acids Research, 2016, 44, gkw897.	6.5	24
79	Genetics of enteric neuropathies. Developmental Biology, 2016, 417, 198-208.	0.9	44
80	Gene set analysis for interpreting genetic studies. Human Molecular Genetics, 2016, 25, R133-R140.	1.4	12
81	Data and programs in support of network analysis of genes and their association with diseases. Data in Brief, 2016, 8, 1036-1039.	0.5	3
82	Opportunities and technical challenges in next-generation sequencing for diagnosis of rare pediatric diseases. Expert Review of Molecular Diagnostics, 2016, 16, 1073-1082.	1.5	20
83	The Qatar genome: a population-specific tool for precision medicine in the Middle East. Human Genome Variation, 2016, 3, 16016.	0.4	103
84	Mutational patterns in oncogenes and tumour suppressors. Biochemical Society Transactions, 2016, 44, 925-931.	1.6	16
85	Protein function in precision medicine: deep understanding with machine learning. FEBS Letters, 2016, 590, 2327-2341.	1.3	43
86	Structural Chromosomal Rearrangements Require Nucleotide-Level Resolution: Lessons from Next-Generation Sequencing in Prenatal Diagnosis. American Journal of Human Genetics, 2016, 99, 1015-1033.	2.6	53
87	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	5.8	68
88	BATMAN-TCM: a Bioinformatics Analysis Tool for Molecular mechANism of Traditional Chinese Medicine. Scientific Reports, 2016, 6, 21146.	1.6	530
89	To Unveil the Molecular Mechanisms of Qi and Blood through Systems Biology-Based Investigation into Si-Jun-Zi-Tang and Si-Wu-Tang formulae. Scientific Reports, 2016, 6, 34328.	1.6	24
90	Lessons learned from the search for genes responsible for rare Mendelian disorders. Molecular Genetics & Genomic Medicine, 2016, 4, 371-375.	0.6	7
91	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw100.	1.4	1,085
92	The Chinchilla Research Resource Database: resource for an otolaryngology disease model. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw073.	1.4	20

#	Article	IF	Citations
93	Network analysis of genes and their association with diseases. Gene, 2016, 590, 68-78.	1.0	31
94	Weighted mutual information analysis substantially improves domain-based functional network models. Bioinformatics, 2016, 32, 2824-2830.	1.8	20
95	StructMAn: annotation of single-nucleotide polymorphisms in the structural context. Nucleic Acids Research, 2016, 44, W463-W468.	6.5	32
96	g:Profilerâ€"a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	6.5	1,179
97	Inference of domain-disease associations from domain-protein, protein-disease and disease-disease relationships. BMC Systems Biology, 2016, 10, 4.	3.0	16
98	A novel mutation in CELSR1 is associated with hereditary lymphedema. Vascular Cell, 2016, 8, 1.	0.2	38
99	Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. Journal of Biomedical Semantics, 2016, 7, 8.	0.9	28
100	The Somatic Nature of Cancer Allows It to Affect Highly Constrained Genes. Genome Biology and Evolution, 2016, 8, 1614-1620.	1.1	3
101	The UniProtKB guide to the human proteome. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav120.	1.4	130
102	Identifying network-based biomarkers of complex diseases from high-throughput data. Biomarkers in Medicine, 2016, 10, 633-650.	0.6	35
103	Lynx: a knowledge base and an analytical workbench for integrative medicine. Nucleic Acids Research, 2016, 44, D882-D887.	6.5	8
104	Integrated Genomic and Network-Based Analyses of Complex Diseases and Human Disease Network. Journal of Genetics and Genomics, 2016, 43, 349-367.	1.7	21
105	SEA: a super-enhancer archive. Nucleic Acids Research, 2016, 44, D172-D179.	6.5	88
106	MitoMiner v3.1, an update on the mitochondrial proteomics database. Nucleic Acids Research, 2016, 44, D1258-D1261.	6.5	182
107	DIDA: A curated and annotated digenic diseases database. Nucleic Acids Research, 2016, 44, D900-D907.	6.5	84
108	PCOSKB: A KnowledgeBase on genes, diseases, ontology terms and biochemical pathways associated with PolyCystic Ovary Syndrome. Nucleic Acids Research, 2016, 44, D1032-D1035.	6.5	46
109	ClinVar: public archive of interpretations of clinically relevant variants. Nucleic Acids Research, 2016, 44, D862-D868.	6.5	2,198
110	Rare disease relations through common genes and protein interactions. Molecular and Cellular Probes, 2016, 30, 178-181.	0.9	4

#	Article	IF	Citations
111	Transitive closure of subsumption and causal relations in a large ontology of radiological diagnosis. Journal of Biomedical Informatics, 2016, 61, 27-33.	2.5	8
112	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. American Journal of Human Genetics, 2016, 98, 744-754.	2.6	146
113	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. Nucleic Acids Research, 2016, 44, D555-D559.	6.5	30
114	WormBase 2016: expanding to enable helminth genomic research. Nucleic Acids Research, 2016, 44, D774-D780.	6.5	329
115	dbPTM 2016: 10-year anniversary of a resource for post-translational modification of proteins. Nucleic Acids Research, 2016, 44, D435-D446.	6.5	154
116	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
117	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
118	Integrating 400 million variants from 80,000 human samples with extensive annotations: towards a knowledge base to analyze disease cohorts. BMC Bioinformatics, 2016, 17, 24.	1.2	13
119	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	6.5	184
120	Dynamic software design for clinical exome and genome analyses: insights from bioinformaticians, clinical geneticists, and genetic counselors. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 257-268.	2.2	9
121	On the Analysis of Diseases and Their Related Geographical Data. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 228-237.	3.9	17
122	Genomics pipelines and data integration: challenges and opportunities in the research setting. Expert Review of Molecular Diagnostics, 2017, 17, 225-237.	1.5	54
123	RNF43 germline and somatic mutation in serrated neoplasia pathway and its association with BRAF mutation. Gut, 2017, 66, 1645-1656.	6.1	157
124	The Human Phenotype Ontology in 2017. Nucleic Acids Research, 2017, 45, D865-D876.	6.5	699
125	The 24th annualNucleic Acids Researchdatabase issue: a look back and upcoming changes. Nucleic Acids Research, 2017, 45, D1-D11.	6.5	144
126	Global Prioritizing Disease Candidate lncRNAs via a Multi-level Composite Network. Scientific Reports, 2017, 7, 39516.	1.6	47
127	MalaCards: an amalgamated human disease compendium with diverse clinical and genetic annotation and structured search. Nucleic Acids Research, 2017, 45, D877-D887.	6.5	398
128	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. Nature Genetics, 2017, 49, 387-394.	9.4	147

#	Article	IF	Citations
129	â€˜IRDiRC Recognized Resourcesâ€™: a new mechanism to support scientists to conduct efficient, high-quality research for rare diseases. European Journal of Human Genetics, 2017, 25, 162-165.	1.4	30
130	ChiTaRS-3.1â€”the enhanced chimeric transcripts and RNA-seq database matched with proteinâ€“protein interactions. Nucleic Acids Research, 2017, 45, D790-D795.	6.5	44
131	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	1.2	46
132	Annotating Mutational Effects on Proteins and Protein Interactions: Designing Novel and Revisiting Existing Protocols. Methods in Molecular Biology, 2017, 1550, 235-260.	0.4	18
133	Neurology Individualized Medicine: When to Use Next-Generation Sequencing Panels. Mayo Clinic Proceedings, 2017, 92, 292-305.	1.4	55
134	Genome-wide predicting disease-related protein complexes by walking on the heterogeneous network based on data integration and laplacian normalization. Computational Biology and Chemistry, 2017, 69, 41-47.	1.1	3
135	Interactome-based approaches to human disease. Current Opinion in Systems Biology, 2017, 3, 88-94.	1.3	77
136	Harnessing public domain data to discover and validate therapeutic targets. Expert Opinion on Drug Discovery, 2017, 12, 687-693.	2.5	6
137	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. American Journal of Human Genetics, 2017, 100, 843-853.	2.6	181
138	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	2.6	305
139	CLINICAL PROGRESS IN INHERITED RETINAL DEGENERATIONS. Retina, 2017, 37, 417-423.	1.0	51
140	Network-Based Gene Function Prediction in Mouse and Other Model Vertebrates Using MouseNet Server. Methods in Molecular Biology, 2017, 1611, 183-198.	0.4	3
141	Discovering relationships between nuclear receptor signaling pathways, genes, and tissues in Transcriptomine. Science Signaling, 2017, 10, .	1.6	35
142	Large differences in proportions of harmful and benign amino acid substitutions between proteins and diseases. Human Mutation, 2017, 38, 839-848.	1.1	17
143	Protein Function Prediction. Methods in Molecular Biology, 2017, , .	0.4	15
144	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
145	Cancer Cytogenetics. Methods in Molecular Biology, 2017, , .	0.4	4
146	Cytogenetic Resources and Information. Methods in Molecular Biology, 2017, 1541, 311-331.	0.4	1

#	Article	IF	Citations
147	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
148	GeMSTONE: orchestrated prioritization of human germline mutations in the cloud. Nucleic Acids Research, 2017, 45, W207-W214.	6.5	2
149	Integration of over 9,000 mass spectrometry experiments builds a global map of human proteinÂcomplexes. Molecular Systems Biology, 2017, 13, 932.	3.2	177
150	Genomic databases: A WHO affair. Science, 2017, 356, 812-813.	6.0	5
151	Identification of active components in Yixinshu Capsule with protective effects against myocardial dysfunction on human induced pluripotent stem cell-derived cardiomyocytes by an integrative approach. Molecular BioSystems, 2017, 13, 1469-1480.	2.9	23
152	Clinical sequencing using a nextâ€generation sequencingâ€based multiplex gene assay in patients with advanced solid tumors. Cancer Science, 2017, 108, 1440-1446.	1.7	57
153	Sources of discordance among germ-line variant classifications in ClinVar. Genetics in Medicine, 2017, 19, 1118-1126.	1.1	88
154	FlyBase at 25: looking to the future. Nucleic Acids Research, 2017, 45, D663-D671.	6.5	563
155	Remodeling adipose tissue through in silico modulation of fat storage for the prevention of type 2 diabetes. BMC Systems Biology, 2017, 11, 60.	3.0	6
156	Meta-analysis of host response networks identifies a common core in tuberculosis. Npj Systems Biology and Applications, 2017, 3, 4.	1.4	55
157	Bioinformatic resources for the investigation of proteins and proteomes. Peptidomics, 2017, 3, 1-10.	0.3	2
158	Pathogenic variants in the healthy elderly: unique ethical and practical challenges. Journal of Medical Ethics, 2017, 43, 714-722.	1.0	10
159	The Human Gene Mutation Database: towards a comprehensive repository of inherited mutation data for medical research, genetic diagnosis and next-generation sequencing studies. Human Genetics, 2017, 136, 665-677.	1.8	1,106
160	In silico analysis of nonsynonymous single nucleotide polymorphisms of the human adiponectin receptor 2 (ADIPOR2) gene. Computational Biology and Chemistry, 2017, 68, 175-185.	1.1	20
161	Network analysis reveals crosstalk between autophagy genes and disease genes. Scientific Reports, 2017, 7, 44391.	1.6	5
162	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
163	Network-Based Approach to Identify Potential Targets and Drugs that Promote Neuroprotection and Neurorepair in Acute Ischemic Stroke. Scientific Reports, 2017, 7, 40137.	1.6	38
164	DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. Nucleic Acids Research, 2017, 45, D833-D839.	6.5	1,865

#	Article	IF	Citations
165	The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic Acids Research, 2017, 45, D712-D722.	6.5	306
166	The STRING database in 2017: quality-controlled proteinâ€“protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	6.5	6,303
167	A comprehensive global genotypeâ€“phenotype database for rare diseases. Molecular Genetics & Genomic Medicine, 2017, 5, 66-75.	0.6	57
168	Gene discovery in amyotrophic lateral sclerosis: implications for clinical management. Nature Reviews Neurology, 2017, 13, 96-104.	4.9	245
169	Identification of susceptible genes for complex chronic diseases based on disease risk functional SNPs and interaction networks. Journal of Biomedical Informatics, 2017, 74, 137-144.	2.5	6
170	Quantitative and Systems Pharmacology. 1. In Silico Prediction of Drugâ€“Target Interactions of Natural Products Enables New Targeted Cancer Therapy. Journal of Chemical Information and Modeling, 2017, 57, 2657-2671.	2.5	76
171	A Problem-Driven Approach for Building a Bioinformatics GraphDB. Lecture Notes in Computer Science, 2017, , 134-144.	1.0	0
172	Mouse Genome Informatics (MGI) Resource: Genetic, Genomic, and Biological Knowledgebase for the Laboratory Mouse. ILAR Journal, 2017, 58, 17-41.	1.8	77
173	Zebrafish Models of Human Disease: Gaining Insight into Human Disease at ZFIN. ILAR Journal, 2017, 58, 4-16.	1.8	117
174	An Integrated Patient Genomic Information Management and Analysis System for Healthcare Professionals. , 2017, , .		1
175	Decoding disease-causing mechanisms of missense mutations from supramolecular structures. Scientific Reports, 2017, 7, 8541.	1.6	26
176	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	1.6	44
177	MRC Centre Neuromuscular Biobank (Newcastle and London): Supporting and facilitating rare and neuromuscular disease research worldwide. Neuromuscular Disorders, 2017, 27, 1054-1064.	0.3	15
178	The transformative potential of an integrative approach to pregnancy. Placenta, 2017, 57, 204-215.	0.7	12
179	Settling the score: variant prioritization and Mendelian disease. Nature Reviews Genetics, 2017, 18, 599-612.	7.7	213
180	From Peas to Disease: Modifier Genes, Network Resilience, and the Genetics of Health. American Journal of Human Genetics, 2017, 101, 177-191.	2.6	108
181	Intellectual Disability & Rare Disorders: A Diagnostic Challenge. Advances in Experimental Medicine and Biology, 2017, 1031, 39-54.	0.8	27
182	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. Advances in Experimental Medicine and Biology, 2017, 1031, 55-94.	0.8	20

#	Article	IF	Citations
183	Functional mapping and annotation of genetic associations with FUMA. Nature Communications, 2017, 8, 1826.	5.8	2,400
184	Functional germline variants as potential co-oncogenes. Npj Breast Cancer, 2017, 3, 46.	2.3	14
185	Network pharmacology exploration reveals endothelial inflammation as a common mechanism for stroke and coronary artery disease treatment of Danhong injection. Scientific Reports, 2017, 7, 15427.	1.6	84
186	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	5.8	200
187	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
188	Searching Online Mendelian Inheritance in Man (OMIM): A Knowledgebase of Human Genes and Genetic Phenotypes. Current Protocols in Bioinformatics, 2017, 58, 1.2.1-1.2.12.	25.8	378
189	A new era in the interpretation of human genomic variation. Genetics in Medicine, 2017, 19, 1092-1095.	1.1	34
190	Soft Sweeps Are the Dominant Mode of Adaptation in the Human Genome. Molecular Biology and Evolution, 2017, 34, 1863-1877.	3.5	164
191	brain-coX: investigating and visualising gene co-expression in seven human brain transcriptomic datasets. Genome Medicine, 2017, 9, 55.	3.6	13
192	The integration of weighted human gene association networks based on link prediction. BMC Systems Biology, 2017, 11, 12.	3.0	5
193	Accurate and equitable medical genomic analysis requires an understanding of demography and its influence on sample size and ratio. Genome Biology, 2017, 18, 42.	3.8	3
194	GLADIATOR: a global approach for elucidating disease modules. Genome Medicine, 2017, 9, 48.	3.6	23
195	Geneticization in MIM/OMIMÂ®? Exploring Historic and Epistemic Drivers of Contemporary Understandings of Genetic Disease. Journal of Medicine and Philosophy, 2017, 42, 367-384.	0.4	2
196	The Gene Ontology Handbook. Methods in Molecular Biology, 2017, , .	0.4	63
197	The Comparative Toxicogenomics Database: update 2017. Nucleic Acids Research, 2017, 45, D972-D978.	6.5	526
198	Next Generation Sequencing for Next Generation Diagnostics and Therapy. , 2017, , 87-102.		0
199	Drug repurposing by integrated literature mining and drugâ€“geneâ€“disease triangulation. Drug Discovery Today, 2017, 22, 615-619.	3.2	45
200	Integrated Transcriptome Map Highlights Structural and Functional Aspects of the Normal Human Heart. Journal of Cellular Physiology, 2017, 232, 759-770.	2.0	28

#	Article	IF	Citations
201	Computational analysis unravels novel destructive single nucleotide polymorphisms in the non-synonymous region of human caveolin gene. Gene Reports, 2017, 6, 142-157.	0.4	7
202	POSTAR: a platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. Nucleic Acids Research, 2017, 45, D104-D114.	6.5	115
203	Systematic reanalysis of clinical exome data yields additional diagnoses: implications for providers. Genetics in Medicine, 2017, 19, 209-214.	1.1	261
204	CeNDR, theCaenorhabditis elegansnatural diversity resource. Nucleic Acids Research, 2017, 45, D650-D657.	6.5	287
205	Mining cross-ontology weighted association rules between GO and HPO. , 2017, , .		0
206	Candidate SNP markers of social dominance, which may affect the affinity of the TATA-binding protein for human gene promoters. Russian Journal of Genetics: Applied Research, 2017, 7, 523-537.	0.4	12
207	dbSAP: single amino-acid polymorphism database for protein variation detection. Nucleic Acids Research, 2017, 45, D827-D832.	6.5	27
208	Excessive burden of lysosomal storage disorder gene variants in Parkinsonâ€™s disease. Brain, 2017, 140, 3191-3203.	3.7	323
209	HereditÃre Hauterkrankungen â€•Klinisch und genetisch heterogen. JDDG - Journal of the German Society of Dermatology, 2017, 15, 881-882.	0.4	5
210	Stable solution to l 2,1-based robust inductive matrix completion and its application in linking long noncoding RNAs to human diseases. BMC Medical Genomics, 2017, 10, 77.	0.7	0
211	Functional protein networks underlying the comorbidity of gout and hyperuricemia. , 2017, , .		0
212	Identification of potential cancer-related pseudogenes in lung adenocarcinoma based on ceRNA hypothesis. Oncotarget, 2017, 8, 59036-59047.	0.8	21
213	Access to medicines: the plot thickens in 24 Season 2 (Indian series). Journal of Intellectual Property Law and Practice, 2017, 12, 619-620.	0.2	0
214	Enhancing the Promise of Drug Repositioning through Genetics. Frontiers in Pharmacology, 2017, 8, 896.	1.6	59
215	Genomic Databases. , 2017, , 353-369.		0
216	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. Genes, 2017, 8, 392.	1.0	5
217	A molecular view of the normal human thyroid structure and function reconstructed from its reference transcriptome map. BMC Genomics, 2017, 18, 739.	1.2	27
218	SNP TATA Comparator genomewide landmarks for preventive personalized medicine. Frontiers in Bioscience - Scholar, 2017, 9, 276-306.	0.8	19

#	Article	IF	Citations
219	Network Diffusion-Based Prioritization of Autism Risk Genes Identifies Significantly Connected Gene Modules. Frontiers in Genetics, 2017, 8, 129.	1.1	20
220	Candidate SNP Markers of Familial and Sporadic Alzheimer's Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Aging Neuroscience, 2017, 9, 231.	1.7	23
221	Trends in Precision Medicine. , 2017, , 269-299.		8
222	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. BMC Genomics, 2017, 18, 554.	1.2	52
223	NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	60
224	In silico search for modifier genes associated with pancreatic and liver disease in Cystic Fibrosis. PLoS ONE, 2017, 12, e0173822.	1.1	14
225	Chronic obstructive pulmonary disease candidate gene prioritization based on metabolic networks and functional information. PLoS ONE, 2017, 12, e0184299.	1.1	6
226	Computational analysis of multimorbidity between asthma, eczema and rhinitis. PLoS ONE, 2017, 12, e0179125.	1.1	33
227	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. BMC Systems Biology, 2017, 11, 132.	3.0	28
228	Towards a more molecular taxonomy of disease. Journal of Biomedical Semantics, 2017, 8, 25.	0.9	11
229	Mimvec: a deep learning approach for analyzing the human phenome. BMC Systems Biology, 2017, 11, 76.	3.0	5
230	Iteratively collective prediction of disease-gene associations through the incomplete network. , 2017, , .		8
231	PCOSBase: a manually curated database of polycystic ovarian syndrome. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	10
232	Mouse Genome Database (MGD)-2017: community knowledge resource for the laboratory mouse. Nucleic Acids Research, 2017, 45, D723-D729.	6.5	255
233	A systematic survey to identify lethal recessive variation in highly managed pig populations. BMC Genomics, 2017, 18, 858.	1.2	37
235	VarfromPDB: An Automated and Integrated Tool to Mine Disease-Gene-Variant Relations from the Public Databases and Literature. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	4
236	Consistency ofBRCA1andBRCA2Variant Classifications Among Clinical Diagnostic Laboratories. JCO Precision Oncology, 2017, 1, 1-10.	1.5	24
237	DLREFD: a database providing associations of long non-coding RNAs, environmental factors and phenotypes. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	12

#	Article	IF	Citations
238	Bipartite graphs in systems biology and medicine: a survey of methods and applications. GigaScience, 2018, 7, 1-31.	3.3	117
239	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. Cell, 2018, 172, 924-936.e11.	13.5	103
240	Text-mined phenotype annotation and vector-based similarity to improve identification of similar phenotypes and causative genes in monogenic disease patients. Human Mutation, 2018, 39, 643-652.	1.1	4
241	ClinVar: improving access to variant interpretations and supporting evidence. Nucleic Acids Research, 2018, 46, D1062-D1067.	6.5	2,746
242	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
243	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	0.7	22
244	Interleukins and their signaling pathways in the Reactome biological pathway database. Journal of Allergy and Clinical Immunology, 2018, 141, 1411-1416.	1.5	11
245	Human disease MiRNA inference by combining target information based on heterogeneous manifolds. Journal of Biomedical Informatics, 2018, 80, 26-36.	2.5	23
246	Genome Variation Map: a data repository of genome variations in BIG Data Center. Nucleic Acids Research, 2018, 46, D944-D949.	6.5	53
247	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	6.5	148
248	Recognition of the polycistronic nature of human genes is critical to understanding the genotype-phenotype relationship. Genome Research, 2018, 28, 609-624.	2.4	54
249	Transcriptome-wide discovery of coding and noncoding RNA-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3879-E3887.	3.3	138
250	Rare Disease Mechanisms Identified by Genealogical Proteomics of Copper Homeostasis Mutant Pedigrees. Cell Systems, 2018, 6, 368-380.e6.	2.9	16
251	Paediatric genomics: diagnosing rare disease in children. Nature Reviews Genetics, 2018, 19, 253-268.	7.7	369
252	Cancer genetics meets biomolecular mechanismâ€”bridging an ageâ€old gulf. FEBS Letters, 2018, 592, 463-474.	1.3	9
253	Causes of Congenital Malformations. Birth Defects Research, 2018, 110, 87-91.	0.8	42
254	PhenoRank: reducing study bias in gene prioritization through simulation. Bioinformatics, 2018, 34, 2087-2095.	1.8	30
255	Textâ€based phenotypic profiles incorporating biochemical phenotypes of inborn errors of metabolism improve phenomicsâ€based diagnosis. Journal of Inherited Metabolic Disease, 2018, 41, 555-562.	1.7	5

#	Article	IF	Citations
256	Malformations among 289,365 Births Attributed to Mutations with Autosomal Dominant and Recessive and Xâ€Linked Inheritance. Birth Defects Research, 2018, 110, 92-97.	0.8	1
257	The role of the clinician in the multiâ€omics era: are you ready?. Journal of Inherited Metabolic Disease, 2018, 41, 571-582.	1.7	55
258	Quantitative Missense Variant Effect Prediction Using Large-Scale Mutagenesis Data. Cell Systems, 2018, 6, 116-124.e3.	2.9	176
259	Identifying pathways affected by cancer mutations. Genomics, 2018, 110, 318-328.	1.3	5
260	WNT Signaling Perturbations Underlie the Genetic Heterogeneity of Robinow Syndrome. American Journal of Human Genetics, 2018, 102, 27-43.	2.6	88
261	Histone Lysine Methylases and Demethylases in the Landscape of Human Developmental Disorders. American Journal of Human Genetics, 2018, 102, 175-187.	2.6	204
262	Machine learning annotation of human branchpoints. Bioinformatics, 2018, 34, 920-927.	1.8	52
263	Precision oncology in the age of integrative genomics. Nature Biotechnology, 2018, 36, 46-60.	9.4	104
264	eRAM: encyclopedia of rare disease annotations for precision medicine. Nucleic Acids Research, 2018, 46, D937-D943.	6.5	56
265	Systematic analyses of drugs and disease indications in RepurposeDB reveal pharmacological, biological and epidemiological factors influencing drug repositioning. Briefings in Bioinformatics, 2018, 19, 656-678.	3.2	81
266	A 35-gene signature discriminates between rapidly- and slowly-progressing glioblastoma multiforme and predicts survival in known subtypes of the cancer. BMC Cancer, 2018, 18, 377.	1.1	27
267	Divergence of Noncoding Regulatory Elements Explains Geneâ€“Phenotype Differences between Human and Mouse Orthologous Genes. Molecular Biology and Evolution, 2018, 35, 1653-1667.	3.5	12
268	Relationship between Deleterious Variation, Genomic Autozygosity, and Disease Risk: Insights from The 1000 Genomes Project. American Journal of Human Genetics, 2018, 102, 658-675.	2.6	29
269	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. Circulation Genomic and Precision Medicine, 2018, 11, e001978.	1.6	65
270	Looking for Broken TAD Boundaries and Changes on DNA Interactions: Clinical Guide to 3D Chromatin Change Analysis in Complex Chromosomal Rearrangements and Chromothripsis. Methods in Molecular Biology, 2018, 1769, 353-361.	0.4	7
271	A Data Fusion Pipeline for Generating and Enriching Adverse Outcome Pathway Descriptions. Toxicological Sciences, 2018, 162, 264-275.	1.4	51
272	A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. Nature Communications, 2018, 9, 1215.	5.8	177
273	Adding biological meaning to human protein-protein interactions identified by yeast two-hybrid screenings: A guide through bioinformatics tools. Journal of Proteomics, 2018, 171, 127-140.	1.2	9

#	Article	IF	Citations
274	Association of MEOX2 polymorphism with nonsyndromic cleft palate only in a Vietnamese population. Congenital Anomalies (discontinued), 2018, 58, 124-129.	0.3	2
275	The DifferentialNet database of differential proteinâ€“protein interactions in human tissues. Nucleic Acids Research, 2018, 46, D522-D526.	6.5	71
276	Rare Diseases: Drug Discovery and Informatics Resource. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 195-204.	2.2	21
277	tmVar 2.0: integrating genomic variant information from literature with dbSNP and ClinVar for precision medicine. Bioinformatics, 2018, 34, 80-87.	1.8	79
278	WormBase 2017: molting into a new stage. Nucleic Acids Research, 2018, 46, D869-D874.	6.5	172
279	Inferred inheritance of MorbidMap genes without OMIM clinical synopsis. Genetics in Medicine, 2018, 20, 470-473.	1.1	0
280	Modernizing Human Cancer Risk Assessment of Therapeutics. Trends in Pharmacological Sciences, 2018, 39, 232-247.	4.0	17
281	Merging in-silico and in vitro salivary protein complex partners using the STRING database: A tutorial. Journal of Proteomics, 2018, 171, 87-94.	1.2	51
282	Future of Rare Diseases Research 2017â€“2027: An IRDiRC Perspective. Clinical and Translational Science, 2018, 11, 21-27.	1.5	154
283	An Integrative Framework for the Construction of Big Functional Networks. , 2018, , .		1
284	Wholeâ€genome sequencing of a monozygotic twin discordant for systemic lupus erythematosus. Molecular Medicine Reports, 2018, 17, 8391-8396.	1.1	8
285	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	377
286	INTEGRO: an algorithm for data-integration and disease-gene association. , 2018, , .		10
287	GRIPT: a novel case-control analysis method for Mendelian disease gene discovery. Genome Biology, 2018, 19, 203.	3.8	3
288	Database Resources of the BIG Data Center in 2018. Nucleic Acids Research, 2018, 46, D14-D20.	6.5	128
289	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. PeerJ, 2018, 6, e5298.	0.9	27
290	Selecting Multiple Biomarker Subsets with Similarly Effective Binary Classification Performances. Journal of Visualized Experiments, 2018, , .	0.2	5
291	Distributed gene clinical decision support system based on cloud computing. BMC Medical Genomics, 2018, 11, 100.	0.7	2

#	Article	IF	Citations
292	Widespread Genotype-Phenotype Correlations in Intellectual Disability. Frontiers in Psychiatry, 2018, 9, 535.	1.3	15
293	AGD: Aneurysm Gene Database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	7
294	Bioinformatics Analysis Reveals Potential Candidate Genes for Different Glioma Subtypes (Astrocytoma, Ependymoma, and Oligodendroglioma). Cancer Biotherapy and Radiopharmaceuticals, 2018, 33, 478-490.	0.7	0
295	RDAD: A Machine Learning System to Support Phenotype-Based Rare Disease Diagnosis. Frontiers in Genetics, 2018, 9, 587.	1.1	33
296	The unsolved rare genetic disease atlas? An analysis of the unexplained phenotypic descriptions in OMIMÂ®. , 2018, 178, 458-463.		25
297	Identifying mouse developmental essential genes using machine learning. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	18
298	Bioinformatics Tools and Databases to Assess the Pathogenicity of Mitochondrial DNA Variants in the Field of Next Generation Sequencing. Frontiers in Genetics, 2018, 9, 632.	1.1	48
299	Identification of gene expression profiles in myocardial infarction: a systematic review and meta-analysis. BMC Medical Genomics, 2018, 11, 109.	0.7	17
300	The accuracy of computerâ€based diagnostic tools for the identification of concurrent genetic disorders. American Journal of Medical Genetics, Part A, 2018, 176, 2704-2709.	0.7	5
301	A nomenclature and classification for the congenital myasthenic syndromes: preparing for FAIR data in the genomic era. Orphanet Journal of Rare Diseases, 2018, 13, 211.	1.2	17
302	ATD: a comprehensive bioinformatics resource for deciphering the association of autophagy and diseases. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	7
303	PTMD: A Database of Human Disease-associated Post-translational Modifications. Genomics, Proteomics and Bioinformatics, 2018, 16, 244-251.	3.0	129
304	Topological alternate centrality measure capturing drug targets in the network of MAPK pathways. IET Systems Biology, 2018, 12, 226-232.	0.8	1
305	Gold biotechnology: Development and advancements. AIP Conference Proceedings, 2018, , .	0.3	1
306	Improved ontology-based similarity calculations using a study-wise annotation model. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	11
307	Exome-Wide Rare Variant Analyses in Sudden Infant Death Syndrome. Journal of Pediatrics, 2018, 203, 423-428.e11.	0.9	17
308	Network-Based Methods for Prediction of Drug-Target Interactions. Frontiers in Pharmacology, 2018, 9, 1134.	1.6	131
310	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. International Journal of Computational Biology and Drug Design, 2018, 11, 135.	0.3	1

#	Article	IF	Citations
311	A Platform for Comprehensive Genomic Profiling in Human Cancers and Pharmacogenomics Therapy Selection. Methods in Molecular Biology, 2018, 1825, 413-424.	0.4	0
312	Dme-Hsa Disease Database (DHDD): Conserved Human Disease-Related miRNA and Their Targeting Genes in Drosophila melanogaster. International Journal of Molecular Sciences, 2018, 19, 2642.	1.8	6
313	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	1.6	13
314	<scp>DNA</scp> repair in trinucleotide repeat ataxias. FEBS Journal, 2018, 285, 3669-3682.	2.2	12
315	The impact of genome-wide association studies on biomedical research publications. Human Genomics, 2018, 12, 38.	1.4	11
316	Mouse Genome Database (MGD)-2018: knowledgebase for the laboratory mouse. Nucleic Acids Research, 2018, 46, D836-D842.	6.5	241
317	Saccharomyces genome database informs human biology. Nucleic Acids Research, 2018, 46, D736-D742.	6.5	27
318	Xenbase: a genomic, epigenomic and transcriptomic model organism database. Nucleic Acids Research, 2018, 46, D861-D868.	6.5	181
319	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. Nucleic Acids Research, 2018, 46, W65-W70.	6.5	59
320	Small-Molecule Screening for Genetic Diseases. Annual Review of Genomics and Human Genetics, 2018, 19, 263-288.	2.5	9
321	A Census of Disease Ontologies. Annual Review of Biomedical Data Science, 2018, 1, 305-331.	2.8	29
322	Using WormBase: A Genome Biology Resource for Caenorhabditis elegans and Related Nematodes. Methods in Molecular Biology, 2018, 1757, 399-470.	0.4	28
323	ClinVar Miner: Demonstrating utility of a Web-based tool for viewing and filtering ClinVar data. Human Mutation, 2018, 39, 1051-1060.	1.1	81
324	Sorting Five Human Tumor Types Reveals Specific Biomarkers and Background Classification Genes. Scientific Reports, 2018, 8, 8180.	1.6	8
325	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102
326	Protein Interactomics by Two-Hybrid Methods. Methods in Molecular Biology, 2018, 1794, 1-14.	0.4	6
327	Bioinformatics-based tools in drug discovery: the cartography from single gene to integrative biological networks. Drug Discovery Today, 2018, 23, 1658-1665.	3.2	14
328	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	5.8	63

#	Article	IF	Citations
329	PopViz: a webserver for visualizing minor allele frequencies and damage prediction scores of human genetic variations. Bioinformatics, 2018, 34, 4307-4309.	1.8	55
330	Computational Techniques in Data Integration and Big Data Handling in Omics. , 2018, , 209-222.		0
332	Novel application of normalized pointwise mutual information (NPMI) to mine biomedical literature for gene sets associated with disease: Use case in breast carcinogenesis. Computational Toxicology, 2018, 7, 46-57.	1.8	9
333	Reappraisal of Reported Genes for Sudden Arrhythmic Death. Circulation, 2018, 138, 1195-1205.	1.6	271
335	Automatic extraction of gene-disease associations from literature using joint ensemble learning. PLoS ONE, 2018, 13, e0200699.	1.1	50
336	Phenotype-oriented network analysis for discovering pharmacological effects of natural compounds. Scientific Reports, 2018, 8, 11667.	1.6	11
337	Hepatoprotective Effect of San-Cao Granule on Con A-Induced Liver Injury in Mice and Mechanisms of Action Exploration. Frontiers in Pharmacology, 2018, 9, 624.	1.6	11
338	In silico prediction of novel residues involved in amyloid primary nucleation of human I56T and D67H lysozyme. BMC Structural Biology, 2018, 18, 9.	2.3	6
339	iCopyDAV: Integrated platform for copy number variationsâ€"Detection, annotation and visualization. PLoS ONE, 2018, 13, e0195334.	1.1	43
340	Identification of Shared Molecular Signatures Indicate the Susceptibility of Endometriosis to Multiple Sclerosis. Frontiers in Genetics, 2018, 9, 42.	1.1	16
341	CDG: An Online Server for Detecting Biologically Closest Disease-Causing Genes and its Application to Primary Immunodeficiency. Frontiers in Immunology, 2018, 9, 1340.	2.2	6
342	Pharmacological usage of a selective inhibitor of 3-mercaptopyruvate sulfurtransferase to control H 2 S and polysulfide generation. , 2018, , 579-617.		0
343	Zebrafish Models of Rare Hereditary Pediatric Diseases. Diseases (Basel, Switzerland), 2018, 6, 43.	1.0	17
344	Predicting Gene-Disease Associations with Manifold Learning. Lecture Notes in Computer Science, 2018, , 265-271.	1.0	5
345	Network-based approach to prediction and population-based validation of in silico drug repurposing. Nature Communications, 2018, 9, 2691.	5.8	351
346	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. Journal of Genetics, 2018, 97, 589-609.	0.4	4
347	Preg<scp>OMICS</scp>â€"Leveraging systems biology and bioinformatics for drug repurposing in maternalâ€child health. American Journal of Reproductive Immunology, 2018, 80, e12971.	1.2	8
348	VAReporter: variant reporter for cancer research of massive parallel sequencing. BMC Genomics, 2018, 19, 86.	1.2	2

#	Article	IF	Citations
349	PhenoDis: a comprehensive database for phenotypic characterization of rare cardiac diseases. Orphanet Journal of Rare Diseases, 2018, 13, 22.	1.2	15
350	PedAM: a database for Pediatric Disease Annotation and Medicine. Nucleic Acids Research, 2018, 46, D977-D983.	6.5	27
351	Human Genomic Databases in Translational Medicine. , 2018, , 195-222.		2
352	Mitochondrial DNA copy number is associated with psychosis severity and anti-psychotic treatment. Scientific Reports, 2018, 8, 12743.	1.6	34
353	The IUPHAR/BPS Guide to PHARMACOLOGY in 2018: updates and expansion to encompass the new guide to IMMUNOPHARMACOLOGY. Nucleic Acids Research, 2018, 46, D1091-D1106.	6.5	1,584
354	Genetic Epidemiology. Methods in Molecular Biology, 2018, , .	0.4	1
355	Genomic atlas of the human plasma proteome. Nature, 2018, 558, 73-79.	13.7	1,180
356	Bioinformatics and genomic databases. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 147, 75-92.	1.0	15
357	Methods for Polygenic Traits. Methods in Molecular Biology, 2018, 1793, 145-156.	0.4	5
358	Whole Exome Sequencing of Patients from Multicase Families with Systemic Lupus Erythematosus Identifies Multiple Rare Variants. Scientific Reports, 2018, 8, 8775.	1.6	32
359	Patient similarity by joint matrix trifactorization to identify subgroups in acute myeloid leukemia. JAMIA Open, 2018, 1, 75-86.	1.0	15
360	VarAFT: a variant annotation and filtration system for human next generation sequencing data. Nucleic Acids Research, 2018, 46, W545-W553.	6.5	136
361	A proposed nosology of inborn errors of metabolism. Genetics in Medicine, 2019, 21, 102-106.	1.1	181
362	Congenital eye anomalies: More mosaic than thought?. Congenital Anomalies (discontinued), 2019, 59, 56-73.	0.3	15
363	Disease classification: from phenotypic similarity to integrative genomics and beyond. Briefings in Bioinformatics, 2019, 20, 1769-1780.	3.2	19
364	Computational resources associating diseases with genotypes, phenotypes and exposures. Briefings in Bioinformatics, 2019, 20, 2098-2115.	3.2	27
365	Genome-Wide Haplotype Association Study. , 2019, , 441-446.		0
366	The applications of big data in molecular diagnostics. Expert Review of Molecular Diagnostics, 2019, 19, 905-917.	1.5	4

#	Article	IF	Citations
367	GCN-MF. , 2019, , .		87
369	RNA Editing by ADAR Adenosine Deaminases: From Molecular Plasticity of Neural Proteins to the Mechanisms of Human Cancer. Biochemistry (Moscow), 2019, 84, 896-904.	0.7	12
370	Encoding Clinical Data with the Human Phenotype Ontology for Computational Differential Diagnostics. Current Protocols in Human Genetics, 2019, 103, e92.	3.5	29
371	Dutch genome diagnostic laboratories accelerated and improved variant interpretation and increased accuracy by sharing data. Human Mutation, 2019, 40, 2230-2238.	1.1	32
372	Understanding protein multifunctionality: from short linear motifs to cellular functions. Cellular and Molecular Life Sciences, 2019, 76, 4407-4412.	2.4	36
374	PhenPath: a tool for characterizing biological functions underlying different phenotypes. BMC Genomics, 2019, 20, 548.	1.2	8
375	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	1.1	8
376	EPIC: software toolkit for elution profile-based inference of protein complexes. Nature Methods, 2019, 16, 737-742.	9.0	67
377	Annotating and detecting phenotypic information for chronic obstructive pulmonary disease. JAMIA Open, 2019, 2, 261-271.	1.0	4
378	Prioritization and comprehensive analysis of genes associated with melanoma. Oncology Letters, 2019, 18, 127-136.	0.8	1
379	Disease gene prediction for molecularly uncharacterized diseases. PLoS Computational Biology, 2019, 15, e1007078.	1.5	26
380	Sirius: A Resource for Analyzing Drug-Disease Relationships for Drug Repositioning. Lecture Notes in Electrical Engineering, 2019, , 235-244.	0.3	0
381	Quantifying gene selection in cancer through protein functional alteration bias. Nucleic Acids Research, 2019, 47, 6642-6655.	6.5	21
382	Disease classification via gene network integrating modules and pathways. Royal Society Open Science, 2019, 6, 190214.	1.1	14
383	An emerging ribosomopathy affecting the skeleton due to biallelic variations in NEPRO. American Journal of Medical Genetics, Part A, 2019, 179, 1709-1717.	0.7	3
384	Comprehensive elaboration of database resources utilized in next-generation sequencing-based tumor somatic mutation detection. Biochimica Et Biophysica Acta: Reviews on Cancer, 2019, 1872, 122-137.	3.3	5
385	Fusion of multiple heterogeneous networks for predicting circRNA-disease associations. Scientific Reports, 2019, 9, 9605.	1.6	37
386	Eli Nathans. Peter von Zahnâ€™s Cold War Broadcasts to West Germany: Assessing America. American Historical Review, 2019, 124, 1539-1540.	0.0	0

#	Article	IF	Citations
387	Ubiquitin Ligases Involved in the Regulation of Wnt, TGF-Î², and Notch Signaling Pathways and Their Roles in Mouse Development and Homeostasis. Genes, 2019, 10, 815.	1.0	18
388	Biological Network Approaches and Applications in Rare Disease Studies. Genes, 2019, 10, 797.	1.0	30
389	Candidate SNP Markers of Atherosclerosis That May Significantly Change the Affinity of the TATA-Binding Protein for the Human Gene Promoters. Russian Journal of Genetics, 2019, 55, 1137-1151.	0.2	4
390	Autosomal recessive hypercholesterolemia: Case report. Journal of Clinical Lipidology, 2019, 13, 887-893.	0.6	4
391	Toward Clinical Implementation of Next-Generation Sequencing-Based Genetic Testing in Rare Diseases: Where Are We?. Trends in Genetics, 2019, 35, 852-867.	2.9	65
392	A start codon mutation of the TSPAN12 gene in Chinese families causes clinical heterogeneous familial exudative vitreoretinopathy. Molecular Genetics & Genomic Medicine, 2019, 7, e00948.	0.6	9
393	Ensembles of natural language processing systems for portable phenotyping solutions. Journal of Biomedical Informatics, 2019, 100, 103318.	2.5	19
394	Gene4Denovo: an integrated database and analytic platform for de novo mutations in humans. Nucleic Acids Research, 2020, 48, D913-D926.	6.5	41
395	PanelApp crowdsources expert knowledge to establish consensus diagnostic gene panels. Nature Genetics, 2019, 51, 1560-1565.	9.4	294
396	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	4
397	The IUPHAR/BPS Guide to PHARMACOLOGY in 2020: extending immunopharmacology content and introducing the IUPHAR/MMV Guide to MALARIA PHARMACOLOGY. Nucleic Acids Research, 2020, 48, D1006-D1021.	6.5	131
398	PhenoModifier: a genetic modifier database for elucidating the genetic basis of human phenotypic variation. Nucleic Acids Research, 2019, 48, D977-D982.	6.5	10
399	The NIH microphysiological systems program: developing in vitro tools for safety and efficacy in drug development. Current Opinion in Pharmacology, 2019, 48, 146-154.	1.7	34
400	Characterization of the C584R variant in the mtDNA depletion syndrome gene FBXL4, reveals a novel role for FBXL4 as a regulator of mitochondrial fusion. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 165536.	1.8	25
401	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. Genome Research, 2019, 29, 1555-1565.	2.4	28
402	National Center for Biotechnology Information (NCBI) database search for rubber plant Hevea brasiliensis. IOP Conference Series: Earth and Environmental Science, 2019, 260, 012171.	0.2	0
403	MSTO1 mutations cause mtDNA depletion, manifesting as muscular dystrophy with cerebellar involvement. Acta Neuropathologica, 2019, 138, 1013-1031.	3.9	31
404	C: Consensus Cancer Driver Gene Caller. Genomics, Proteomics and Bioinformatics, 2019, 17, 311-318.	3.0	3

#	Article	IF	Citations
405	A Convolutional Neural Network for the automatic diagnosis of collagen VI-related muscular dystrophies. Applied Soft Computing Journal, 2019, 85, 105772.	4.1	5
406	Predicting circRNA-Disease Associations Based on circRNA Expression Similarity and Functional Similarity. Frontiers in Genetics, 2019, 10, 832.	1.1	16
407	Homozygous TANGO2 Single Nucleotide Variants Presenting with Additional Manifestations Resembling Alternating Hemiplegia of Childhoodâ€“Expanding the Phenotype of a Recently Reported Condition. Neuropediatrics, 2019, 50, 122-125.	0.3	15
408	Genetic and genomic analyses of testicular hypoplasia in Nellore cattle. PLoS ONE, 2019, 14, e0211159.	1.1	9
409	Network Analysis Reveals TNF as a Major Hub of Reactive Inflammation Following Spinal Cord Injury. Scientific Reports, 2019, 9, 928.	1.6	12
410	The utility of phenomics in diagnosis of inherited metabolic disorders. Clinical Medicine, 2019, 19, 30-36.	0.8	15
411	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. American Journal of Human Genetics, 2019, 104, 275-286.	2.6	158
412	The ATP-dependent chromatin remodelling enzyme Uls1 prevents Topoisomerase II poisoning. Nucleic Acids Research, 2019, 47, 6172-6183.	6.5	4
413	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. Nucleic Acids Research, 2019, 47, W242-W247.	6.5	11
414	MutationDistiller: user-driven identification of pathogenic DNA variants. Nucleic Acids Research, 2019, 47, W114-W120.	6.5	37
415	Targeted gene panel sequencing for the rapid diagnosis of acutely ill infants. Molecular Genetics & Genomic Medicine, 2019, 7, e00796.	0.6	34
416	Proteomics INTegrator (PINT): An Online Tool To Store, Query, and Visualize Large Proteomics Experiment Results. Journal of Proteome Research, 2019, 18, 2999-3008.	1.8	0
417	Mechanisms of Compound Kushen Injection for the Treatment of Lung Cancer Based on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2019, 2019, 1-15.	0.5	28
418	Proteinâ€“Protein Interaction Network Analysis Reveals Several Diseases Highly Associated with Polycystic Ovarian Syndrome. International Journal of Molecular Sciences, 2019, 20, 2959.	1.8	31
419	Active repurposing of drug candidates for melanoma based on GWAS, PheWAS and a wide range of omics data. Molecular Medicine, 2019, 25, 30.	1.9	21
420	Endometriosis Knowledgebase: a gene-based resource on endometriosis. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	16
421	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. Challenges and Advances in Computational Chemistry and Physics, 2019, , 75-97.	0.6	1
422	AmyCo: the amyloidoses collection. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2019, 26, 112-117.	1.4	12

#	Article	IF	Citations
423	Towards the automated economic assessment of newborn screening for rare diseases. Journal of Biomedical Informatics, 2019, 95, 103216.	2.5	2
424	Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919.	15.2	221
425	Meta-analysis of genomic variants and gene expression data in schizophrenia suggests the potential need for adjunctive therapeutic interventions for neuropsychiatric disorders. Journal of Genetics, 2019, 98, 1.	0.4	5
426	BEERE: a web server for biomedical entity expansion, ranking and explorations. Nucleic Acids Research, 2019, 47, W578-W586.	6.5	5
427	Pathway-specific protein domains are predictive for human diseases. PLoS Computational Biology, 2019, 15, e1007052.	1.5	8
428	WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. Nucleic Acids Research, 2019, 47, W199-W205.	6.5	2,234
429	Identifying Disease-Gene Associations With Graph-Regularized Manifold Learning. Frontiers in Genetics, 2019, 10, 270.	1.1	19
430	Bioinformatics Analysis of the Core Genes Related to Lupus Nephritis Through a Network and Pathway-Based Approach. DNA and Cell Biology, 2019, 38, 639-650.	0.9	4
431	Biomolecular Data Resources: Bioinformatics Infrastructure for Biomedical Data Science. Annual Review of Biomedical Data Science, 2019, 2, 199-222.	2.8	8
432	Optimal control nodes in disease-perturbed networks as targets for combination therapy. Nature Communications, 2019, 10, 2180.	5.8	37
433	De Novo Transcriptome Assembly and Functional Annotation in Five Species of Bats. Scientific Reports, 2019, 9, 6222.	1.6	23
434	Cardioprotective effects of Aconiti Lateralis Radix Praeparata combined with Zingiberis Rhizoma on doxorubicin-induced chronic heart failure in rats and potential mechanisms. Journal of Ethnopharmacology, 2019, 238, 111880.	2.0	30
435	Novel Characterization of Antioxidant Enzyme, 3-Mercaptopyruvate Sulfurtransferase-Knockout Mice: Overexpression of the Evolutionarily-Related Enzyme Rhodanese. Antioxidants, 2019, 8, 116.	2.2	22
437	Prioritization of candidate metabolites for postmenopausal osteoporosis using multi-omics composite network. Experimental and Therapeutic Medicine, 2019, 17, 3155-3161.	0.8	6
438	Natural Selection Equally Supports the Human Tendencies in Subordination and Domination: A Genome-Wide Study With in silico Confirmation and in vivo Validation in Mice. Frontiers in Genetics, 2019, 10, 73.	1.1	14
439	Network Medicine. , 2019, , 414-458.		0
440	Using genetic drug-target networks to develop new drug hypotheses for major depressive disorder. Translational Psychiatry, 2019, 9, 117.	2.4	37
441	Using Human Genetics to Drive Drug Discovery: A Perspective. American Journal of Kidney Diseases, 2019, 74, 111-119.	2.1	7

#	Article	IF	Citations
442	Identification of Important Effector Proteins in the FOXJ1 Transcriptional Network Associated With Ciliogenesis and Ciliary Function. Frontiers in Genetics, 2019, 10, 23.	1.1	28
443	Enhancing the prediction of diseaseâ€“gene associations with multimodal deep learning. Bioinformatics, 2019, 35, 3735-3742.	1.8	52
444	Isoform-specific GSK3A activity is negatively correlated with human sperm motility. Molecular Human Reproduction, 2019, 25, 171-183.	1.3	18
445	Achieving the targets of sustainable development goals (2030 agenda) for congenital disorders in Asia: Bottlenecks and interventions. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2019, 181, 254-261.	0.7	2
446	Exomic and transcriptomic alterations of hereditary gingival fibromatosis. Oral Diseases, 2019, 25, 1374-1383.	1.5	6
447	How good are pathogenicity predictors in detecting benign variants?. PLoS Computational Biology, 2019, 15, e1006481.	1.5	79
448	Phenotypes associated with genes encoding drug targets are predictive of clinical trial side effects. Nature Communications, 2019, 10, 1579.	5.8	61
449	The Promoter Regions of Intellectual Disability-Associated Genes Are Uniquely Enriched in LTR Sequences of the MER41 Primate-Specific Endogenous Retrovirus: An Evolutionary Connection Between Immunity and Cognition. Frontiers in Genetics, 2019, 10, 321.	1.1	10
450	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	1.3	17
451	Candidate gene prioritization for non-communicable diseases based on functional information: Case studies. Journal of Biomedical Informatics, 2019, 93, 103155.	2.5	2
452	The combination of wholeâ€exome sequencing and copy number variation sequencing enables the diagnosis of rare neurological disorders. Clinical Genetics, 2019, 96, 140-150.	1.0	30
453	An enhanced workflow for variant interpretation in UniProtKB/Swiss-Prot improves consistency and reuse in ClinVar. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	7
454	A Model Information Management Plan for Molecular Pathology Sequence Data Using Standards. Journal of Molecular Diagnostics, 2019, 21, 408-417.	1.2	5
455	Ranking Cancer Proteins by Integrating PPI Network and Protein Expression Profiles. BioMed Research International, 2019, 2019, 1-8.	0.9	8
456	Identifying Windows of Susceptibility by Temporal Gene Analysis. Scientific Reports, 2019, 9, 2740.	1.6	9
457	Data-driven multiple-level analysis of gut-microbiome-immune-joint interactions in rheumatoid arthritis. BMC Genomics, 2019, 20, 124.	1.2	30
458	Debutant iOS app and geneâ€disease complexities in clinical genomics and precision medicine. Clinical and Translational Medicine, 2019, 8, 26.	1.7	17
459	Healing Functions of Carthami Flos against Contusion and Other Potential Damages. , 2019, , .		0

#	Article	IF	Citations
460	Factors Affecting Network-Based Gene Prediction Across Diverse Diseases. , 2019, , .		0
461	TexAnASD: Text Analytics for ASD Risk Gene Predictions. , 2019, , .		0
462	Healing Functions of Carthami Flos against Contusion and Other Potential Damages. , 2019, , .		0
463	Modeling and Predicting Protein-Protein Interactions of Type 2 Diabetes Mellitus Using Feedforward Neural Networks. , 2019, , .		0
464	Integrating Deep Textual Features to Probability Matrix Factorization for Metabolite-disease Association Prediction. , 2019, , .		1
465	GTX.Digest.VCF: an online NGS data interpretation system based on intelligent gene ranking and large-scale text mining. BMC Medical Genomics, 2019, 12, 193.	0.7	3
466	ChiTaRS 5.0: the comprehensive database of chimeric transcripts matched with druggable fusions and 3D chromatin maps. Nucleic Acids Research, 2020, 48, D825-D834.	6.5	22
467	Comparative analysis of cellular expression pattern of schizophrenia risk genes in human versus mouse cortex. Cell and Bioscience, 2019, 9, 89.	2.1	8
468	Gene- and Disease-Based Expansion of the Knowledge on Inborn Errors of Immunity. Frontiers in Immunology, 2019, 10, 2475.	2.2	6
469	MGeND: an integrated database for Japanese clinical and genomic information. Human Genome Variation, 2019, 6, 53.	0.4	6
470	Rapid Whole Genome Sequencing and Fulfilling the Promise of Precision Pediatric Critical Care*. Pediatric Critical Care Medicine, 2019, 20, 1085-1086.	0.2	7
471	Cardiac disorders and structural brain abnormalities are commonly associated with hypospadias in children with neurodevelopmental disorders. Clinical Dysmorphology, 2019, 28, 112-117.	0.1	5
472	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	14
473	Representing glycophenotypes: semantic unification of glycobiology resources for disease discovery. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
474	Bioinformatics Approaches for Anti-cancer Drug Discovery. Current Drug Targets, 2019, 21, 3-17.	1.0	73
475	Genome analysis and knowledge-driven variant interpretation with TGex. BMC Medical Genomics, 2019, 12, 200.	0.7	30
476	The distributions of protein coding genes within chromatin domains in relation to human disease. Epigenetics and Chromatin, 2019, 12, 72.	1.8	7
477	Clinical evidence-guided network pharmacology analysis reveals a critical contribution of Î²1-adrenoreceptor upregulation to bradycardia alleviation by Shenxian-Shengmai. BMC Complementary and Alternative Medicine, 2019, 19, 357.	3.7	13

#	Article	IF	Citations
478	CYP1B1 Gene and Phenotypic Correlation in Patients From Northeastern Brazil With Primary Congenital Glaucoma. Journal of Glaucoma, 2019, 28, 161-164.	0.8	11
479	Genomic analysis of a spinal muscular atrophy (SMA) discordant family identifies a novel mutation in TLL2, an activator of growth differentiation factor 8 (myostatin): a case report. BMC Medical Genetics, 2019, 20, 204.	2.1	8
480	Unveiling Active Constituents and Potential Targets Related to the Hematinic Effect of Steamed Panax notoginseng Using Network Pharmacology Coupled With Multivariate Data Analyses. Frontiers in Pharmacology, 2018, 9, 1514.	1.6	18
481	Molecular diagnostics of disorders of sexual development: an Indian survey and systems biology perspective. Systems Biology in Reproductive Medicine, 2019, 65, 105-120.	1.0	8
482	A Computational Bipartite Graph-Based Drug Repurposing Method. Methods in Molecular Biology, 2019, 1903, 115-127.	0.4	7
483	MitoMiner v4.0: an updated database of mitochondrial localization evidence, phenotypes and diseases. Nucleic Acids Research, 2019, 47, D1225-D1228.	6.5	97
484	STRING v11: proteinâ€“protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
485	HmtVar: a new resource for human mitochondrial variations and pathogenicity data. Nucleic Acids Research, 2019, 47, D1202-D1210.	6.5	58
486	Human Disease Ontology 2018 update: classification, content and workflow expansion. Nucleic Acids Research, 2019, 47, D955-D962.	6.5	383
487	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. Nucleic Acids Research, 2019, 47, D1090-D1101.	6.5	45
488	Repurposing of Approved Cardiovascular Drugs against Ischemic Cerebrovascular Disease by Diseaseâ€“Disease Associated Network-Assisted Prediction. Chemical and Pharmaceutical Bulletin, 2019, 67, 32-40.	0.6	4
489	Designing an Elusive Câ€¢Gâ†'Gâ€¢C CRISPR Base Editor. Trends in Biochemical Sciences, 2019, 44, 91-94.	3.7	10
490	Distant Supervision for Large-Scale Extraction of Geneâ€“Disease Associations from Literature Using DeepDive. Lecture Notes in Networks and Systems, 2019, , 367-374.	0.5	4
491	Dysfunctional Mechanism of Liver Cancer Mediated by Transcription Factor and Non-coding RNA. Current Bioinformatics, 2019, 14, 100-107.	0.7	20
492	Biological Knowledge Graph Construction, Search, and Navigation. , 2019, , 107-120.		1
493	PopHumanScan: the online catalog of human genome adaptation. Nucleic Acids Research, 2019, 47, D1080-D1089.	6.5	22
494	Cofactors revisited â€“ Predicting the impact of flavoprotein-related diseases on a genome scale. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 360-370.	1.8	10
495	iDog: an integrated resource for domestic dogs and wild canids. Nucleic Acids Research, 2019, 47, D793-D800.	6.5	33

#	Article	IF	Citations
496	The Comparative Toxicogenomics Database: update 2019. Nucleic Acids Research, 2019, 47, D948-D954.	6.5	731
497	Quantitative and systems pharmacology 4. Network-based analysis of drug pleiotropy on coronary artery disease. European Journal of Medicinal Chemistry, 2019, 161, 192-204.	2.6	25
498	Genomic and Phenomic Research in the 21st Century. Trends in Genetics, 2019, 35, 29-41.	2.9	20
499	Genetic variants of erythropoietin (EPO) and EPO receptor genes in familial erythrocytosis. International Journal of Laboratory Hematology, 2019, 41, 162-167.	0.7	25
500	Computational Methods for Drug Repurposing. Methods in Molecular Biology, 2019, , .	0.4	7
501	Integrating molecular networks with genetic variant interpretation for precision medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2019, 11, e1443.	6.6	34
502	ClinPhen extracts and prioritizes patient phenotypes directly from medical records to expedite genetic disease diagnosis. Genetics in Medicine, 2019, 21, 1585-1593.	1.1	67
503	OMIM.org: leveraging knowledge across phenotypeâ€“gene relationships. Nucleic Acids Research, 2019, 47, D1038-D1043.	6.5	562
504	15 years of PhosphoSitePlusÂ®: integrating post-translationally modified sites, disease variants and isoforms. Nucleic Acids Research, 2019, 47, D433-D441.	6.5	208
505	Developing a â€˜personalomeâ€™ for precision medicine: emerging methods that compute interpretable effect sizes from single-subject transcriptomes. Briefings in Bioinformatics, 2019, 20, 789-805.	3.2	24
506	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. Genomics, 2019, 111, 612-618.	1.3	5
507	Prioritizing complex disease risk genes by integrating multiple data. Genomics, 2019, 111, 590-597.	1.3	2
508	Integrating Multiple Heterogeneous Networks for Novel LncRNA-Disease Association Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 396-406.	1.9	103
509	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	1.9	29
510	The diagnosis of inborn errors of metabolism by an integrative â€œmultiâ€•omicsâ€•approach: A perspective encompassing genomics, transcriptomics, and proteomics. Journal of Inherited Metabolic Disease, 2020, 43, 25-35.	1.7	47
511	100 Years of evolving geneâ€“disease complexities and scientific debutants. Briefings in Bioinformatics, 2020, 21, 885-905.	3.2	36
513	AVADA: toward automated pathogenic variant evidence retrieval directly from the full-text literature. Genetics in Medicine, 2020, 22, 362-370.	1.1	24
514	A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. Human Molecular Genetics, 2020, 29, 159-167.	1.4	54

#	Article	IF	Citations
515	VarSite: Disease variants and protein structure. Protein Science, 2020, 29, 111-119.	3.1	77
516	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	13.7	441
517	Microphthalmia, Linear Skin Defects, Callosal Agenesis, and Cleft Palate in a Patient with Deletion at Xp22.3p22.2. Journal of Pediatric Genetics, 2020, 09, 258-262.	0.3	1
518	Broadâ€Spectrum Profiling of Drug Safety via Learning Complex Network. Clinical Pharmacology and Therapeutics, 2020, 107, 1373-1382.	2.3	1
519	Computational network biology: Data, models, and applications. Physics Reports, 2020, 846, 1-66.	10.3	126
520	Plant Metabolite Databases: From Herbal Medicines to Modern Drug Discovery. Journal of Chemical Information and Modeling, 2020, 60, 1101-1110.	2.5	37
521	Translational Tools and Databases in Genomic Medicine. , 2020, , 171-187.		0
522	Genetic Counseling and Genome Sequencing in Pediatric Rare Disease. Cold Spring Harbor Perspectives in Medicine, 2020, 10, a036632.	2.9	18
523	LDAH2V: Exploring Meta-Paths Across Multiple Networks for lncRNA-Disease Association Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1572-1581.	1.9	29
524	Interviews with experts in rare diseases for the development of clinical decision support system software - a qualitative study. BMC Medical Informatics and Decision Making, 2020, 20, 230.	1.5	8
525	The similarity of inherited diseases (II): clinical and biological similarity between the phenotypic series. BMC Medical Genomics, 2020, 13, 139.	0.7	2
526	Clinical Evaluation of a Custom Gene Panel as a Tool for Precision Male Infertility Diagnosis by Next-Generation Sequencing. Life, 2020, 10, 242.	1.1	12
527	Using Drosophila to drive the diagnosis and understand the mechanisms of rare human diseases. Development (Cambridge), 2020, 147, .	1.2	37
528	Functional relationships between recessive inherited genes and genes with de novo variants in autism spectrum disorder. Molecular Autism, 2020, 11, 75.	2.6	5
529	inCNV: An Integrated Analysis Tool for Copy Number Variation on Whole Exome Sequencing. Evolutionary Bioinformatics, 2020, 16, 117693432095657.	0.6	3
530	The case for open science: rare diseases. JAMIA Open, 2020, 3, 472-486.	1.0	33
531	A Genetic Screen for Genes That Impact Peroxisomes in Drosophila Identifies Candidate Genes for Human Disease. G3: Genes, Genomes, Genetics, 2020, 10, 69-77.	0.8	6
532	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	2.9	199

#	Article	IF	Citations
533	metPropagate: network-guided propagation of metabolomic information for prioritization of metabolic disease genes. Npj Genomic Medicine, 2020, 5, 25.	1.7	13
534	A pipelineâ€friendly software tool for genome diagnostics to prioritize genes by matching patient symptoms to literature. Genetics & Genomics Next, 2020, 1, e10023.	0.8	3
535	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. Cell Reports, 2020, 32, 108050.	2.9	64
536	A molecular cell atlas of the human lung from single-cell RNA sequencing. Nature, 2020, 587, 619-625.	13.7	963
537	Study on Medication Rules of Traditional Chinese Medicine against Antineoplastic Drug-Induced Cardiotoxicity Based on Network Pharmacology and Data Mining. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-15.	0.5	17
538	The Underlying Mechanism of Paeonia lactiflora Pall. in Parkinsonâ€™s Disease Based on a Network Pharmacology Approach. Frontiers in Pharmacology, 2020, 11, 581984.	1.6	29
539	Frameshift Variant in Novel Adenosine-A1-Receptor Homolog Associated With Bovine Spastic Syndrome/Late-Onset Bovine Spastic Paresis in Holstein Sires. Frontiers in Genetics, 2020, 11, 591794.	1.1	3
540	An Investigation of the Molecular Mechanisms Underlying the Analgesic Effect of Jakyak-Gamcho Decoction: A Network Pharmacology Study. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-20.	0.5	8
541	Analysis of Glucocorticoid-Related Genes Reveal CCHCR1 as a New Candidate Gene for Type 2 Diabetes. Journal of the Endocrine Society, 2020, 4, bvaa121.	0.1	8
542	A Network Pharmacology to Explore the Mechanism of Astragalus Membranaceus in the Treatment of Diabetic Retinopathy. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-11.	0.5	10
543	Alternative Applications of Genotyping Array Data Using Multivariant Methods. Trends in Genetics, 2020, 36, 857-867.	2.9	7
544	Drug discovery strategies for modulating oxidative stress in gastrointestinal disorders. Expert Opinion on Drug Discovery, 2020, 15, 1309-1341.	2.5	18
545	Decipher the connections between proteins and phenotypes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140503.	1.1	8
546	Limitations and challenges in protein stability prediction upon genome variations: towards future applications in precision medicine. Computational and Structural Biotechnology Journal, 2020, 18, 1968-1979.	1.9	88
547	A Novel Network Pharmacology Strategy to Decode Metabolic Biomarkers and Targets Interactions for Depression. Frontiers in Psychiatry, 2020, 11, 667.	1.3	10
548	DNA Sequencing Resolves Misdiagnosed and Rare Genetic Disorders. , 2020, , .		0
549	Bioinformatics resources, databases, and tools for human mtDNA. , 2020, , 277-304.		0
550	Development of Multiscale Transcriptional Regulatory Network in Esophageal Cancer Based on Integrated Analysis. BioMed Research International, 2020, 2020, 1-17.	0.9	2

#	Article	IF	Citations
551	Analyzing Active Constituents and Optimal Steaming Conditions Related to the Hematopoietic Effect of Steamed Panax notoginseng by Network Pharmacology Coupled with Response Surface Methodology. BioMed Research International, 2020, 2020, 1-15.	0.9	9
552	Network Pharmacology-Based Study on the Mechanism of Pinellia ternata in Asthma Treatment. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-12.	0.5	8
553	Proteinâ€“protein and protein-nucleic acid binding residues important for common and rare sequence variants in human. BMC Bioinformatics, 2020, 21, 452.	1.2	4
554	The Phenotypic Consequences of Genetic Divergence between Admixed Latin American Populations: Antioquia and ChocÃ³, Colombia. Genome Biology and Evolution, 2020, 12, 1516-1527.	1.1	3
555	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.	3.9	26
556	Optic nerve coloboma as extension of the phenotype of 22q11.23 duplication syndrome: a case report. BMC Ophthalmology, 2020, 20, 333.	0.6	0
557	Assessing the Anti-cancer Therapeutic Mechanism of a Herbal Combination for Breast Cancer on System-level by a Network Pharmacological Approach. Anticancer Research, 2020, 40, 5097-5106.	0.5	5
558	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
559	An Effective Disease Risk Indicator Tool. , 2020, 2020, 5284-5287.		0
560	Computational Drug Repositioning: Current Progress and Challenges. Applied Sciences (Switzerland), 2020, 10, 5076.	1.3	24
561	Myosin XVI in the Nervous System. Cells, 2020, 9, 1903.	1.8	5
562	Tek/Tie2 is not required for cardiovascular development in zebrafish. Development (Cambridge), 2020, 147, .	1.2	14
563	Improving diagnosis for rare diseases: the experience of the Italian undiagnosed Rare diseases network. Italian Journal of Pediatrics, 2020, 46, 130.	1.0	14
564	A flexible computational pipeline for research analyses of unsolved clinical exome cases. Npj Genomic Medicine, 2020, 5, 54.	1.7	4
565	A comprehensive survey on computational methods of non-coding RNA and disease association prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	38
566	Systems Pharmacology Study of the Anticervical Cancer Mechanisms of FDY003. Natural Product Communications, 2020, 15, 1934578X2097736.	0.2	1
567	Meta-Analysis of Differentially Expressed Genes in the Substantia Nigra in Parkinsonâ€™s Disease Supports Phenotype-Specific Transcriptome Changes. Frontiers in Neuroscience, 2020, 14, 596105.	1.4	11
568	A Wide Spectrum of Genetic Disorders Causing Severe Childhood Epilepsy in Taiwan: A Case Series of Ultrarare Genetic Cause and Novel Mutation Analysis in a Pilot Study. Journal of Personalized Medicine, 2020, 10, 281.	1.1	15

#	Article	IF	Citations
569	The Shuganhuazheng Formula in Triple-Negative Breast Cancer: A Study Based on Network Pharmacology and In Vivo Experiments. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-10.	0.5	1
570	Unraveling the Molecular Mechanisms of Fructus Anisi Stellati as a Remedy for Infantile Colic by Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-9.	0.5	5
571	Microenvironment Remodeling and Subsequent Clinical Implications in Diffuse Large B-Cell Histologic Variant of Richter Syndrome. Frontiers in Immunology, 2020, 11, 594841.	2.2	11
572	A Network Pharmacology Study on the Effects of Ma Xing Shi Gan Decoction on Influenza. Digital Chinese Medicine, 2020, 3, 163-179.	0.5	3
573	Paediatric Horner syndrome. A case series of 14 patients in a tertiary hospital. Archivos De La Sociedad Espanola De Oftalmologia, 2020, 96, 356-365.	0.1	0
574	nMAGMA: a network-enhanced method for inferring risk genes from GWAS summary statistics and its application to schizophrenia. Briefings in Bioinformatics, 2021, 22, .	3.2	4
575	Utilizing network pharmacology to explore the underlying mechanism of Qiangzhi decoction in treating Touretteâ€™s syndrome. Annals of Palliative Medicine, 2020, 9, 4194-4210.	0.5	0
576	Pathway information extracted from 25 years of pathway figures. Genome Biology, 2020, 21, 273.	3.8	21
577	Network pharmacology and molecular docking analyses on Lianhua Qingwen capsule indicate Akt1 is a potential target to treat and prevent COVIDâ€19. Cell Proliferation, 2020, 53, e12949.	2.4	161
578	Cohesion of Cortical Language Networks During Word Processing Is Predicted by a Common Polymorphism in the SETBP1 Gene. New Directions for Child and Adolescent Development, 2020, 2020, 131-155.	1.3	1
579	Signaling Inclusivity in Undergraduate Biology Courses through Deliberate Framing of Genetics Topics Relevant to Gender Identity, Disability, and Race. CBE Life Sciences Education, 2020, 19, es2.	1.1	14
580	MACSNVdb: a high-quality SNV database for interspecies genetic divergence investigation among macaques. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	0
581	Resveratrol: Multi-Targets Mechanism on Neurodegenerative Diseases Based on Network Pharmacology. Frontiers in Pharmacology, 2020, 11, 694.	1.6	25
582	PathWalks: identifying pathway communities using a disease-related map of integrated information. Bioinformatics, 2020, 36, 4070-4079.	1.8	7
583	Human gene and disease associations for clinicalâ€genomics and precision medicine research. Clinical and Translational Medicine, 2020, 10, 297-318.	1.7	57
584	Identification of CDC5L as bridge gene between chronic obstructive pulmonary disease and lung adenocarcinoma. Epigenomics, 2020, 12, 1515-1529.	1.0	4
585	Exploring the mechanism of TCM formulae in the treatment of different types of coronary heart disease by network pharmacology and machining learning. Pharmacological Research, 2020, 159, 105034.	3.1	56
586	Assessment of the Retina of Plp-Î±-Syn Mice as a Model for Studying Synuclein-Dependent Diseases. , 2020, 61, 12.		5

#	Article	IF	Citations
587	A comprehensive map of disease networks and molecular drug discoveries for glaucoma. Scientific Reports, 2020, 10, 9719.	1.6	3
588	Relieving Sore Throat Formula Exerts a Therapeutic Effect on Pharyngitis through Immunoregulation and NF-Î°B Pathway. Mediators of Inflammation, 2020, 2020, 1-21.	1.4	5
589	Screening novel drug candidates for Alzheimerâ€™s disease by an integrated network and transcriptome analysis. Bioinformatics, 2020, 36, 4626-4632.	1.8	26
590	pyMeSHSim: an integrative python package for biomedical named entity recognition, normalization, and comparison of MeSH terms. BMC Bioinformatics, 2020, 21, 252.	1.2	8
591	Aralar Sequesters GABA into Hyperactive Mitochondria, Causing Social Behavior Deficits. Cell, 2020, 180, 1178-1197.e20.	13.5	62
592	New age-related hearing loss candidate genes in humans: an ongoing challenge. Gene, 2020, 742, 144561.	1.0	9
593	Benchmarking analysis of deleterious SNP prediction tools on CYP2D6 enzyme. Chemical Biology and Drug Design, 2020, 96, 984-994.	1.5	6
594	A Genome-wide ER-phagy Screen Highlights Key Roles of Mitochondrial Metabolism and ER-Resident UFMylation. Cell, 2020, 180, 1160-1177.e20.	13.5	163
595	Ethnogeographic and inter-individual variability of human ABC transporters. Human Genetics, 2020, 139, 623-646.	1.8	34
596	Network pharmacology analysis of Chaihu Lizhong Tang treating non-alcoholic fatty liver disease. Computational Biology and Chemistry, 2020, 86, 107248.	1.1	32
597	Runx2 (Runt-Related Transcription Factor 2)-Mediated Microcalcification Is a Novel Pathological Characteristic and Potential Mediator of Abdominal Aortic Aneurysm. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 1352-1369.	1.1	24
598	Fibroblastâ€specific genomeâ€scale modelling predicts an imbalance in amino acid metabolism in Refsum disease. FEBS Journal, 2020, 287, 5096-5113.	2.2	8
599	Investigating the multi-target pharmacological mechanism of danhong injection acting on unstable angina by combined network pharmacology and molecular docking. BMC Complementary Medicine and Therapies, 2020, 20, 66.	1.2	8
600	Pathogenic Gene Prediction Algorithm Based on Heterogeneous Information Fusion. Frontiers in Genetics, 2020, 11, 5.	1.1	5
601	Exploring the mechanism of action Xianlingubao Prescription in the treatment of osteoporosis by network pharmacology. Computational Biology and Chemistry, 2020, 85, 107240.	1.1	50
602	Genome sequencing of human in vitro fertilisation embryos for pathogenic variation screening. Scientific Reports, 2020, 10, 3795.	1.6	15
603	Quantitative analysis of proteins which are members of the same protein complex but cause locus heterogeneity in disease. Scientific Reports, 2020, 10, 10423.	1.6	3
604	Constructing knowledge graphs and their biomedical applications. Computational and Structural Biotechnology Journal, 2020, 18, 1414-1428.	1.9	132

#	Article	IF	Citations
605	Computational Systems Analysis on Polycystic Ovarian Syndrome (PCOS). , 2020, , .		2
606	A Census and Categorization Method of Epitranscriptomic Marks. International Journal of Molecular Sciences, 2020, 21, 4684.	1.8	29
607	UFO: A tool for unifying biomedical ontology-based semantic similarity calculation, enrichment analysis and visualization. PLoS ONE, 2020, 15, e0235670.	1.1	9
608	Systematic comparison of the protein-protein interaction databases from a user's perspective. Journal of Biomedical Informatics, 2020, 103, 103380.	2.5	51
609	The IUPHAR Guide to Immunopharmacology: connecting immunology and pharmacology. Immunology, 2020, 160, 10-23.	2.0	7
610	SmartPhase: Accurate and fast phasing of heterozygous variant pairs for genetic diagnosis of rare diseases. PLoS Computational Biology, 2020, 16, e1007613.	1.5	13
611	Candidate SNP Markers of Atherogenesis Significantly Shifting the Affinity of TATA-Binding Protein for Human Gene Promoters Show Stabilizing Natural Selection as a Sum of Neutral Drift Accelerating Atherogenesis and Directional Natural Selection Slowing It. International Journal of Molecular Sciences, 2020, 21, 1045.	1.8	7
612	MicroRNA sequencing of rat hippocampus and human biofluids identifies acute, chronic, focal and diffuse traumatic brain injuries. Scientific Reports, 2020, 10, 3341.	1.6	16
613	Transcriptome analysis reveals the difference between â€œhealthyâ€•and â€œcommonâ€•aging and their connection with ageâ€•related diseases. Aging Cell, 2020, 19, e13121.	3.0	22
614	ncRPheno: a comprehensive database platform for identification and validation of disease related noncoding RNAs. RNA Biology, 2020, 17, 943-955.	1.5	23
615	MetaOmGraph: a workbench for interactive exploratory data analysis of large expression datasets. Nucleic Acids Research, 2020, 48, e23-e23.	6.5	19
616	An ENU-induced mutation in Twist1 transactivation domain causes hindlimb polydactyly with complete penetrance and dominant-negatively impairs E2A-dependent transcription. Scientific Reports, 2020, 10, 2501.	1.6	5
617	Network Pharmacology-Based Investigation of the System-Level Molecular Mechanisms of the Hematopoietic Activity of Samul-Tang, a Traditional Korean Herbal Formula. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-17.	0.5	15
618	Target identification among known drugs by deep learning from heterogeneous networks. Chemical Science, 2020, 11, 1775-1797.	3.7	193
619	Differential network analysis of multiple human tissue interactomes highlights tissue-selective processes and genetic disorder genes. Bioinformatics, 2020, 36, 2821-2828.	1.8	28
620	MicroRNA and transcription factor co-regulatory networks and subtype classification of seminoma and non-seminoma in testicular germ cell tumors. Scientific Reports, 2020, 10, 852.	1.6	43
621	Steamed Panax notoginseng Attenuates Anemia in Mice With Blood Deficiency Syndrome via Regulating Hematopoietic Factors and JAK-STAT Pathway. Frontiers in Pharmacology, 2019, 10, 1578.	1.6	30
622	A transcriptome-wide association study based on 27 tissues identifies 106 genes potentially relevant for disease pathology in age-related macular degeneration. Scientific Reports, 2020, 10, 1584.	1.6	39

#	Article	IF	Citations
623	Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165714.	1.8	3
624	Significantly different clinical phenotypes associated with mutations in synthesis and transamidase+remodeling glycosylphosphatidylinositol (GPI)-anchor biosynthesis genes. Orphanet Journal of Rare Diseases, 2020, 15, 40.	1.2	21
625	A Systems Pharmacology Approach for Identifying the Multiple Mechanisms of Action for the Rougui-Fuzi Herb Pair in the Treatment of Cardiocerebral Vascular Diseases. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-17.	0.5	21
626	Identifying the regulation mechanism of phytochemicals on triple negative breast cancer's biological network. Gene Reports, 2020, 19, 100656.	0.4	1
627	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	13.7	724
628	The Predicted Key Molecules, Functions, and Pathways That Bridge Mild Cognitive Impairment (MCI) and Alzheimer's Disease (AD). Frontiers in Neurology, 2020, 11, 233.	1.1	43
629	Genomic Data Sharing for Novel Mendelian Disease Gene Discovery: The Matchmaker Exchange. Annual Review of Genomics and Human Genetics, 2020, 21, 305-326.	2.5	36
630	Large-Scale Transgenic Drosophila Resource Collections for Loss- and Gain-of-Function Studies. Genetics, 2020, 214, 755-767.	1.2	81
631	Systems Biochemistry Approaches to Defining Mitochondrial Protein Function. Cell Metabolism, 2020, 31, 669-678.	7.2	16
632	A network pharmacology approach to investigate the mechanism of Shuxuening injection in the treatment of ischemic stroke. Journal of Ethnopharmacology, 2020, 257, 112891.	2.0	61
633	Investigation of cardiovascular protective effect of Shenmai injection by network pharmacology and pharmacological evaluation. BMC Complementary Medicine and Therapies, 2020, 20, 112.	1.2	18
634	Medical diagnosis and treatment is NP-complete. Journal of Experimental and Theoretical Artificial Intelligence, 2021, 33, 297-312.	1.8	3
635	Detection of copy-number variations from NGS data using read depth information: a diagnostic performance evaluation. European Journal of Human Genetics, 2021, 29, 99-109.	1.4	23
636	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in Bioinformatics, 2021, 22, 1656-1678.	3.2	66
637	PsychENCODE and beyond: transcriptomics and epigenomics of brain development and organoids. Neuropsychopharmacology, 2021, 46, 70-85.	2.8	15
638	Systematic identification of genetic systems associated with phenotypes in patients with rare genomic copy number variations. Human Genetics, 2021, 140, 457-475.	1.8	8
639	Integrative pharmacological mechanism of vitamin C combined with glycyrrhizic acid against COVID-19: findings of bioinformatics analyses. Briefings in Bioinformatics, 2021, 22, 1161-1174.	3.2	51
640	MoonProt 3.0: an update of the moonlighting proteins database. Nucleic Acids Research, 2021, 49, D368-D372.	6.5	38

#	Article	IF	Citations
641	Systematic analysis of molecular mechanisms of heart failure through the pathway and network-based approach. Life Sciences, 2021, 265, 118830.	2.0	9
642	OrthoDB in 2020: evolutionary and functional annotations of orthologs. Nucleic Acids Research, 2021, 49, D389-D393.	6.5	103
643	Fineâ€tuning ERâ€phagy by postâ€translational modifications. BioEssays, 2021, 43, e2000212.	1.2	9
644	Computational Tools for Causal Inference in Genetics. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039248.	2.9	3
645	The burden of rare damaging variants in hereditary atypical parkinsonism genes is increased in patients with Parkinsonâ€™s disease. Neurobiology of Aging, 2021, 100, 118.e5-118.e13.	1.5	2
646	A guide to plasma membrane solute carrier proteins. FEBS Journal, 2021, 288, 2784-2835.	2.2	168
647	The Proteomics Study of Compounded HFE/TF/TfR2/HJV Genetic Variations in a Thai Family with Iron Overload, Chronic Anemia, and Motor Neuron Disorder. Journal of Molecular Neuroscience, 2021, 71, 545-555.	1.1	4
648	Genetic Etiology of Leftâ€sided Obstructive Heart Lesions: A Story in Development. Journal of the American Heart Association, 2021, 10, e019006.	1.6	23
650	The human GPCR signal transduction network. Network Modeling Analysis in Health Informatics and Bioinformatics, 2021, 10, 1.	1.2	1
651	Study of the active ingredients and mechanism of Sparganii rhizoma in gastric cancer based on HPLC-Q-TOFâ€“MS/MS and network pharmacology. Scientific Reports, 2021, 11, 1905.	1.6	20
652	Formononetin protects against ox-LDL-induced endothelial dysfunction by activating PPAR-Î³ signaling based on network pharmacology and experimental validation. Bioengineered, 2021, 12, 4887-4898.	1.4	24
654	Biallelic variants in SLC38A3 encoding a glutamine transporter cause epileptic encephalopathy. Brain, 2022, 145, 909-924.	3.7	17
655	Data sharing and gene variant databases. , 2021, , 221-236.		0
656	Manganese exposure in juvenile C57BL/6 mice increases glial inflammatory responses in the substantia nigra following infection with H1N1 influenza virus. PLoS ONE, 2021, 16, e0245171.	1.1	6
657	Human disease genes website series: An international, open and dynamic library for upâ€toâ€date clinical information. American Journal of Medical Genetics, Part A, 2021, 185, 1039-1046.	0.7	19
658	Transcriptome-directed analysis for Mendelian disease diagnosis overcomes limitations of conventional genomic testing. Journal of Clinical Investigation, 2021, 131, .	3.9	87
659	Common Network Pharmacology Databases. , 2021, , 75-126.		1
660	Potential therapeutic targets and molecular details of anthocyan-treated inflammatory bowel disease: a systematic bioinformatics analysis of network pharmacology. RSC Advances, 2021, 11, 8239-8249.	1.7	3

#	Article	IF	Citations
661	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, .	1.4	27
662	Personizing the prediction of future susceptibility to a specific disease. PLoS ONE, 2021, 16, e0243127.	1.1	3
663	Mechanism of Modified Danggui Sini Decoction for Knee Osteoarthritis Based on Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-11.	0.5	18
664	The similarity of inherited diseases (I): clinical similarity within the phenotypic series. BMC Medical Genomics, 2021, 14, 52.	0.7	0
665	Linking clinotypes to phenotypes and genotypes from laboratory test results in comprehensive physical exams. BMC Medical Informatics and Decision Making, 2021, 21, 51.	1.5	2
666	Network pharmacologyâ€‘based study to explore the mechanism of the Yiqi Gubiao pill in lung cancer treatment. Oncology Letters, 2021, 21, 321.	0.8	4
667	Machine learning approaches for predicting biomoleculeâ€“disease associations. Briefings in Functional Genomics, 2021, 20, 273-287.	1.3	10
668	Theoretical Study of the Molecular Mechanism of Maxingyigan Decoction Against COVID-19: Network Pharmacology-based Strategy. Combinatorial Chemistry and High Throughput Screening, 2021, 24, 294-305.	0.6	7
669	Uncovering the Anti-Lung-Cancer Mechanisms of the Herbal Drug FDY2004 by Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	0
671	A Network Pharmacology Study on the Molecular Mechanisms of FDY003 for Breast Cancer Treatment. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-18.	0.5	6
672	Prioritizing Pain-Associated Targets with Machine Learning. Biochemistry, 2021, 60, 1430-1446.	1.2	5
673	Impaired eIF5A function causes a Mendelian disorder that is partially rescued in model systems by spermidine. Nature Communications, 2021, 12, 833.	5.8	41
675	Disturbance of Mitochondrial Dynamics and Mitochondrial Therapies in Atherosclerosis. Life, 2021, 11, 165.	1.1	15
676	De novo Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning. Frontiers in Genetics, 2021, 12, 630379.	1.1	4
678	<scp>DbStRiPs</scp>: Database of structural repeats in proteins. Protein Science, 2022, 31, 23-36.	3.1	6
679	Hedgehog acylâ€transferaseâ€related multiple congenital anomalies: Report of an additional family and delineation of the syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 2756-2765.	0.7	3
680	Chlorogenic Acid Inhibits Human Glioma U373 Cell Progression via Regulating the SRC/MAPKs Signal Pathway: Based on Network Pharmacology Analysis. Drug Design, Development and Therapy, 2021, Volume 15, 1369-1383.	2.0	9
682	Animation or leaflet: Does it make a difference when educating young people about genome sequencing?. Patient Education and Counseling, 2021, 104, 2522-2530.	1.0	2

#	Article	IF	Citations
683	Reducing Sanger confirmation testing through false positive prediction algorithms. Genetics in Medicine, 2021, 23, 1255-1262.	1.1	8
684	A Comprehensive Understanding of the Anticancer Mechanisms of FDY2004 Against Cervical Cancer Based on Network Pharmacology. Natural Product Communications, 2021, 16, 1934578X2110043.	0.2	2
685	A scalable random walk with restart on heterogeneous networks with Apache Spark for ranking disease-related genes through type-II fuzzy data fusion. Journal of Biomedical Informatics, 2021, 115, 103688.	2.5	12
686	The Impact of Modern Technologies on Molecular Diagnostic Success Rates, with a Focus on Inherited Retinal Dystrophy and Hearing Loss. International Journal of Molecular Sciences, 2021, 22, 2943.	1.8	6
687	Whole Genome Interpretation for a Family of Five. Frontiers in Genetics, 2021, 12, 535123.	1.1	3
688	Prediction of Synergistic Drug Combinations for Prostate Cancer by Transcriptomic and Network Characteristics. Frontiers in Pharmacology, 2021, 12, 634097.	1.6	10
689	A Combined Phytochemistry and Network Pharmacology Approach to Reveal Potential Anti-NSCLC Effective Substances and Mechanisms in Marsdenia tenacissima (Roxb.) Moon (Stem). Frontiers in Pharmacology, 2021, 12, 518406.	1.6	7
690	The Role of RNA-Sequencing as a New Genetic Diagnosis Tool. Current Genetic Medicine Reports, 2021, 9, 13-21.	1.9	12
691	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. Cell Systems, 2021, 12, 353-362.e6.	2.9	24
692	Traditional Chinese Formula Xiaoyaosan Alleviates Depressive-Like Behavior in CUMS Mice by Regulating PEBP1-GPX4-Mediated Ferroptosis in the Hippocampus. Neuropsychiatric Disease and Treatment, 2021, Volume 17, 1001-1019.	1.0	36
693	Investigation of the Mechanism of Traditional Chinese Medicines in Angiogenesis through Network Pharmacology and Data Mining. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-13.	0.5	7
694	Whole-Transcriptome RNA Sequencing Reveals Significant Differentially Expressed mRNAs, miRNAs, and lncRNAs and Related Regulating Biological Pathways in the Peripheral Blood of COVID-19 Patients. Mediators of Inflammation, 2021, 2021, 1-22.	1.4	50
695	Leveraging proteomics in orphan disease research: pitfalls and potential. Expert Review of Proteomics, 2021, 18, 315-327.	1.3	2
696	An Overview of Benefits and Challenges of Rare Disease Biobanking in Africa, Focusing on South Africa. Biopreservation and Biobanking, 2021, 19, 143-150.	0.5	7
697	Comparative transcriptomics and network pharmacology analysis to identify the potential mechanism of celastrol against osteoarthritis. Clinical Rheumatology, 2021, 40, 4259-4268.	1.0	6
698	The VRNetzer platform enables interactive network analysis in Virtual Reality. Nature Communications, 2021, 12, 2432.	5.8	33
699	Analysis of circulating exosomes reveals a peripheral signature of astrocytic pathology in schizophrenia. World Journal of Biological Psychiatry, 2022, 23, 33-45.	1.3	19
700	The Use of Traditional Chinese Medicine in Relieving EGFR-TKI-Associated Diarrhea Based on Network Pharmacology and Data Mining. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-16.	0.5	3

#	Article	IF	Citations
701	Monogenic Epilepsies: Channelopathies, Synaptopathies, mTorpathies, and Otheropathies. Journal of Pediatric Neurology, 0, , .	0.0	0
702	Two novel biâ€allelic <scp>KDELR2</scp> missense variants cause osteogenesis imperfecta with neurodevelopmental features. American Journal of Medical Genetics, Part A, 2021, 185, 2241-2249.	0.7	7
703	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. Journal of Molecular Biology, 2021, 433, 166840.	2.0	15
705	Inferring Genome-Wide Correlations of Mutation Fitness Effects between Populations. Molecular Biology and Evolution, 2021, 38, 4588-4602.	3.5	23
706	Network pharmacology integrated with experimental validation revealed the anti-inflammatory effects of Andrographis paniculata. Scientific Reports, 2021, 11, 9752.	1.6	12
707	CNVxplorer: a web tool to assist clinical interpretation of CNVs in rare disease patients. Nucleic Acids Research, 2021, 49, W93-W103.	6.5	14
708	Hepatoprotective effect of forsythiaside a against acetaminophen-induced liver injury in zebrafish: Coupling network pharmacology with biochemical pharmacology. Journal of Ethnopharmacology, 2021, 271, 113890.	2.0	19
709	Mapping OMIM Diseaseâ€"Related Variations on Protein Domains Reveals an Association Among Variation Type, Pfam Models, and Disease Classes. Frontiers in Molecular Biosciences, 2021, 8, 617016.	1.6	5
711	Coregulation Analysis of Mechanistic Biomarkers in Autosomal Dominant Polycystic Kidney Disease. International Journal of Molecular Sciences, 2021, 22, 6885.	1.8	6
712	Updating MoonProt From Home: An Online Student Research Project During the COVID-19 Pandemic. The Biophysicist, 2021, 2, 23-27.	0.1	2
713	Network Pharmacology-Based Dissection of the Active Ingredients and Protective Mechanism of the Salvia Miltiorrhiza and Panax Notoginseng Herb Pair against Insulin Resistance. ACS Omega, 2021, 6, 17276-17288.	1.6	5
714	Mechnetor: a web server for exploring protein mechanism and the functional context of genetic variants. Nucleic Acids Research, 2021, 49, W366-W374.	6.5	3
715	Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions. Scientific Reports, 2021, 11, 12358.	1.6	40
716	G-Protein-Coupled Receptors and Ischemic Stroke: a Focus on Molecular Function and Therapeutic Potential. Molecular Neurobiology, 2021, 58, 4588-4614.	1.9	9
717	Summarizing the Effective Herbs for the Treatment of Hypertensive Nephropathy by Complex Network and Machine Learning. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-12.	0.5	5
718	Metabolomics and Network Pharmacology-Based Investigation into the Mechanisms Underlying the Therapeutic Effect of a New Chinese Traditional Medicine (Cui Nai Ling) on Bromocriptine-Induced Hypogalactia. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	2
719	Semen Cuscutae-Fructus Lycii improves spermatogenic dysfunction by repairing the blood-testis barrier in rats according to in silico and in vitro methods. Journal of Ethnopharmacology, 2021, 274, 114022.	2.0	3
720	Precision omics data integration and analysis with interoperable ontologies and their application for COVID-19 research. Briefings in Functional Genomics, 2021, 20, 235-248.	1.3	8

#	Article	IF	Citations
721	DGLinker: flexible knowledge-graph prediction of diseaseâ€“gene associations. Nucleic Acids Research, 2021, 49, W153-W161.	6.5	19
722	Online Mendelian Inheritance in Man (<scp>OMIM</scp>Â®): Victor <scp>McKusick</scp>'s magnum opus. American Journal of Medical Genetics, Part A, 2021, 185, 3259-3265.	0.7	63
724	Disruptive Selection of Human Immunostimulatory and Immunosuppressive Genes Both Provokes and Prevents Rheumatoid Arthritis, Respectively, as a Self-Domestication Syndrome. Frontiers in Genetics, 2021, 12, 610774.	1.1	5
725	Diagnostic yield of rare skeletal dysplasia conditions in the radiogenomics era. BMC Medical Genomics, 2021, 14, 148.	0.7	7
726	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. Molecular Diversity, 2022, 26, 1175-1190.	2.1	14
727	Mechanism of protective effect of xuan-bai-cheng-qi decoction on LPS-induced acute lung injury based on an integrated network pharmacology and RNA-sequencing approach. Respiratory Research, 2021, 22, 188.	1.4	25
728	Advancing clinical genomics and precision medicine with GVViZ: FAIR bioinformatics platform for variable gene-disease annotation, visualization, and expression analysis. Human Genomics, 2021, 15, 37.	1.4	15
729	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	1.4	34
730	SÃndrome de Horner pediÃ¡trico. A propÃ³sito de una serie de 14 casos en un hospital terciario. Archivos De La Sociedad Espanola De Oftalmologia, 2021, 96, 356-365.	0.1	0
731	Advances in protein-protein interaction network analysis for Parkinson's disease. Neurobiology of Disease, 2021, 155, 105395.	2.1	31
732	Clinical Exome Reanalysis: Current Practice and Beyond. Molecular Diagnosis and Therapy, 2021, 25, 529-536.	1.6	27
733	A review on network pharmacology based phytotherapy in treating diabetes- An environmental perspective. Environmental Research, 2021, 202, 111656.	3.7	10
734	Joint disease-specificity at the regulatory base-pair level. Nature Communications, 2021, 12, 4161.	5.8	18
735	Retinoblastoma genetics screening and clinical management. BMC Medical Genomics, 2021, 14, 188.	0.7	5
736	RNA Sequencing of CD4+ T Cells in Relapsingâ€“Remitting Multiple Sclerosis Patients at Relapse: Deciphering the Involvement of Novel genes and Pathways. Journal of Molecular Neuroscience, 2021, 71, 2628-2645.	1.1	3
737	A data-driven architecture using natural language processing to improve phenotyping efficiency and accelerate genetic diagnoses of rare disorders. Human Genetics and Genomics Advances, 2021, 2, 100035.	1.0	4
738	Exploring the Mechanism of Scutellaria baicalensis Georgi Efficacy against Oral Squamous Cell Carcinoma Based on Network Pharmacology and Molecular Docking Analysis. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	4
739	InpherNet accelerates monogenic disease diagnosis using patientsâ€™ candidate genesâ€™ neighbors. Genetics in Medicine, 2021, 23, 1984-1992.	1.1	1

#	Article	IF	Citations
740	Effect of dapagliflozin on diabetic patients with cardiovascular disease via MAPK signalling pathway. Journal of Cellular and Molecular Medicine, 2021, 25, 7500-7512.	1.6	7
742	From late fatherhood to prenatal screening of monogenic disorders: evidence and ethical concerns. Human Reproduction Update, 2021, 27, 1056-1085.	5.2	7
744	Network-Based Analysis of Fatal Comorbidities of COVID-19 and Potential Therapeutics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1271-1280.	1.9	23
745	Mechanism Prediction of Astragalus membranaceus against Cisplatin-Induced Kidney Damage by Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	5
746	Exploring targets and signaling pathways of paeonol involved in relieving inflammation based on modern technology. Molecular Diversity, 2022, 26, 1731-1742.	2.1	3
747	Verification of immunology-related genetic associations in BPD supports ABCA3 and five other genes. Pediatric Research, 2022, 92, 190-198.	1.1	4
748	nf-LO: A Scalable, Containerized Workflow for Genome-to-Genome Lift Over. Genome Biology and Evolution, 2021, 13, .	1.1	10
749	Investigating the Mechanism of Scutellariae barbata Herba in the Treatment of Colorectal Cancer by Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-18.	0.5	8
750	Identification of Potential Bioactive Ingredients and Mechanisms of the Guanxin Suhe Pill on Angina Pectoris by Integrating Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-13.	0.5	2
751	Assigning function to SNPs: Considerations when interpreting genetic variation. Seminars in Cell and Developmental Biology, 2022, 121, 135-142.	2.3	13
752	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. Biomolecules, 2021, 11, 1245.	1.8	17
753	PhenoDB, GeneMatcher and VariantMatcher, tools for analysis and sharing of sequence data. Orphanet Journal of Rare Diseases, 2021, 16, 365.	1.2	24
754	Magnitude of Mendelian versus complex inheritance of rare disorders. American Journal of Medical Genetics, Part A, 2021, 185, 3287-3293.	0.7	12
755	Genetic testing in ambulatory cardiology clinics reveals high rate of findings with clinical management implications. Genetics in Medicine, 2021, 23, 2404-2414.	1.1	14
757	Exploring the Biological Mechanism of Huang Yam in Treating Tumors and Preventing Antitumor Drug-Induced Cardiotoxicity Using Network Pharmacology and Molecular Docking Technology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	2
758	Rare variant contribution to human disease in 281,104 UK Biobank exomes. Nature, 2021, 597, 527-532.	13.7	224
759	Predicting functional consequences of mutations using molecular interaction network features. Human Genetics, 2022, 141, 1195-1210.	1.8	9
760	Protein Interaction Network-based Deep Learning Framework for Identifying Disease-Associated Human Proteins. Journal of Molecular Biology, 2021, 433, 167149.	2.0	4

#	Article	IF	Citations
761	Technological Improvements in the Genetic Diagnosis of Rett Syndrome Spectrum Disorders. International Journal of Molecular Sciences, 2021, 22, 10375.	1.8	3
762	Mechanisms of Paeoniflorin against myocardial ischemia reperfusion injury based on network pharmacology. Materials Express, 2021, 11, 1505-1515.	0.2	3
765	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	9.4	69
766	WTD Attenuating Rheumatoid Arthritis via Suppressing Angiogenesis and Modulating the PI3K/AKT/mTOR/HIF-1Î± Pathway. Frontiers in Pharmacology, 2021, 12, 696802.	1.6	20
767	The clinical utility of pediatric cardiomyopathy genetic testing: From diagnosis to a precision medicine-based approach to care. Progress in Pediatric Cardiology, 2021, 62, 101413.	0.2	9
768	Identifying digenic disease genes via machine learning in the Undiagnosed Diseases Network. American Journal of Human Genetics, 2021, 108, 1946-1963.	2.6	25
769	Network Pharmacology-Based Dissection of the Comprehensive Molecular Mechanisms of the Herbal Prescription FDY003 Against Estrogen Receptor-Positive Breast Cancer. Natural Product Communications, 2021, 16, 1934578X2110443.	0.2	1
770	Candidate gene prioritization for chronic obstructive pulmonary disease using expression information in proteinâ€“protein interaction networks. BMC Pulmonary Medicine, 2021, 21, 280.	0.8	4
771	The Key Ingredient Acacetin in Weishu Decoction Alleviates Gastrointestinal Motility Disorder Based on Network Pharmacology Analysis. Mediators of Inflammation, 2021, 2021, 1-12.	1.4	5
772	COVID19db: a comprehensive database platform to discover potential drugs and targets of COVID-19 at whole transcriptomic scale. Nucleic Acids Research, 2022, 50, D747-D757.	6.5	27
773	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
774	Analysis of the Composition and Anti-Rheumatoid Arthritis Mechanism of Qintengtongbi Decoction Based on Network Pharmacology. Natural Product Communications, 2021, 16, 1934578X2110414.	0.2	1
775	Formins in Human Disease. Cells, 2021, 10, 2554.	1.8	16
776	The Enzyme Portal: an integrative tool for enzyme information and analysis. FEBS Journal, 2021, , .	2.2	2
777	Repurposing new drug candidates and identifying crucial molecules underlying PCOS Pathogenesis Based On Bioinformatics Analysis. DARU, Journal of Pharmaceutical Sciences, 2021, 29, 353-366.	0.9	11
778	Integrative Network Pharmacology of Moringa oleifera Combined with Gemcitabine against Pancreatic Cancer. Processes, 2021, 9, 1742.	1.3	0
780	Integrating network pharmacology and experimental evidence to decipher the cardioprotective mechanism of Yiqihuoxue decoction in rats after myocardial infarction. Journal of Ethnopharmacology, 2021, 279, 114062.	2.0	8
781	Xinnaokang improves cecal microbiota and lipid metabolism to target atherosclerosis. Letters in Applied Microbiology, 2021, 73, 779-792.	1.0	4

#	Article	IF	Citations
782	Protein deep profile and model predictions for identifying the causal genes of male infertility based on deep learning. Information Fusion, 2021, 75, 70-89.	11.7	6
783	Reproductive genetics. , 2022, , 21-46.e3.		0
784	Rare and de novo coding variants in chromodomain genes in Chiari I malformation. American Journal of Human Genetics, 2021, 108, 100-114.	2.6	17
785	Current approaches to genetic testingÂinÂpediatric disease. , 2021, , 15-36.		0
786	Comprehensive computational target fishing approach to identify Xanthorrhizol putative targets. Scientific Reports, 2021, 11, 1594.	1.6	17
787	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	5
788	Identification of the active substances and mechanisms of ginger for the treatment of colon cancer based on network pharmacology and molecular docking. BioData Mining, 2021, 14, 1.	2.2	92
789	Prediction of Protein Interactions by Structural Matching: Prediction of PPI Networks and the Effects of Mutations on PPIs that Combines Sequence and Structural Information. Methods in Molecular Biology, 2017, 1558, 255-270.	0.4	6
790	Target Safety Assessment: Strategies and Resources. Methods in Molecular Biology, 2017, 1641, 213-228.	0.4	9
791	A Collection of Benchmark Data Sets for Knowledge Graph-based Similarity in the Biomedical Domain. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	9
824	Network Pharmacology Identifies the Mechanisms of Action of Shaoyao Gancao Decoction in the Treatment of Osteoarthritis. Medical Science Monitor, 2019, 25, 6051-6073.	0.5	40
825	Research on the Potential Mechanism of Gypenosides on Treating Thyroid-Associated Ophthalmopathy Based on Network Pharmacology. Medical Science Monitor, 2019, 25, 4923-4932.	0.5	11
826	Network Pharmacology to Uncover the Molecular Mechanisms of Action of LeiGongTeng for the Treatment of Nasopharyngeal Carcinoma. Medical Science Monitor Basic Research, 2020, 26, e923431.	2.6	9
827	Protein-mRNA interactome capture: cartography of the mRNP landscape. F1000Research, 2016, 5, 2627.	0.8	10
828	Community Approaches for Integrating Environmental Exposures into Human Models of Disease. Environmental Health Perspectives, 2020, 128, 125002.	2.8	11
829	A Review of Mathematical Models for Muscular Dystrophy: A Systems Biology Approach. PLOS Currents, 0, , .	1.4	2
830	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	1.5	149
831	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. PLoS Computational Biology, 2017, 13, e1005221.	1.5	31

#	Article	IF	Citations
832	Network Analysis of Human Genes Influencing Susceptibility to Mycobacterial Infections. PLoS ONE, 2016, 11, e0146585.	1.1	14
833	Association between mitochondrial DNA variations and schizophrenia in the northern Chinese Han population. PLoS ONE, 2017, 12, e0182769.	1.1	11
834	Rare genetic variants in the endocannabinoid system genes CNR1 and DAGLA are associated with neurological phenotypes in humans. PLoS ONE, 2017, 12, e0187926.	1.1	55
835	dictyBase and the Dicty Stock Center (version 2.0) - a progress report. International Journal of Developmental Biology, 2019, 63, 563-572.	0.3	20
836	Unweaving the role of nuclear Lamins in neural circuit integrity. Cell Stress, 2018, 2, 219-224.	1.4	3
837	Congenital disorders of glycosylation. Part I. Defects of protein N-glycosylation.. Acta Biochimica Polonica, 2013, 60, .	0.3	30
838	Identification of potential genes for human ischemic cardiomyopathy based on RNA-Seq data. Oncotarget, 2016, 7, 82063-82073.	0.8	7
839	Systemically identifying and prioritizing risk lncRNAs through integration of pan-cancer phenotype associations. Oncotarget, 2017, 8, 12041-12051.	0.8	12
840	Prioritizing chronic obstructive pulmonary disease (COPD) candidate genes in COPD-related networks. Oncotarget, 2017, 8, 103375-103384.	0.8	5
841	GÎ±o (GNAO1) encephalopathies: plasma membrane vs. Golgi functions. Oncotarget, 2018, 9, 23846-23847.	0.8	13
842	Discovery and validation of a glioblastoma co-expressed gene module. Oncotarget, 2018, 9, 10995-11008.	0.8	15
843	Đ¡andidate SNP-markers of rheumatoid arthritis that can significantly alter the affinity of the TATA-binding protein for human gene promoters. Vavilovskii Zhurnal Genetiki I Selektsii, 2020, 23, 1047-1058.	0.4	1
844	Investigating the dysfunctional pathogenesis of Wilmsâ€™ tumor through a multidimensional integration strategy. Annals of Translational Medicine, 2019, 7, 136-136.	0.7	7
845	The pathogenic AGT c.856+1G>T mutation of a patient with multiple renal cysts and hypertension. Annals of Translational Medicine, 2019, 7, 699-699.	0.7	1
846	An Overview of Bioinformatics Methods for Analyzing Autism Spectrum Disorders. Current Pharmaceutical Design, 2020, 25, 4552-4559.	0.9	4
847	Integration and Querying of Heterogeneous Omics Semantic Annotations for Biomedical and Biomolecular Knowledge Discovery. Current Bioinformatics, 2020, 15, 41-58.	0.7	4
848	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. Journal of Medical Internet Research, 2017, 19, e212.	2.1	5
849	Exome Sequencing in Children. Deutsches Ärzteblatt International, 2019, 116, 197-204.	0.6	25

#	Article	IF	Citations
850	Genetic tests by next-generation sequencing in children with developmental delay and/or intellectual disability. Clinical and Experimental Pediatrics, 2020, 63, 195-202.	0.9	29
851	Global pathway view analysis of microRNA clusters in myasthenia gravis. Molecular Medicine Reports, 2019, 19, 2350-2360.	1.1	3
852	New markers for regulation of transcription and macromolecule metabolic process in porcine oocytes during in vitro maturation. Molecular Medicine Reports, 2020, 21, 1537-1551.	1.1	16
853	Next-generation sequencing reveals a novel NDP gene mutation in a Chinese family with Norrie disease. Indian Journal of Ophthalmology, 2017, 65, 1161.	0.5	3
854	Systematic morphological profiling of human gene and allele function via Cell Painting. ELife, 2017, 6, .	2.8	129
855	Biotea: semantics for Pubmed Central. PeerJ, 2018, 6, e4201.	0.9	5
856	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. Nucleic Acids Research, 2022, 50, D326-D332.	6.5	92
857	Gene4HL: An Integrated Genetic Database for Hearing Loss. Frontiers in Genetics, 2021, 12, 773009.	1.1	3
858	Investigation of the Active Ingredients and Mechanism of Hudi Enteric-Coated Capsules in DSS-Induced Ulcerative Colitis Mice Based on Network Pharmacology and Experimental Verification. Drug Design, Development and Therapy, 2021, Volume 15, 4259-4273.	2.0	5
859	Elucidate multidimensionality of type 1 diabetes mellitus heterogeneity by multifaceted information. Scientific Reports, 2021, 11, 20965.	1.6	2
860	Predicting the Molecular Mechanism of Shenling Baizhu San in Treating Convalescent Patients With COVID-19 Based on Network Pharmacology and Molecular Docking. Natural Product Communications, 2021, 16, 1934578X2110460.	0.2	0
861	Huanglianjiedu Decoction as an effective treatment for oral squamous cell carcinoma based on network pharmacology and experimental validation. Cancer Cell International, 2021, 21, 553.	1.8	3
863	A Network Pharmacology Analysis of the Systems-Perspective Anticancer Mechanisms of the Herbal Drug FDY2004 for Breast Cancer. Natural Product Communications, 2021, 16, 1934578X2110491.	0.2	0
864	Facilitating Antiviral Drug Discovery Using Genetic and Evolutionary Knowledge. Viruses, 2021, 13, 2117.	1.5	3
865	Effects and Components of Herb Pair Huanglian-Banxia on Diabetic Gastroparesis by Network Pharmacology. BioMed Research International, 2021, 2021, 1-14.	0.9	7
866	An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. IScience, 2021, 24, 103221.	1.9	27
867	Current Tools, Databases, and Resources for Phenotype and Variant Analysis of Clinical Exome Sequencing. Advances in Molecular Pathology, 2021, 4, 1-15.	0.2	0
871	IFGFA: Identification of featured genes from genomic data using factor analysis. Genetics and Molecular Research, 2016, 15, .	0.3	0

#	Article	IF	Citations
872	Complementary Sources of Protein Functional Information: The Far Side of GO. Methods in Molecular Biology, 2017, 1446, 263-274.	0.4	1
878	Investigating Alzheimerâ€™s Disease Candidate Genes Based on Combined Network Using Subnetwork Extraction Algorithms. Lecture Notes in Computer Science, 2017, , 559-565.	1.0	0
879	Relating Diseases Based on Disease Module Theory. Lecture Notes in Computer Science, 2017, , 24-33.	1.0	1
880	Hypersensitivity to Aspirin as a Factor for Poor Control in Hereditary Angioedema. Journal of Biosciences and Medicines, 2017, 05, 39-54.	0.1	0
888	Technical Tools for Computational Drug Repositioning. , 2017, , 83-104.		0
890	SEMANTIC-ENABLED HYBRID GENETIC DISEASE DIAGNOSTICS IN NEXT-GENERATION SEQUENCED DATA. Computer Science, 2018, 19, 179.	0.4	0
891	Application of Bioinformatics to Asthma. Translational Bioinformatics, 2018, , 349-359.	0.0	0
892	Connecting human disease phenotype to genetic mutation and protein function: A modular data mining short course with an independent project sequence for lecture or lab. , 0, , .		0
893	Immune System Promiscuity in Human and Nonhuman Primate Evolution. Human Biology, 2018, 90, 251.	0.4	4
894	Malformations cÃ©rÃ©brales. , 2018, , 637-673.e7.		0
895	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. International Journal of Computational Biology and Drug Design, 2018, 11, 135.	0.3	0
906	Celastrol Binds to HSP90 Trigger Functional Protein Interaction Network Against Pancreatic Cancer. Advances in Intelligent Systems and Computing, 2019, , 413-419.	0.5	0
907	Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. SSRN Electronic Journal, 0, , .	0.4	3
908	Systems Biology: Generating and Understanding Big Data. Success in Academic Surgery, 2019, , 233-243.	0.1	0
910	Identification of Key Metabolites for Acute Lung Injury in Patients with Sepsis. Iranian Journal of Public Health, 0, , .	0.3	2
914	Personalized and Precision Medicine Informatics Education. Computers in Health Care, 2020, , 319-330.	0.2	0
922	Leveraging the UMLS As a Data Standard for Rare Disease Data Normalization and Harmonization. Methods of Information in Medicine, 2020, 59, 131-139.	0.7	2
923	Congenital disorder of glycosylation caused by starting site-specific variant in syntaxin-5. Nature Communications, 2021, 12, 6227.	5.8	14

#	Article	IF	Citations
924	Network Pharmacological Dissection of the Mechanisms of Eucommiae Cortex-Achyranthis Radix Combination for Intervertebral Disc Herniation Treatment. Natural Product Communications, 2021, 16, 1934578X2110550.	0.2	0
925	Knowledge-based approaches to drug discovery for rare diseases. Drug Discovery Today, 2022, 27, 490-502.	3.2	15
926	Study on the Mechanism of Liuwei Dihuang Pills in Treating Parkinsonâ€™s Disease Based on Network Pharmacology. BioMed Research International, 2021, 2021, 1-12.	0.9	6
931	Mechanism of Salviae Miltiorrhizae Radix et Rhizoma in the Treatment of Knee Osteoarthritis Based on Network Pharmacology. Natural Product Communications, 2020, 15, 1934578X2098313.	0.2	0
932	A Collection of Benchmark Data Sets for Knowledge Graph-Based Similarity in the Biomedical Domain. Lecture Notes in Computer Science, 2020, , 50-55.	1.0	1
933	Differential Expression Analysis on Schizophrenia Dataset Suggests Pseudogene RNU6-505P as under Selective Pressure. International Annals of Science, 2019, 9, 86-99.	0.4	0
935	A Network Pharmacology Study on the Mechanisms of the Herbal Extract, Christina Loosestrife, for the Treatment of Nephrolithiasis. Medical Science Monitor, 2020, 26, e919360.	0.5	6
938	The Rat Genome Database (RGD) facilitates genomic and phenotypic data integration across multiple species for biomedical research. Mammalian Genome, 2022, 33, 66-80.	1.0	14
939	BioKG. , 2020, , .		24
943	Vaxar: A Web-Based Database of Laboratory Animal Responses to Vaccinations and Its Application in the Meta-Analysis of Different Animal Responses to Tuberculosis Vaccinations. Comparative Medicine, 2016, 66, 119-28.	0.4	1
944	Targeted next-generation sequencing analysis identifies novel mutations in families with severe familial exudative vitreoretinopathy. Molecular Vision, 2017, 23, 605-613.	1.1	9
945	A one-stop shop for biomedical and genomic data. AMIA Summits on Translational Science Proceedings, 2018, 2017, 118-123.	0.4	0
946	Combining mechanism-based prediction with patient-based profiling for psoriasis metabolomics biomarker discovery. AMIA ... Annual Symposium proceedings, 2017, 2017, 1734-1743.	0.2	3
947	Genetic Testing in Endocrinology. Clinical Biochemist Reviews, 2018, 39, 17-28.	3.3	7
948	Identification of Key Metabolites for Acute Lung Injury in Patients with Sepsis. Iranian Journal of Public Health, 2019, 48, 77-84.	0.3	2
949	Regulation of the mitochondrial permeability transition pore and its effects on aging. Microbial Cell, 2020, 7, 222-233.	1.4	0
950	A novel strategy to reveal clinical advantages and molecular mechanism of aidi injection in the treatment of pancreatic cancer based on network meta-analysis and network pharmacology. Journal of Ethnopharmacology, 2022, 285, 114852.	2.0	5
951	Network Pharmacology Analysis on the Mechanism of Huangqi Sijunzi Decoction in Treating Cancer-Related Fatigue. Journal of Healthcare Engineering, 2021, 2021, 1-10.	1.1	16

#	Article	IF	Citations
952	A Novel Mutation of the KLK6 Gene in a Family With Knee Osteoarthritis. Frontiers in Genetics, 2021, 12, 784176.	1.1	3
953	Pharmacological Mechanism of Danggui-Sini Formula for Intervertebral Disc Degeneration: A Network Pharmacology Study. BioMed Research International, 2021, 2021, 1-12.	0.9	3
954	Mechanism of quercetin therapeutic targets for Alzheimer disease and type 2 diabetes mellitus. Scientific Reports, 2021, 11, 22959.	1.6	29
955	Genetic architecture of orbital telorism. Human Molecular Genetics, 2021, , .	1.4	1
956	Investigation on the antitumor effects of paeonol against renal cell carcinoma based on network pharmacology and experimental validation. Journal of Ethnopharmacology, 2022, 285, 114857.	2.0	7
957	Mechanistic insights into the renoprotective role of curcumin in cisplatin-induced acute kidney injury: network pharmacology analysis and experimental validation. Bioengineered, 2021, 12, 11039-11054.	1.4	5
958	Antidepressant Mechanism of Traditional Chinese Medicine Formula Xiaoyaosan in CUMS-Induced Depressed Mouse Model via RIPK1-RIPK3-MLKL Mediated Necroptosis Based on Network Pharmacology Analysis. Frontiers in Pharmacology, 2021, 12, 773562.	1.6	21
959	In Silico Prediction of Potential Drug Combinations for Type 2 Diabetes Mellitus by an Integrated Network and Transcriptome Analysis. ChemMedChem, 2022, 17, .	1.6	3
960	Computational Network Pharmacologyâ€“Based Strategy to Capture Key Functional Components and Decode the Mechanism of Chai-Hu-Shu-Gan-San in Treating Depression. Frontiers in Pharmacology, 2021, 12, 782060.	1.6	6
961	Meningitis Caused by the Live Varicella Vaccine Virus: Metagenomic Next Generation Sequencing, Immunology Exome Sequencing and Cytokine Multiplex Profiling. Viruses, 2021, 13, 2286.	1.5	11
962	Uncovering Bupi Yishen Formula Pharmacological Mechanisms Against Chronic Kidney Disease by Network Pharmacology and Experimental Validation. Frontiers in Pharmacology, 2021, 12, 761572.	1.6	1
963	Quantitative dissection of multilocus pathogenic variation in an Egyptian infant with severe neurodevelopmental disorder resulting from multiple molecular diagnoses. American Journal of Medical Genetics, Part A, 2022, 188, 735-750.	0.7	14
964	Comparable Number of Genes Having Experienced Positive Selection among Great Ape Species. Animals, 2021, 11, 3264.	1.0	0
965	The possible mechanism of Hippophae fructus oil applied in tympanic membrane repair identified based on network pharmacology and molecular docking. Journal of Clinical Laboratory Analysis, 2021, , e24157.	0.9	4
966	Network Pharmacology and Experimental Validation to Reveal the Pharmacological Mechanisms of Liuwei Dihuang Decoction Against Intervertebral Disc Degeneration. Drug Design, Development and Therapy, 2021, Volume 15, 4911-4924.	2.0	23
967	Integrative Network Analysis Interweaves the Missing Links in Cardiomyopathy Diseasome. SSRN Electronic Journal, 0, , .	0.4	0
968	Network pharmacology analysis and experimental study strategy reveals the potential mechanism of puerarin against rotavirus. Annals of Translational Medicine, 2022, 10, 14-14.	0.7	2
969	A Practical Strategy for Exploring the Pharmacological Mechanism of Luteolin Against COVID-19/Asthma Comorbidity: Findings of System Pharmacology and Bioinformatics Analysis. Frontiers in Immunology, 2021, 12, 769011.	2.2	21

#	Article	IF	Citations
971	Study on the mechanism of Yupingfeng powder in the treatment of immunosuppression based on UPLCâƒQTOFâƒMS, network pharmacology and molecular biology verification. Life Sciences, 2022, 289, 120211.	2.0	8
973	Regulation of the mitochondrial permeability transition pore and its effects on aging. Microbial Cell, 2020, 7, 222-233.	1.4	4
975	Informationstechnik (IT) und Seltene Erkrankungen. , 2021, , 93-114.		0
976	What Has the Undiagnosed Diseases Network Taught Us About the Clinical Applications of Genomic Testing?. Annual Review of Medicine, 2022, 73, 575-585.	5.0	11
977	Integration of Network Pharmacology and Experimental Validation to Explore the Pharmacological Mechanisms of Zhuanggu Busui Formula Against Osteoporosis. Frontiers in Endocrinology, 2021, 12, 841668.	1.5	4
978	Population-Based Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 350.	3.8	34
979	A Network Pharmacology Perspective Investigation of the Pharmacological Mechanisms of the Herbal Drug FDY003 in Gastric Cancer. Natural Product Communications, 2022, 17, 1934578X2110730.	0.2	0
980	The QChip1 knowledgebase and microarray for precision medicine in Qatar. Npj Genomic Medicine, 2022, 7, 3.	1.7	4
981	Network Pharmacology and Molecular Docking Analysis on Pharmacological Mechanisms of Astragalus membranaceus in the Treatment of Gastric Ulcer. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-11.	0.5	3
982	An evaluation of pipelines for DNA variant detection can guide a reanalysis protocol to increase the diagnostic ratio of genetic diseases. Npj Genomic Medicine, 2022, 7, 7.	1.7	8
983	Systematic Pharmacology-Based Strategy to Explore the Molecular Network Mechanism of Modified Taohong Siwu Decoction in the Treatment of Premature Ovarian Failure. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	3
984	Targets of Tripterygium glycosides in systemic lupus erythematosus treatment: A network-pharmacology study. Lupus, 2022, 31, 319-329.	0.8	9
985	Tissue-specific multi-omics analysis of atrial fibrillation. Nature Communications, 2022, 13, 441.	5.8	17
986	Identification of cardiomyopathy-related core genes through human metabolic networks and expression data. BMC Genomics, 2022, 23, 47.	1.2	2
987	DBHR: a collection of databases relevant to human research. Future Science OA, 2022, 8, FSO780.	0.9	3
988	Evaluation of Evidence for Pathogenicity Demonstrates That BLK, KLF11, and PAX4 Should Not Be Included in Diagnostic Testing for MODY. Diabetes, 2022, 71, 1128-1136.	0.3	27
989	A Framework of Critical Considerations in Clinical Exome Reanalyses by Clinical and Laboratory Standards Institute. Journal of Molecular Diagnostics, 2022, 24, 177-188.	1.2	4
990	Herbal Formula Modified Bu-Shen-Huo-Xue Decoction Attenuates Intervertebral Disc Degeneration via Regulating Inflammation and Oxidative Stress. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-12.	0.5	2

#	Article	IF	Citations
991	Syndromic obesity with neurodevelopmental delay: Opportunities for targeted interventions. European Journal of Medical Genetics, 2022, 65, 104443.	0.7	4
992	Identifying patients and assessing variant pathogenicity for an autosomal dominant disease-driving gene. STAR Protocols, 2022, 3, 101150.	0.5	4
993	Anemone chinensis Bunge aqueous enema alleviates dextran sulfate sodium-induced colitis via inhibition of inflammation and regulation of the colonic mucosal microbiota. Journal of Ethnopharmacology, 2022, 288, 114916.	2.0	7
994	Lingguizhugan decoction dynamically regulates MAPKs and AKT signaling pathways to retrogress the pathological progression of cardiac hypertrophy to heart failure. Phytomedicine, 2022, 98, 153951.	2.3	9
995	In vitro anti-Helicobacter pylori activity of Syzygium aromaticum and the preliminary mechanism of action. Journal of Ethnopharmacology, 2022, 288, 114995.	2.0	11
996	Multimodal reasoning based on knowledge graph embedding for specific diseases. Bioinformatics, 2022, 38, 2235-2245.	1.8	15
997	Elucidating the material basis and potential mechanisms of Ershiwuwei Lvxue Pill acting on rheumatoid arthritis by UPLC-Q-TOF/MS and network pharmacology. PLoS ONE, 2022, 17, e0262469.	1.1	4
998	Network Pharmacology Prediction and Molecular Docking-Based Strategy to Discover the Potential Pharmacological Mechanism of Wen-Yu-Jin against Pulmonary Fibrosis in a Mouse Model. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-16.	0.5	5
999	A Network Pharmacology Study to Uncover the Mechanism of FDY003 for Ovarian Cancer Treatment. Natural Product Communications, 2022, 17, 1934578X2210754.	0.2	1
1000	Answer ALS, a large-scale resource for sporadic and familial ALS combining clinical and multi-omics data from induced pluripotent cell lines. Nature Neuroscience, 2022, 25, 226-237.	7.1	66
1001	Uncovering the Potential Mechanisms of Coptis chinensis Franch. for Serious Mental Illness by Network Pharmacology and Pharmacology-Based Analysis. Drug Design, Development and Therapy, 2022, Volume 16, 325-342.	2.0	4
1002	Growth and Pubertal Features in a Cohort of 83 Patients with Osteogenesis Imperfecta. Klinische Padiatrie, 2022, 234, 199-205.	0.2	3
1003	Proapoptotic Effect of Icariin on Human Ovarian Cancer Cells via the NF-Î¹B/PI3K-AKT Signaling Pathway: A Network Pharmacology-Directed Experimental Investigation. The American Journal of Chinese Medicine, 2022, 50, 589-619.	1.5	6
1004	Analysis of missense variants in the human genome reveals widespread gene-specific clustering and improves prediction of pathogenicity. American Journal of Human Genetics, 2022, 109, 457-470.	2.6	29
1005	Disentangling glial diversity in peripheral nerves at single-nuclei resolution. Nature Neuroscience, 2022, 25, 238-251.	7.1	35
1006	Inferring Retinal Degeneration-Related Genes Based on Xgboost. Frontiers in Molecular Biosciences, 2022, 9, 843150.	1.6	3
1007	Deep learning for drug repurposing: Methods, databases, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	48
1008	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. Journal of Genetics, 2018, 97, 589-609.	0.4	0

#	Article	IF	Citations
1009	Meta-analysis of genomic variants and gene expression data in schizophrenia suggests the potential need for adjunctive therapeutic interventions for neuropsychiatric disorders. Journal of Genetics, 2019, 98, .	0.4	2
1010	WikiPathways: Integrating Pathway Knowledge with Clinical Data. , 2022, , 1457-1466.		2
1011	Network Pharmacology Analysis on the Mechanism of Zuogui Pill Against Osteoporosis. SSRN Electronic Journal, 0, , .	0.4	0
1012	Study on the Mechanism of Danqi Tongluo Recipe in Treating Cervical Spondylosis Based on Network Pharmacology. Traditional Chinese Medicine, 2022, 11, 213-223.	0.1	1
1013	åŸºäºŽç½‘ç»œè¯ºå›¾åˆ†æžæ¢ç©¶é¢ˆæ¤ç—…...åŸºå›¢„æµ‹. Scientia Sinica Vitae, 2022, , .	0.1	0
1014	A guide for the diagnosis of rare and undiagnosed disease: beyond the exome. Genome Medicine, 2022, 14, 23.	3.6	101
1015	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	1.1	18
1016	GeneTerpret: a customizable multilayer approach to genomic variant prioritization and interpretation. BMC Medical Genomics, 2022, 15, 31.	0.7	1
1017	Analysis of Novel Variants Associated with Three Human Ovarian Cancer Cell Lines. Current Bioinformatics, 2022, 17, 380-392.	0.7	1
1018	Overcoming Drug Resistance in Advanced Prostate Cancer by Drug Repurposing. Medical Sciences (Basel, Switzerland), 2022, 10, 15.	1.3	13
1019	Network pharmacology and molecular docking analysis reveals the mechanism of asiaticoside on COVID-19. Annals of Translational Medicine, 2022, 10, 174-174.	0.7	4
1020	Revealing Calcium Signaling Pathway as Novel Mechanism of Danhong Injection for Treating Acute Myocardial Infarction by Systems Pharmacology and Experiment Validation. Frontiers in Pharmacology, 2022, 13, 839936.	1.6	0
1021	The Role of VHL in the Development of von Hippel-Lindau Disease and Erythrocytosis. Genes, 2022, 13, 362.	1.0	14
1022	Network pharmacology reveals potential functional components and underlying molecular mechanisms of Andrographis paniculata in esophageal cancer treatment. Phytotherapy Research, 2022, 36, 1748-1760.	2.8	4
1023	An Integrated Pharmacology-Based Strategy to Investigate the Potential Mechanism of Xiebai San in Treating Pediatric Pneumonia. Frontiers in Pharmacology, 2022, 13, 784729.	1.6	5
1024	Zebrafish information network, the knowledgebase for Danio rerio research. Genetics, 2022, 220, .	1.2	89
1025	Network pharmacology-based predictions of active components and pharmacological mechanisms of Artemisia annua L. for the treatment of the novel Corona virus disease 2019 (COVID-19). BMC Complementary Medicine and Therapies, 2022, 22, 56.	1.2	12
1026	Drug repurposing in silico screening platforms. Biochemical Society Transactions, 2022, 50, 747-758.	1.6	14

#	Article	IF	Citations
1027	Computational and Experimental Analysis of Genetic Variants. , 2022, 12, 3303-3336.		5
1028	Syndromic male subfertility: A network view of genomeâ€“phenome associations. Andrology, 2022, 10, 720-732.	1.9	5
1029	Molecular Mechanism Underlying Effects of Wumeiwan on Steroid-Dependent Asthma: A Network Pharmacology, Molecular Docking, and Experimental Verification Study. Drug Design, Development and Therapy, 2022, Volume 16, 909-929.	2.0	7
1030	Exploring the Potential Antidepressant Mechanisms of Pinellia by Using the Network Pharmacology and Molecular Docking. Metabolic Brain Disease, 2022, 37, 1071-1094.	1.4	11
1031	Identification of the potential mechanism of Radix pueraria in colon cancer based on network pharmacology. Scientific Reports, 2022, 12, 3765.	1.6	4
1032	Myopia Genetics and Heredity. Children, 2022, 9, 382.	0.6	20
1033	Pervasive occurrence of splice-site-creating mutations and their possible involvement in genetic disorders. Npj Genomic Medicine, 2022, 7, 22.	1.7	3
1034	The Mechanism of Ginseng and Astragalus Decoction in the Treatment of Malignant Pleural Effusion Based on Network Pharmacology and Molecular Docking Technology. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-11.	0.5	0
1036	Use of Network Pharmacology and Molecular Docking Methods to Elucidate the Curative Effect of Epimediumâ€“Anemarrhen on Osteoporosis. Natural Product Communications, 2022, 17, 1934578X2210869.	0.2	0
1037	Uncovering the Pharmacological Mechanisms of Gexia-Zhuyu Formula (GXZY) in Treating Liver Cirrhosis by an Integrative Pharmacology Strategy. Frontiers in Pharmacology, 2022, 13, 793888.	1.6	4
1038	Anticancer Activity of Erianin: Cancer-Specific Target Prediction Based on Network Pharmacology. Frontiers in Molecular Biosciences, 2022, 9, 862932.	1.6	13
1039	Complex Changes in the Efficiency of the Expression of Many Genes in Monogenic Diseases, Mucopolysaccharidoses, May Arise from Significant Disturbances in the Levels of Factors Involved in the Gene Expression Regulation Processes. Genes, 2022, 13, 593.	1.0	11
1040	Functional Enrichment Analysis of Regulatory Elements. Biomedicines, 2022, 10, 590.	1.4	53
1041	PatientMatcher: A customizable Pythonâ€based openâ€source tool for matching undiagnosed rare disease patients via the Matchmaker Exchange network. Human Mutation, 2022, , .	1.1	5
1043	Genome Alert!: A standardized procedure for genomicÂvariant reinterpretation and automated geneâ€“phenotype reassessment in clinical routine. Genetics in Medicine, 2022, 24, 1316-1327.	1.1	5
1044	Comprehensive Metabolomics and Network Pharmacology to Explore the Mechanism of 5-Hydroxymethyl Furfural in the Treatment of Blood Deficiency Syndrome. Frontiers in Pharmacology, 2021, 12, 811331.	1.6	6
1045	seqr : A webâ€based analysis and collaboration tool for rare disease genomics. Human Mutation, 2022, , .	1.1	31
1046	The impact of GeneMatcher on international data sharing and collaboration. Human Mutation, 2022, , .	1.1	7

#	Article	IF	Citations
1047	Darling: A Web Application for Detecting Disease-Related Biomedical Entity Associations with Literature Mining. Biomolecules, 2022, 12, 520.	1.8	9
1048	Systematic analysis of the mechanism of aged citrus peel (Chenpi) in oral squamous cell carcinoma treatment via network pharmacology, molecular docking and experimental validation. Journal of Functional Foods, 2022, 91, 105012.	1.6	10
1049	Identifying the Mechanism of Polygoni Cuspidati Rhizoma et Radix in Treating Acute Liver Failure Based on Network Pharmacology and Molecular Docking. Gastroenterology Research and Practice, 2022, 2022, 1-14.	0.7	2
1050	Structural basis of activation of the tumor suppressor protein neurofibromin. Molecular Cell, 2022, 82, 1288-1296.e5.	4.5	14
1051	16p13.11p11.2 triplication syndrome: a new recognizable genomic disorder characterized by optical genome mapping and whole genome sequencing. European Journal of Human Genetics, 2022, , .	1.4	5
1052	A network pharmacology technique used to investigate the potential mechanism of Ligustilide's effect on atherosclerosis. Journal of Food Biochemistry, 2022, 46, e14146.	1.2	2
1053	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. American Journal of Human Genetics, 2022, 109, 692-709.	2.6	2
1054	Protecting effect of emodin in experimental autoimmune encephalomyelitis mice by inhibiting microglia activation and inflammation via Myd88/PI3K/Akt/NF-ÎºB signalling pathway. Bioengineered, 2022, 13, 9322-9344.	1.4	16
1055	Loss-of-function variants in TIAM1 are associated with developmental delay, intellectual disability, and seizures. American Journal of Human Genetics, 2022, 109, 571-586.	2.6	19
1056	Systems pharmacology, proteomics and in vivo studies identification of mechanisms of cerebral ischemia injury amelioration by Huanglian Jiedu Decoction. Journal of Ethnopharmacology, 2022, 293, 115244.	2.0	9
1057	Disrupted long-range gene regulations elucidate shared tissue-specific mechanisms of neuropsychiatric disorders. Molecular Psychiatry, 2022, 27, 2720-2730.	4.1	1
1058	Exploration of the Potential Mechanisms of Lingqihuangban Granule for Treating Diabetic Retinopathy Based on Network Pharmacology. Combinatorial Chemistry and High Throughput Screening, 2023, 26, 14-29.	0.6	0
1059	Network pharmacology prediction and molecular docking-based strategy to explore the potential mechanism of Huanglian Jiedu Decoction against sepsis. Computers in Biology and Medicine, 2022, 144, 105389.	3.9	137
1060	Mechanisms underlying the therapeutic effects of Qingfeiyin in treating acute lung injury based on GEO datasets, network pharmacology and molecular docking. Computers in Biology and Medicine, 2022, 145, 105454.	3.9	42
1061	Caffeoyl malic acid is a potential dual inhibitor targeting TNFÎ±/IL-4 evaluated by a combination strategy of network analysis-deep learning-molecular simulation. Computers in Biology and Medicine, 2022, 145, 105410.	3.9	4
1062	Myasthenia gravis: The pharmacological basis of traditional Chinese medicine for its clinical application. BioFactors, 2022, 48, 228-238.	2.6	1
1063	Novel In-Frame Deletion in HTRA1 Gene, Responsible for Stroke at a Young Age and Dementiaâ€"A Case Study. Genes, 2021, 12, 1955.	1.0	4
1064	Target engagement of ginsenosides in mild cognitive impairment using mass spectrometry-based drug affinity responsive target stability. Journal of Ginseng Research, 2021, , .	3.0	1

#	Article	IF	Citations
1065	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.	0.5	5
1066	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. Human Molecular Genetics, 2021, , .	1.4	2
1067	Total Flavonoids of Chuju Decrease Oxidative Stress and Cell Apoptosis in Ischemic Stroke Rats: Network and Experimental Analyses. Frontiers in Neuroscience, 2021, 15, 772401.	1.4	6
1068	Network Pharmacology and Inflammatory Microenvironment Strategy Approach to Finding the Potential Target of Siraitia grosvenorii (Luo Han Guo) for Glioblastoma. Frontiers in Genetics, 2021, 12, 799799.	1.1	2
1069	Predicting the Molecular Mechanism of Sini Jia Renshen Decoction in Treating Severe COVID-19 Patients Based on Network Pharmacology and Molecular Docking. Natural Product Communications, 2021, 16, 1934578X2110592.	0.2	2
1070	A cis-regulatory-directed pipeline for the identification of genes involved in cardiac development and disease. Genome Biology, 2021, 22, 335.	3.8	4
1071	Systems biology and machine learning approaches identify drug targets in diabetic nephropathy. Scientific Reports, 2021, 11, 23452.	1.6	6
1073	Network Pharmacology-Based Investigation and Experimental Exploration of the Antiapoptotic Mechanism of Colchicine on Myocardial Ischemia Reperfusion Injury. Frontiers in Pharmacology, 2021, 12, 804030.	1.6	10
1074	Rare Genetic Syndromes and Oral Anomalies: A Review of the Literature and Case Series with a New Classification Proposal. Children, 2022, 9, 12.	0.6	2
1076	Leveraging Integrative Knowledge Graphs to Improve Health Information Access for Rare Diseases. , 2021, , .		0
1078	The Mechanism of Dendrobium officinale as a Treatment for Hyperlipidemia Based on Network Pharmacology and Experimental Validation. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-23.	0.5	2
1079	Computational Methods for the Study of Peroxisomes in Health and Disease. Physiology, 0, , .	4.0	0
1080	PPVED: A machine learning tool for predicting the effect of single amino acid substitution on protein function in plants. Plant Biotechnology Journal, 2022, 20, 1417-1431.	4.1	9
1081	Radix Bupleuri-Radix Paeoniae Alba couplet medicine in the treatment of type 2 diabetes mellitus - A network pharmacology and cellular experimental assessment. European Journal of Integrative Medicine, 2022, 52, 102132.	0.8	1
1083	Diagnostic yield of whole exome data in fetuses aborted for conotruncal malformations. Prenatal Diagnosis, 2022, 42, 852-861.	1.1	1
1084	Icariin: A Potential Molecule for Treatment of Knee Osteoarthritis. Frontiers in Pharmacology, 2022, 13, 811808.	1.6	10
1137	Utilizing Network Pharmacology and Molecular Docking Integrated Surface Plasmon Resonance Technology to Investigate the Potential Targets and Mechanisms of Tripterygium wilfordii against Pulmonary Artery Hypertension. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-13.	0.5	3
1138	Wuzi Yanzong pill attenuates MPTP-induced Parkinsonâ€™s Disease via PI3K/Akt signaling pathway. Metabolic Brain Disease, 2022, 37, 1435-1450.	1.4	7

#	Article	IF	Citations
1139	Leveraging omic features with F3UTER enables identification of unannotated 3â€™UTRs for synaptic genes. Nature Communications, 2022, 13, 2270.	5.8	4
1141	Systematic Elaboration of the Pharmacological Targets and Potential Mechanisms of ZhiKe GanCao Decoction for Preventing and Delaying Intervertebral Disc Degeneration. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-11.	0.5	3
1142	Rules of Chinese Herbal Intervention of Radiation Pneumonia Based on Network Pharmacology and Data Mining. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-13.	0.5	7
1143	The Brain Research Hotspot Database (BRHD): A Panoramic Database of the Latest Hotspots in Brain Research. Brain Sciences, 2022, 12, 638.	1.1	0
1145	Exploring Molecular Mechanisms of Aloe barbadmsis Miller on Diphenoxylate-Induced Constipation in Mice. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-16.	0.5	9
1146	An exploratory study on the mechanism of Huangqi Guizhi Wuwu Decoction in the treatment of neuropathic pain. , 2022, 8, 127-140.		2
1147	Examining the Mechanisms of Huachansu Injection on Liver Cancer through Integrated Bioinformatics Analysis. Recent Patents on Anti-Cancer Drug Discovery, 2023, 18, 408-425.	0.8	2
1148	Network Pharmacology and Absolute Bacterial Quantification-Combined Approach to Explore the Mechanism of Tianqi Pingchan Granule Against 6-OHDA-Induced Parkinsonâ€™s Disease in Rats. Frontiers in Nutrition, 2022, 9, .	1.6	2
1149	Germline predisposition to pediatric Ewing sarcoma is characterized by inherited pathogenic variants in DNA damage repair genes. American Journal of Human Genetics, 2022, 109, 1026-1037.	2.6	19
1150	Exploration of the System-Level Mechanisms of the Herbal Drug FDY003 for Pancreatic Cancer Treatment: A Network Pharmacological Investigation. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-16.	0.5	0
1151	Mechanism of Peitu Shengjin Formula Shenlingbaizhu Powder in Treating Bronchial Asthma and Allergic Colitis through Different Diseases with Simultaneous Treatment Based on Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-23.	0.5	2
1152	Evaluation of tea (Camellia sinensis L.) phytochemicals as multi-disease modulators, a multidimensional in silico strategy with the combinations of network pharmacology, pharmacophore analysis, statistics and molecular docking. Molecular Diversity, 2023, 27, 487-509.	2.1	4
1153	Dihydrosanguinarine based RNA-seq approach couple with network pharmacology attenuates LPS-induced inflammation through TNF/IL-17/PI3K/AKT pathways in mice liver. International Immunopharmacology, 2022, 109, 108779.	1.7	6
1154	Dynamic network biomarker analysis and system pharmacology methods to explore the therapeutic effects and targets of Xiaoyaosan against liver cirrhosis. Journal of Ethnopharmacology, 2022, 294, 115324.	2.0	2
1155	Translation into Russian of the Classification of inborn errors of immunity in humans updated by experts from a Committee on Congenital Immunity Errors of International Union of Immunological Societies (Russian version 2019). Russian Journal of Immunology: RJI: Official Journal of Russian Society of Immunology, 2021, 24, 7-68.	0.2	1
1156	Integrated Network Pharmacology and Clinical Study to Reveal the Effects and Mechanisms of Bushen Huoxue Huatan Decoction on Polycystic Ovary Syndrome. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-16.	0.5	4
1157	Network pharmacology and bioinformatics analysis identified essential genes of Jingulian in the treatment of rheumatoid arthritis and COVID-19. Annals of Translational Medicine, 2022, 10, 635-635.	0.7	2
1158	Silencing XIST on the future active X: Searching human and bovine preimplantation embryos for the repressor. European Journal of Human Genetics, 2022, , .	1.4	2

#	Article	IF	Citations
1159	Feasibility analysis and mechanism exploration of Rhei Radix et Rhizomeâ^'Schisandrae Sphenantherae Fructus (RS) against COVID-19. Journal of Medical Microbiology, 2022, 71, .	0.7	11
1160	A basement membrane discovery pipeline uncovers network complexity, regulators, and human disease associations. Science Advances, 2022, 8, eabn2265.	4.7	76
1161	The potential effects and mechanisms ofâ€,hispidulin in the treatment of diabetic retinopathy based onâ€,network pharmacology. BMC Complementary Medicine and Therapies, 2022, 22, 141.	1.2	3
1162	Gene Map. , 2022, , 2892-2894.		0
1163	Study on the Mechanism of Danqi Tongluo Recipe in Treating Lumbar Disc Herniation Based on Network Pharmacology. Traditional Chinese Medicine, 2022, 11, 407-415.	0.1	0
1164	Effects of Musk Volatile Compounds on Attenuated Nerve Injury and Improving Post-cerebral Ischemic Exercise Functions. Current Pharmaceutical Design, 2022, 28, 1932-1948.	0.9	3
1165	Medication Rules in Herbal Medicine for Mild Cognitive Impairment: A Network Pharmacology and Data Mining Study. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	3
1168	Epigenetic Activation of Antiviral Sensors and Effectors of Interferon Response Pathways During SARS-CoV-2 Infection. SSRN Electronic Journal, 0, , .	0.4	0
1169	TangShenWeiNing Formula Prevents Diabetic Nephropathy by Protecting Podocytes Through the SIRT1/HIF-1Î± Pathway. Frontiers in Endocrinology, 2022, 13, .	1.5	6
1171	The Antidiabetic Effect and Mechanism of JinXiaoXiaoKe Decoction in type 2 diabetic Gotoâ€“Kakizaki rats. Clinical Complementary Medicine and Pharmacology, 2022, , 100049.	0.9	1
1172	Case Report: MYO5B Homozygous Variant c.2090+3A>T Causes Intron Retention Related to Chronic Cholestasis and Diarrhea. Frontiers in Genetics, 0, 13, .	1.1	3
1173	A Genomic Information Management System for Maintaining Healthy Genomic States and Application of Genomic Big Data in Clinical Research. International Journal of Molecular Sciences, 2022, 23, 5963.	1.8	6
1175	A Network Pharmacology Study on the Similarities and Differences in the Mechanisms of Zuo Gui Wan/You Gui Wan for the Treatment of Premature Ovarian Failure. Combinatorial Chemistry and High Throughput Screening, 2023, 26, 1167-1179.	0.6	1
1176	A Network Pharmacological Elucidation of the Systematic Treatment Activities and Mechanisms of the Herbal Drug FDY003 Against Esophageal Cancer. Natural Product Communications, 2022, 17, 1934578X2211053.	0.2	0
1177	Investigation of the mechanism of Shen Qi Wan prescription in the treatment of T2DM via network pharmacology and molecular docking. In Silico Pharmacology, 2022, 10, .	1.8	1
1178	Deciphering the pharmacological mechanisms of Scutellaria baicalensis Georgi on oral leukoplakia by combining network pharmacology, molecular docking and experimental evaluations. Phytomedicine, 2022, 103, 154195.	2.3	22
1179	Vitamin C exerts anti-cadmium induced fracture functions/targets: bioinformatic and biostructural findings. Food Science and Human Wellness, 2022, 11, 1384-1391.	2.2	5
1180	Network pharmacology-based analysis of the effects of puerarin on sarcopenia. Annals of Translational Medicine, 2022, 10, 671-671.	0.7	1

#	Article	IF	Citations
1181	Naoluo Xintong Decoction in the Treatment of Ischemic Stroke: A Network Analysis of the Mechanism of Action. Frontiers in Pharmacology, 0, 13, .	1.6	1
1182	Integrating Network Pharmacology and Experimental Validation to Explore the Key Mechanism of Gubitong Recipe in the Treatment of Osteoarthritis. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-25.	0.7	3
1183	Network pharmacology and experimental verification based research into the effect and mechanism of Aucklandiae Radixâ€“Amomi Fructus against gastric cancer. Scientific Reports, 2022, 12, .	1.6	11
1185	New Developments and Possibilities in Reanalysis and Reinterpretation of Whole Exome Sequencing Datasets for Unsolved Rare Diseases Using Machine Learning Approaches. International Journal of Molecular Sciences, 2022, 23, 6792.	1.8	9
1186	Prioritizing Suggestive Candidate Genes in Migraine: An Opinion. Frontiers in Neurology, 0, 13, .	1.1	1
1187	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Communications Biology, 2022, 5, .	2.0	3
1188	Humanized yeast to model human biology, disease and evolution. DMM Disease Models and Mechanisms, 2022, 15, .	1.2	22
1189	A Mechanistic Exploratory Study on the Therapeutic Efficacy of Astragaloside IV Against Diabetic Retinopathy Revealed by Network Pharmacology. Frontiers in Pharmacology, 0, 13, .	1.6	3
1190	Network pharmacology-based strategy to investigate pharmacological mechanisms of Qingbutongluo Pill for treatment of brucellosis. Combinatorial Chemistry and High Throughput Screening, 2022, 25, .	0.6	0
1191	Role of statins in regulating molecular pathways following traumatic brain injury: A system pharmacology study. Biomedicine and Pharmacotherapy, 2022, 153, 113304.	2.5	4
1192	Flavonoids from Rhododendron nivale Hook. f delay aging via modulation of gut microbiota and glutathione metabolism. Phytomedicine, 2022, 104, 154270.	2.3	9
1193	Integrative analysis of network pharmacology and proteomics to identify key targets of Tuomin-Zhiti-Decoction for allergic rhinitis. Journal of Ethnopharmacology, 2022, 296, 115448.	2.0	8
1194	Taohong Siwu Decoction exerts anticancer effects on breast cancer via regulating MYC, BIRC5, EGF and PIK3R1 revealed by HTS2 technology. Computational and Structural Biotechnology Journal, 2022, 20, 3461-3472.	1.9	4
1195	HumanMine: advanced data searching, analysis and cross-species comparison. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	1
1198	Infantile esotropia in a family with TUBB3 mutation associated congenital fibrosis of extraocular muscles. Ophthalmic Genetics, 2022, 43, 716-719.	0.5	2
1199	Pharmacological analysis of Empagliflozin: Acting through the CaMKII pathway in type 2 diabetes and acute cardiovascular events. PLoS ONE, 2022, 17, e0270152.	1.1	1
1200	Modeling Kaempferol as a Potential Pharmacological Agent for COVID-19/PF Co-Occurrence Based on Bioinformatics and System Pharmacological Tools. Frontiers in Pharmacology, 0, 13, .	1.6	8
1201	Mechanism of Action of Yin Nourishing and Heat Clearing Prescription in Treating Cough Variant Asthma Based on Network Pharmacology and Molecular Docking Verification. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-11.	0.7	1

#	Article	IF	Citations
1202	Mechanisms of Action of Semen Ziziphi spinosae in the Treatment of Tourette Syndrome. Degenerative Neurological and Neuromuscular Disease, 0, Volume 12, 85-96.	0.7	0
1203	Network Pharmacology-Based Strategy to Investigate the Mechanisms of Cibotium barometz in Treating Osteoarthritis. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	0
1204	Fucoxanthin Inactivates the PI3K/Akt Signaling Pathway to Mediate Malignant Biological Behaviors of Non-Small Cell Lung Cancer. Nutrition and Cancer, 2022, 74, 3747-3760.	0.9	3
1205	Network Pharmacology-Based Strategy to Reveal the Mechanism of Cassiae Semen against Cataracts. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-18.	0.7	0
1206	The heterogeneous pharmacological medical biochemical network PharMeBINet. Scientific Data, 2022, 9, .	2.4	2
1207	Qin Huang formula enhances the effect of Adriamycin in B-cell lymphoma via increasing tumor infiltrating lymphocytes by targeting toll-like receptor signaling pathway. BMC Complementary Medicine and Therapies, 2022, 22, .	1.2	2
1208	Contexts and contradictions: a roadmap for computational drug repurposing with knowledge inference. Briefings in Bioinformatics, 2022, 23, .	3.2	5
1210	Current landscape of geneâ€editing technology in biomedicine: Applications, advantages, challenges, and perspectives. MedComm, 2022, 3, .	3.1	2
1211	Genetic variation associated with condensate dysregulation in disease. Developmental Cell, 2022, 57, 1776-1788.e8.	3.1	41
1212	Epigenetic activation of antiviral sensors and effectors of interferon response pathways during SARS-CoV-2 infection. Biomedicine and Pharmacotherapy, 2022, 153, 113396.	2.5	5
1213	Network Pharmacology and Molecular Docking on the Molecular Mechanism of Jiawei-Huang Lian-Gan Jiang Decoction in the Treatment of Colorectal Adenomas. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	0
1214	Artificial Intelligence, Healthcare, Clinical Genomics, and Pharmacogenomics Approaches in Precision Medicine. Frontiers in Genetics, 0, 13, .	1.1	23
1215	A novel splice site variant c.1183â€‰+â€‰1 Gâ€‰>â€‰C in DFNA5 causing autosomal dominant nonsyndromic hearing loss in a Chinese family. BMC Medical Genomics, 2022, 15, .	0.7	2
1216	Mechanism of the Combination of KuShen and XiYangShen on Myocarditis Based on Network Pharmacology and Animal Experiments. Pharmacological Research Modern Chinese Medicine, 2022, , 100141.	0.5	0
1217	Analysis of the multi-physiological and functional mechanism of wheat alkylresorcinols based on reverse molecular docking and network pharmacology. Food and Function, 2022, 13, 9091-9107.	2.1	3
1218	Natural history of Myhre syndrome. Orphanet Journal of Rare Diseases, 2022, 17, .	1.2	5
1219	Clair3-trio: high-performance Nanopore long-read variant calling in family trios with trio-to-trio deep neural networks. Briefings in Bioinformatics, 2022, 23, .	3.2	7
1220	Basic Traditional Chinese Medicinal Compound for Adjuvant Treatment of Helicobacter pylori-Related Gastritis: Implication for Anti-H. pylori-Related Gastritis Drug Discovery. Natural Product Communications, 2022, 17, 1934578X2211139.	0.2	0

#	Article	IF	Citations
1221	Uncovering Signals of Positive Selection in Peruvian Populations from Three Ecological Regions. Molecular Biology and Evolution, 2022, 39, .	3.5	4
1222	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.	0.9	3
1223	The common regulatory pathway of COVID-19 and multiple inflammatory diseases and the molecular mechanism of cepharanthine in the treatment of COVID-19. Frontiers in Pharmacology, 0, 13, .	1.6	5
1224	X-CAP improves pathogenicity prediction of stopgain variants. Genome Medicine, 2022, 14, .	3.6	0
1225	Network pharmacology and molecular docking analysis reveal insights into the molecular mechanism of shiliao decoction in the treatment of cancer-associated malnutrition. Frontiers in Nutrition, 0, 9, .	1.6	3
1226	Study on the Mechanism of Improving HIV/AIDS Immune Function with Jian Aikang Concentrated Pill Based on Network Pharmacology Combined with Experimental Validation. Drug Design, Development and Therapy, 0, Volume 16, 2731-2753.	2.0	0
1227	Investigation of the protective mechanism of leonurine against acute myocardial ischemia by an integrated metabolomics and network pharmacology strategy. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	5
1228	A reverse genetics and genomics approach to gene paralog function and disease: Myokymia and the juxtaparanode. American Journal of Human Genetics, 2022, 109, 1713-1723.	2.6	5
1229	CHDbase: A Comprehensive Knowledgebase for Congenital Heart Disease-related Genes and Clinical Manifestations. Genomics, Proteomics and Bioinformatics, 2023, 21, 216-227.	3.0	4
1230	Pinelliae rhizoma alleviated acute lung injury induced by lipopolysaccharide via suppressing endoplasmic reticulum stress-mediated NLRP3 inflammasome. Frontiers in Pharmacology, 0, 13, .	1.6	6
1231	Data Incompleteness May form a Hard-to-Overcome Barrier to Decoding Lifeâ€™s Mechanism. Biology, 2022, 11, 1208.	1.3	4
1232	Integrated Serum Metabolomics and Network Pharmacology to Reveal the Interventional Effects of Quzhi Decoction against Osteoarthritis Pain. International Journal of Analytical Chemistry, 2022, 2022, 1-11.	0.4	3
1233	Functional Pathway and Process Enrichment Analysis of Genes Associated With Morphological Abnormalities of the Outer Ear. Journal of Craniofacial Surgery, 0, Publish Ahead of Print, .	0.3	1
1235	Rare disease-based scientific annotation knowledge graph. Frontiers in Artificial Intelligence, 0, 5, .	2.0	3
1236	High-throughput sequencing analysis of nuclear-encoded mitochondrial genes reveals a genetic signature of human longevity. GeroScience, 2023, 45, 311-330.	2.1	5
1237	Network pharmacology and molecular docking technology-based predictive study of the active ingredients and potential targets of rhubarb for the treatment of diabetic nephropathy. BMC Complementary Medicine and Therapies, 2022, 22, .	1.2	13
1239	Clinical Real-Time Genome Sequencing to Solve the Complex and Confounded Presentation of a Child With Focal Segmental Glomerulosclerosis and Multiple Malignancies. Kidney International Reports, 2022, 7, 2312-2316.	0.4	2
1240	A cross-disorder dosage sensitivity map of the human genome. Cell, 2022, 185, 3041-3055.e25.	13.5	117

#	Article	IF	Citations
1241	Using network pharmacology to explore the mechanism of Danggui-Shaoyao-San in the treatment of diabetic kidney disease. Frontiers in Pharmacology, 0, 13, .	1.6	2
1242	GlioMarker: An integrated database for knowledge exploration of diagnostic biomarkers in gliomas. Frontiers in Oncology, 0, 12, .	1.3	4
1243	Clinical significance of genetic variation in hypertrophic cardiomyopathy: comparison of computational tools to prioritize missense variants. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	5
1244	Cancer-driving mutations are enriched in genic regions intolerant to germline variation. Science Advances, 2022, 8, .	4.7	2
1245	OARD: Open annotations for rare diseases and their phenotypes based on real-world data. American Journal of Human Genetics, 2022, 109, 1591-1604.	2.6	0
1246	Potential Mechanisms of Biejiajian Pill in the Treatment of Diabetic Atherosclerosis Based on Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulation. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	5
1247	Mechanisms of Chinese Medicine in Gastroesophageal Reflux Disease Treatment: Data Mining and Systematic Pharmacology Study. Chinese Journal of Integrative Medicine, 0, , .	0.7	1
1248	Identification of Interleukin-1-Beta Inhibitors in Gouty Arthritis Using an Integrated Approach Based on Network Pharmacology, Molecular Docking, and Cell Experiments. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-18.	0.5	1
1249	Anticancer effects of OSW-1 on glioma cells via regulation of the PI3K/AKT signal pathway: A network pharmacology approach and experimental validation in vitro and in vivo. Frontiers in Pharmacology, 0, 13, .	1.6	4
1251	Systematic analysis of inheritance pattern determination in genes that cause rare neurodevelopmental diseases. Frontiers in Genetics, 0, 13, .	1.1	5
1252	CPMCP: a database of Chinese patent medicine and compound prescription. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	2
1254	Huayu Jiedu Fang Protects Ovarian Function in Mouse with Endometriosis Iron Overload by Inhibiting Ferroptosis. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-18.	0.5	4
1255	Bioinformatics for sperm phenotypic abnormalities:current situation and future trends. Scientia Sinica Vitae, 2023, 53, 274-286.	0.1	4
1256	Exploring potential mechanism of ciwujia tablets for insomnia by UPLC-Q-TOF-MS/MS, network pharmacology, and experimental validation. Frontiers in Pharmacology, 0, 13, .	1.6	2
1257	Investigation of the Potential Mechanism of Danggui Shaoyao San for the Treatment of Non-alcoholic Fatty Liver Disease (NAFLD) with Network Pharmacology and Molecular Docking. Current Computer-Aided Drug Design, 2022, 18, 258-270.	0.8	4
1258	The Mechanisms Underlying the Pharmacological Effects of GuiPi Decoction on Major Depressive Disorder based on Network Pharmacology and Molecular Docking. Combinatorial Chemistry and High Throughput Screening, 2023, 26, 1701-1728.	0.6	1
1259	Integrated bioinformatics analysis and screening of hub genes in polycystic ovary syndrome. Endocrine, 2022, 78, 615-627.	1.1	3
1260	Regulation and bioinformatic analysis of circ_0015891/miR-129-1-3p axis in methamphetamine-induced dopaminergic apoptosis. Frontiers in Endocrinology, 0, 13, .	1.5	2

#	Article	IF	Citations
1262	A Study on the Mechanism of Herbal Drug FDY003 for Colorectal Cancer Treatment by Employing Network Pharmacology. Natural Product Communications, 2022, 17, 1934578X2211269.	0.2	0
1265	Identification of Molecular Targets and Underlying Mechanisms of Xiaoji Recipe against Pancreatic Cancer Based on Network Pharmacology. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-17.	0.7	1
1266	Drug repositioning: A bibliometric analysis. Frontiers in Pharmacology, 0, 13, .	1.6	7
1267	Network pharmacological investigation into the mechanism of Kaixinsan powder for the treatment of depression. Metabolic Brain Disease, 2022, 37, 2903-2914.	1.4	3
1268	Novel clinical, molecular and bioinformatics insights into the genetic background of autism. Human Genomics, 2022, 16, .	1.4	2
1270	Network pharmacology and in vitro experiments-based strategy to investigate the mechanisms of KangXianYiAi formula for hepatitis B virus-related hepatocellular carcinoma. Frontiers in Pharmacology, 0, 13, .	1.6	3
1271	Editorial: Improving medical diagnosis in rare diseases. Frontiers in Genetics, 0, 13, .	1.1	0
1272	Research into the mechanism of intervention of SanQi in endometriosis based on network pharmacology and molecular docking technology. Medicine (United States), 2022, 101, e30021.	0.4	5
1273	Probing the Potential Mechanism of Quercetin and Kaempferol against Heat Stress-Induced Sertoli Cell Injury: Through Integrating Network Pharmacology and Experimental Validation. International Journal of Molecular Sciences, 2022, 23, 11163.	1.8	4
1274	Unveiling the Mechanism of the Traditional Korean Medicinal Formula FDY003 on Glioblastoma Through a Computational Network Pharmacology Approach. Natural Product Communications, 2022, 17, 1934578X2211263.	0.2	0
1275	Investigation of Anti-Liver Cancer Activity of the Herbal Drug FDY003 Using Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	0
1276	Calcium dobesilate efficiency in the treatment of diabetic kidney disease through suppressing MAPK and chemokine signaling pathways based on clinical evaluation and network pharmacology. Frontiers in Pharmacology, 0, 13, .	1.6	2
1277	Icariin: A Potential Lipid Metabolism Regulator in Osteoarthritis. Natural Product Communications, 2022, 17, 1934578X2211260.	0.2	0
1278	Clinical efficacy evaluation and potential mechanism prediction on Pudilan Xiaoyan oral liquid in treatment of mumps in children based on meta-analysis, network pharmacology, and molecular docking. Frontiers in Pharmacology, 0, 13, .	1.6	1
1279	Exploring Genes and Phenotypes Within Chromosomal Regions Using OMIM's GeneScout. Current Protocols, 2022, 2, .	1.3	2
1280	The phers R package: using phenotype risk scores based on electronic health records to study Mendelian disease and rare genetic variants. Bioinformatics, 2022, 38, 4972-4974.	1.8	5
1281	Elucidation of active ingredients and mechanism of action of hawthorn in the prevention and treatment of atherosclerosis. Journal of Food Biochemistry, 2022, 46, .	1.2	5
1282	Network Pharmacology Analyses of the Pharmacological Targets and Therapeutic Mechanisms of Salvianolic Acid A in Myocardial Infarction. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	1

#	Article	IF	Citations
1283	Phenotypic spectrum in recessive STING-associated vasculopathy with onset in infancy: Four novel cases and analysis of previously reported cases. Frontiers in Immunology, 0, 13, .	2.2	5
1285	Mechanism Investigation of Wuwei Shexiang Pills on Gouty Arthritis via Network Pharmacology, Molecule Docking, and Pharmacological Verification. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-19.	0.5	2
1286	Novel active compounds and the anti-diabetic mechanism of mulberry leaves. Frontiers in Pharmacology, 0, 13, .	1.6	8
1287	Network analysis and experimental pharmacology study explore the protective effects of Isoliquiritigenin on 5-fluorouracil-Induced intestinal mucositis. Frontiers in Pharmacology, 0, 13, .	1.6	3
1288	De novo variants in FRMD5 are associated with developmental delay, intellectual disability, ataxia, and abnormalities of eye movement. American Journal of Human Genetics, 2022, 109, 1932-1943.	2.6	12
1289	Analysis of hereditary cancer gene variant classifications from ClinVar indicates a need for regular reassessment of clinical assertions. Human Mutation, 2022, 43, 2054-2062.	1.1	4
1290	Mixed computational-experimental study to reveal the anti-metastasis and anti-angiogenesis effects of Astragalin in human breast cancer. Computers in Biology and Medicine, 2022, 150, 106131.	3.9	6
1291	Integrating network pharmacology and an experimental validation strategy elucidates the protective effect and mechanism of callicarpa nudiflora against neuroinflammation. RSC Advances, 2022, 12, 31124-31141.	1.7	3
1292	Unraveling the Mechanism of Zhibaidihuang Decoction against IgA Nephropathy Using Network Pharmacology and Molecular Docking Analyses. Tohoku Journal of Experimental Medicine, 2023, 259, 37-47.	0.5	1
1293	Machine Learning-Friendly Biomedical Datasets forÂEquivalence andÂSubsumption Ontology Matching. Lecture Notes in Computer Science, 2022, , 575-591.	1.0	6
1294	TWAS Atlas: a curated knowledgebase of transcriptome-wide association studies. Nucleic Acids Research, 2023, 51, D1179-D1187.	6.5	13
1295	Effect of Curcumin on Attenuation of Liver Cirrhosis via Genes/Proteins and Pathways: A System Pharmacology Study. Nutrients, 2022, 14, 4344.	1.7	9
1296	Network pharmacology and molecular docking analysis on the mechanism of Baihe Zhimu decoction in the treatment of postpartum depression. Medicine (United States), 2022, 101, e29323.	0.4	3
1297	Identifying and Targeting Prediction of the PI3K-AKT Signaling Pathway in Drug-Induced Thrombocytopenia in Infected Patients Receiving Linezolid Therapy: A Network Pharmacology-Based Analysis. Journal of Healthcare Engineering, 2022, 2022, 1-10.	1.1	0
1298	Network toxicology and molecular docking analyses on strychnine indicate CHRM1 is a potential neurotoxic target. BMC Complementary Medicine and Therapies, 2022, 22, .	1.2	2
1300	Investigating the effects and mechanisms of Erchen Decoction in the treatment of colorectal cancer by network pharmacology and experimental validation. Frontiers in Pharmacology, 0, 13, .	1.6	2
1301	Identification of the Anti-Inflammatory Compound, Paeoniflorigenone, in Radix Paeoniae Alba for the Treatment of Polycystic Ovary Syndrome Through Network Pharmacology and Molecular Docking. Natural Product Communications, 2022, 17, 1934578X2211291.	0.2	0
1302	Prediction Targets of a Novel Sesquiterpene Lactone From Eupatorium lindleyanum DC. Against Viral Pneumonia Using Computational Pharmacology. Natural Product Communications, 2022, 17, 1934578X2211314.	0.2	0

#	Article	IF	Citations
1303	Using human genetics to improve safety assessment of therapeutics. Nature Reviews Drug Discovery, 2023, 22, 145-162.	21.5	20
1304	Termviewer â€“ A Web Application for Streamlined Human Phenotype Ontology (HPO) Tagging and Document Annotation. Chemistry and Biodiversity, 0, , .	1.0	0
1306	Astaxanthin attenuates ferroptosis via Keap1-Nrf2/HO-1 signaling pathways in LPS-induced acute lung injury. Life Sciences, 2022, 311, 121091.	2.0	23
1307	Anti-cervical cancer effects of Compound Yangshe granule through the PI3K/AKT pathway based on network pharmacology. Journal of Ethnopharmacology, 2023, 301, 115820.	2.0	5
1308	Mechanism of action of Daqinjiao decoction in treating cerebral small vessel disease explored using network pharmacology and molecular docking technology. Phytomedicine, 2023, 108, 154538.	2.3	10
1310	Recent advances in predicting lncRNAâ€“disease associations based on computational methods. Drug Discovery Today, 2023, 28, 103432.	3.2	3
1311	Combining genetic constraint with predictions of alternative splicing to prioritize deleterious splicing in rare disease studies. BMC Bioinformatics, 2022, 23, .	1.2	7
1312	SCAF4â€related syndromic intellectual disability. American Journal of Medical Genetics, Part A, 2023, 191, 570-574.	0.7	2
1313	Integrating network pharmacology and experimental validation to clarify the anti-hyperuricemia mechanism of cortex phellodendri in mice. Frontiers in Pharmacology, 0, 13, .	1.6	6
1314	Genome-wide identification of exon extension/shrinkage events induced by splice-site-creating mutations. RNA Biology, 2022, 19, 1143-1152.	1.5	0
1317	Therapeutic effects of Guilu-Erxian-Glue treatment on oligoasthenospermia: Evidence from network pharmacology, molecular docking, and in vivo experimental validation. Pharmacological Research Modern Chinese Medicine, 2022, , 100188.	0.5	0
1318	Editorial: NGS technologies of rare diseases diagnosis. Frontiers in Pediatrics, 0, 10, .	0.9	0
1319	Integrative network analysis interweaves the missing links in cardiomyopathy diseasome. Scientific Reports, 2022, 12, .	1.6	8
1320	A novel pathogenesis concept of biliary atresia approached by combined molecular strategies. PLoS ONE, 2022, 17, e0277334.	1.1	1
1321	OrthoDB v11: annotation of orthologs in the widest sampling of organismal diversity. Nucleic Acids Research, 2023, 51, D445-D451.	6.5	76
1322	Explore the mechanism and substance basis of Mahuang FuziXixin Decoction for the treatment of lung cancer based on network pharmacology and molecular docking. Computers in Biology and Medicine, 2022, 151, 106293.	3.9	5
1323	Germline Mosaicism in a Family withMBD5Haploinsufficiency. Journal of Physical Education and Sports Management, 0, , mcs.a006253.	0.5	0
1326	Biomedical knowledge graph embeddings for personalized medicine: Predicting diseaseâ€gene associations. Expert Systems, 2023, 40, .	2.9	5

#	Article	IF	Citations
1327	Enhancing systematic review with machine learning modelling for global health research. The Lancet Digital Health, 2023, 5, e2-e3.	5.9	0
1328	Mechanism study of Cordyceps sinensis alleviates renal ischemiaâ€“reperfusion injury. Open Chemistry, 2022, 20, 1402-1415.	1.0	0
1329	Blood transcriptome comparison between sexes and their function in 4-week Rhode Island red chickens. Animal Cells and Systems, 2022, 26, 358-368.	0.8	1
1330	Uncovering the mechanism of Radix Paeoniae Alba in the treatment of restless legs syndrome based on network pharmacology and molecular docking. Medicine (United States), 2022, 101, e31791.	0.4	2
1331	Systematic Analysis Strategy Based on Network Pharmacology to Investigate the Potential Mechanism of Fritillaria thunbergii Miq. against Idiopathic Pulmonary Fibrosis. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-18.	0.5	1
1332	Exploring the mechanism of Tengli Kangliu Decoction in the prevention and treatment of colorectal cancer precancerous based on network pharmacology. Medicine (United States), 2022, 101, e31690.	0.4	0
1333	Drag-and-drop genome insertion of large sequences without double-strand DNA cleavage using CRISPR-directed integrases. Nature Biotechnology, 2023, 41, 500-512.	9.4	121
1334	Identification of CKS2 and RRM2 as potential markers of vitiligo using bioinformatics analysis. Medicine (United States), 2022, 101, e31908.	0.4	1
1335	Hepatoprotective effect of botanical drug formula on high-fat diet-induced non-alcoholic fatty liver disease by inhibiting lipogenesis and promoting anti-oxidation. Frontiers in Pharmacology, 0, 13, .	1.6	0
1336	Network Pharmacology and Molecular Docking Study on the Multi-Target Mechanisms of Aloe vera for Non-Alcoholic Steatohepatitis Treatment. Plants, 2022, 11, 3585.	1.6	1
1337	Genetically transitional disease: a new concept in genomic medicine. Trends in Genetics, 2023, 39, 98-108.	2.9	16
1338	A network pharmacology study of mechanism and efficacy of Jiawei Huanglian-Wendan decoction in polycystic ovary syndrome with insulin resistance. Medicine (United States), 2022, 101, e32057.	0.4	2
1339	Mechanism of Action of a Chinese Herbal Compound Containing Quercetin, Luteolin, and Kaempferol in the Treatment of Vitiligo Based on Network Pharmacology and Experimental Verification. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	1
1340	Targeting de novo loss-of-function variants in constrained disease genes improves diagnostic rates in the 100,000 Genomes Project. Human Genetics, 2023, 142, 351-362.	1.8	7
1341	Integrated bioinformatics and in silico approaches reveal the biological targets and molecular mechanisms of 1,25-dihydroxyvitamin D against COVID-19 and diabetes mellitus. Frontiers in Nutrition, 0, 9, .	1.6	0
1342	A novel <scp>PLS1</scp> c.981+<scp>1G</scp>>A variant causes autosomalâ€dominant hereditary hearing loss in a family. Clinical Genetics, 2023, 103, 413-423.	1.0	1
1343	Gou Qi Zi inhibits proliferation and induces apoptosis through the PI3K/AKT1 signaling pathway in non-small cell lung cancer. Frontiers in Oncology, 0, 12, .	1.3	3
1344	Efficacy and Mechanism of Quercetin in the Treatment of Experimental Colitis Using Network Pharmacology Analysis. Molecules, 2023, 28, 146.	1.7	2

#	Article	IF	Citations
1345	Uncovering the gene regulatory network of type 2 diabetes through multi-omic data integration. Journal of Translational Medicine, 2022, 20, .	1.8	10
1348	A network pharmacology study on mechanism of resveratrol in treating preeclampsia via regulation of AGE-RAGE and HIF-1 signalling pathways. Frontiers in Endocrinology, 0, 13, .	1.5	1
1349	Identification and characterization of novel compound heterozygous variants in FSHR causing primary ovarian insufficiency with resistant ovary syndrome. Frontiers in Endocrinology, 0, 13, .	1.5	1
1350	Investigate the genetic mechanisms of diabetic kidney disease complicated with inflammatory bowel disease through data mining and bioinformatic analysis. Frontiers in Endocrinology, 0, 13, .	1.5	2
1351	Study on the treatment of postmenopausal osteoporosis with quercetin in Liuwei Dihuang Pill based on network pharmacology. Journal of Orthopaedic Surgery and Research, 2023, 18, .	0.9	4
1353	Genetic Variant in GRM1 Underlies Congenital Cerebellar Ataxia with No Obvious Intellectual Disability. International Journal of Molecular Sciences, 2023, 24, 1551.	1.8	3
1354	Deep dental phenotyping and a novel FAM20A variant in patients with amelogenesis imperfecta type IG. Oral Diseases, 2024, 30, 537-550.	1.5	7
1355	Compound Danshen Dripping Pills moderate intestinal flora and the TLR4/MyD88/NF-ÎºB signaling pathway in alleviating cognitive dysfunction in type 2 diabetic KK-Ay mice. Phytomedicine, 2023, 111, 154656.	2.3	1
1356	Molecular Mechanisms Involved in Craniosynostosis. In Vivo, 2023, 37, 36-46.	0.6	1
1357	Data resources and computational methods for lncRNA-disease association prediction. Computers in Biology and Medicine, 2023, 153, 106527.	3.9	10
1358	POT-3 preferentially binds the terminal DNA-repeat on the telomeric G-overhang. Nucleic Acids Research, 2023, 51, 610-618.	6.5	3
1360	PhenoExam: gene set analyses through integration of different phenotype databases. BMC Bioinformatics, 2022, 23, .	1.2	0
1361	The potential mechanism of Bletilla striata in the treatment of ulcerative colitis determined through network pharmacology, molecular docking, and in vivo experimental verification. Naunyn-Schmiedeberg's Archives of Pharmacology, 2023, 396, 983-1000.	1.4	2
1362	KL-RF: Predicting disease-gene associations with model fusion. , 2022, , .		0
1363	Systems Biology Approaches to the Genetic Complexity of Epilepsy. , 2022, , 5-18.		0
1364	Objective hearing threshold identification from auditory brainstem response measurements using supervised and self-supervised approaches. BMC Neuroscience, 2022, 23, .	0.8	1
1365	Network pharmacology- and molecular simulation-based exploration of therapeutic targets and mechanisms of heparin for the treatment of sepsis/COVID-19. Journal of Biomolecular Structure and Dynamics, 2023, 41, 12586-12598.	2.0	5
1366	Distinguish the Characteristic Mechanism of 3 Drug Pairs of Corydalis Rhizome in Ameliorating Angina Pectoris: Network Pharmacology and Meta-Analysis. Natural Product Communications, 2023, 18, 1934578X2311523.	0.2	0

#	Article	IF	Citations
1368	Exploring the molecular mechanism of Gan Shuang granules for the treatment of non-alcoholic steatohepatitis using network pharmacology, molecular docking, and experimental verification. Frontiers in Pharmacology, 0, 14, .	1.6	1
1369	De Novo Variant in the KCNJ9 Gene as a Possible Cause of Neonatal Seizures. Genes, 2023, 14, 366.	1.0	1
1370	Uncovering the effects and molecular mechanism of Astragalus membranaceus (Fisch.) Bunge and its bioactive ingredients formononetin and calycosin against colon cancer: An integrated approach based on network pharmacology analysis coupled with experimental validation and molecular docking. Frontiers in Pharmacology, 0, 14, .	1.6	4
1371	The visualization of Orphadata neurology phenotypes. Frontiers in Digital Health, 0, 5, .	1.5	0
1372	ProtInteract: A deep learning framework for predicting proteinâ€“protein interactions. Computational and Structural Biotechnology Journal, 2023, 21, 1324-1348.	1.9	7
1373	Defining a Taxonomical Map for Craniosynostoses: An Integrated Nomenclature for Interdisciplinary Workflow and Problem Mapping in Craniosynostoses Management: A Feasibility Study. Journal of Craniofacial Surgery, 2023, 34, 1398-1402.	0.3	0
1374	Network pharmacology-based and pharmacological evaluation of the effects of Curcumae Radix on cerebral ischemiaâ€“Reperfusion injury. World Journal of Traditional Chinese Medicine, 2023, .	0.9	0
1375	Integrative genetic and single cell RNA sequencing analysis provides new clues to the amyotrophic lateral sclerosis neurodegeneration. Frontiers in Neuroscience, 0, 17, .	1.4	2
1376	Rescue of neuropsychiatric phenotypes in a mouse model of 16p11.2 duplication syndrome by genetic correction of an epilepsy network hub. Nature Communications, 2023, 14, .	5.8	7
1377	Automated prioritization of sick newborns for whole genome sequencing using clinical natural language processing and machine learning. Genome Medicine, 2023, 15, .	3.6	5
1378	dbCNV: deleteriousness-based model to predict pathogenicity of copy number variations. BMC Genomics, 2023, 24, .	1.2	1
1379	ETCM v2.0: An update with comprehensive resource and rich annotations for traditional Chinese medicine. Acta Pharmaceutica Sinica B, 2023, 13, 2559-2571.	5.7	12
1380	The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits. Cell Metabolism, 2023, 35, 695-710.e6.	7.2	29
1381	Elucidation of the underlying mechanism of Hua-ban decoction in alleviating acute lung injury by an integrative approach of network pharmacology and experimental verification. Molecular Immunology, 2023, 156, 85-97.	1.0	0
1382	Network pharmacology and in vivo studies reveal the pharmacological effects and molecular mechanisms of Celastrol against acute hepatic injury induced by LPS. International Immunopharmacology, 2023, 117, 109898.	1.7	1
1383	Molecular Mechanism of the Therapeutic Effect of Peach Blossom against Constipation: An Exploratory Study Based on Network Pharmacology Analysis and Molecular Docking Verification. Evidence-based Complementary and Alternative Medicine, 2023, 2023, 1-14.	0.5	0
1384	Key ingredients in Verbena officinalis and determination of their anti-atherosclerotic effect using a computer-aided drug design approach. Frontiers in Plant Science, 0, 14, .	1.7	0
1385	Integrating Network Pharmacology and an Experimental Model to Investigate the Effect of Zhenwu Decoction on Doxorubicin-Induced Heart Failure. Combinatorial Chemistry and High Throughput Screening, 2023, 26, .	0.6	1

#	Article	IF	Citations
1386	Paeoniflorin protects against cisplatin-induced acute kidney injury through targeting Hsp90AA1-Akt protein-protein interaction. Journal of Ethnopharmacology, 2023, 310, 116422.	2.0	2
1387	Network pharmacology, a promising approach to reveal the pharmacology mechanism of Chinese medicine formula. Journal of Ethnopharmacology, 2023, 309, 116306.	2.0	89
1388	Exploring the effective components and potential mechanisms of Zukamu granules against acute upper respiratory tract infections by UHPLC-Q-Exactive Orbitrap-MS and network pharmacology analysis. Arabian Journal of Chemistry, 2023, 16, 104875.	2.3	1
1389	Hypoglycemic effect of Moringa oleifera leaf extract and its mechanism prediction based on network pharmacology. Journal of Future Foods, 2023, 3, 383-391.	2.0	0
1390	The genetic background of hydrocephalus in a population-based cohort: implication of ciliary involvement. Brain Communications, 2022, 5, .	1.5	2
1391	A Retrospective Analysis of Clinically Focused Exome Sequencing Results of 372 Infants with Suspected Monogenic Disorders in China. Pharmacogenomics and Personalized Medicine, 0, Volume 16, 81-97.	0.4	1
1392	MedLexSp â€“ a medical lexicon for Spanish medical natural language processing. Journal of Biomedical Semantics, 2023, 14, .	0.9	2
1394	Exploring the active components and potential mechanisms of Rosa roxburghii Tratt in treating type 2 diabetes mellitus based on UPLC-Q-exactive Orbitrap/MS and network pharmacology. Chinese Medicine, 2023, 18, .	1.6	2
1395	Effect of Shan Zha (Hawthorn or Crataegus) on gastrointestinal cancer: A network pharmacology and molecular docking study. , 2023, 1, 229-237.		3
1396	Common and rare variant associations with latent traits underlying depression, bipolar disorder, and schizophrenia. Translational Psychiatry, 2023, 13, .	2.4	2
1398	Aberrant phase separation and nucleolar dysfunction in rare genetic diseases. Nature, 0, , .	13.7	9
1399	The scalable precision medicine open knowledge engine (SPOKE): a massive knowledge graph of biomedical information. Bioinformatics, 2023, 39, .	1.8	16
1400	Rise of Deep Learning Clinical Applications and Challenges in Omics Data: A Systematic Review. Diagnostics, 2023, 13, 664.	1.3	2
1401	Potential Mechanisms of Yiqi Jiedu Huayu Decoction in the Treatment of Diabetic Microvascular Complications Based on Network Analysis, Molecular Docking, and Experimental Validation. Evidence-based Complementary and Alternative Medicine, 2023, 2023, 1-19.	0.5	0
1402	Exploring the mechanism of curcumin in the treatment of colon cancer based on network pharmacology and molecular docking. Frontiers in Pharmacology, 0, 14, .	1.6	15
1404	Systematic analysis on the mechanism of Zhizi-Bopi decoction against hepatitis B via network pharmacology and molecular docking. Biotechnology Letters, 2023, 45, 463-478.	1.1	0
1405	Dapagliflozin alleviates myocardial ischemia/reperfusion injury by reducing ferroptosis via MAPK signaling inhibition. Frontiers in Pharmacology, 0, 14, .	1.6	13
1406	Active substances and molecular mechanisms of the anti-myocardial ischemia effects of Carthami flos by network pharmacology and in vitro experiments. Heliyon, 2023, 9, e13877.	1.4	0

#	Article	IF	Citations
1409	AIMedGraph: a comprehensive multi-relational knowledge graph for precision medicine. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	1.4	2
1411	Wuling San Based on Network Pharmacology and in vivo Evidence Against Hyperuricemia via Improving Oxidative Stress and Inhibiting Inflammation. Drug Design, Development and Therapy, 0, Volume 17, 675-690.	2.0	2
1412	The mechanism of Croci stigma in the treatment of melasma based on network pharmacology and molecular docking. Journal of Cosmetic Dermatology, 2023, 22, 2105-2114.	0.8	3
1413	Marsdenia tenacissima injection induces the apoptosis of prostate cancer by regulating the AKT/GSK3Î²/STAT3 signaling axis. Chinese Journal of Natural Medicines, 2023, 21, 113-126.	0.7	2
1414	The evolution of comprehensive genetic analysis in neurology: Implications for precision medicine. Journal of the Neurological Sciences, 2023, 447, 120609.	0.3	3
1415	Integration of LC-LTQ-Orbitrap-MS and Network Pharmacology to Analyze the Active Components of Sijunzi Decoction and their Mechanism of Action Against Cytotoxicity-associated Premature Ovarian Insufficiency. Combinatorial Chemistry and High Throughput Screening, 2023, 26, .	0.6	0
1416	Predicting functional effects of ion channel variants using new phenotypic machine learning methods. PLoS Computational Biology, 2023, 19, e1010959.	1.5	7
1417	Brain-wide transcriptome-based metabolic alterations in Parkinson's disease: human inter-region and human-experimental model correlations. Molecular Omics, 2023, 19, 522-537.	1.4	1
1418	Prospects for the application of traditional Chinese medicine network pharmacology in food science research. Journal of the Science of Food and Agriculture, 2023, 103, 5183-5200.	1.7	5
1419	Arctiin-encapsulated DSPE-PEG bubble-like nanoparticles inhibit alveolar epithelial type 2 cell senescence to alleviate pulmonary fibrosis via the p38/p53/p21 pathway. Frontiers in Pharmacology, 0, 14, .	1.6	6
1420	Evidence of clinical efficacy and pharmacological mechanism of N-butylphthalide in the treatment of delayed encephalopathy after acute carbon monoxide poisoning. Frontiers in Neurology, 0, 14, .	1.1	0
1421	Total Flavonoids of Polygala fallax Hemsl Induce Apoptosis of Human Ectopic Endometrial Stromal Cells through PI3K/AKT/Bcl-2 Signaling Pathway. Gynecologic and Obstetric Investigation, 2023, 88, 197-213.	0.7	1
1422	Network Pharmacology and Experimental Validation to Explore That Celastrol Targeting PTEN is the Potential Mechanism of Tripterygium wilfordii (LÃ©v.) Hutch Against IgA Nephropathy. Drug Design, Development and Therapy, 0, Volume 17, 887-900.	2.0	0
1424	Pharmacological Mechanism of Aucklandiae Radix against Gastric Ulcer Based on Network Pharmacology and In Vivo Experiment. Medicina (Lithuania), 2023, 59, 666.	0.8	1
1425	Effect of botanical drugs in improving symptoms of hypertensive nephropathy: Analysis of real-world data, retrospective cohort, network, and experimental assessment. Frontiers in Pharmacology, 0, 14, .	1.6	0
1426	DisGeReExT: a knowledge discovery system for exploration of diseaseâ€“gene associations through large-scale literature-wide analysis study. Knowledge and Information Systems, 0, , .	2.1	0
1427	Genomics of perivascular space burden unravels early mechanisms of cerebral small vessel disease. Nature Medicine, 2023, 29, 950-962.	15.2	14
1428	Potential mechanisms of osthole against bladder cancer cells based on network pharmacology, molecular docking, and experimental validation. BMC Complementary Medicine and Therapies, 2023, 23, .	1.2	2

#	Article	IF	Citations
1429	The convergent application of metabolites from Avena sativa and gut microbiota to ameliorate non-alcoholic fatty liver disease: a network pharmacology study. Journal of Translational Medicine, 2023, 21, .	1.8	0
1430	Transcriptome analyses of murine right and left maxillaâ€“mandibular complex. Orthodontics and Craniofacial Research, 2023, 26, 39-47.	1.2	1
1431	A novel self-attention enriching mechanism for biomedical question answering. Expert Systems With Applications, 2023, 225, 120210.	4.4	1
1432	Salvianolic Acid A Improves Rat Kidney Injury by Regulating MAPKs and TGF-Î²1/Smads Signaling Pathways. Molecules, 2023, 28, 3630.	1.7	5
1443	Foundations of pharmacogenomics and personalized medicine. , 2023, , 15-32.		0
1481	The omics era: a nexus of untapped potential for Mendelian chromatinopathies. Human Genetics, 0, , .	1.8	5
1501	A 20-Year Journey ofÂTracing theÂDevelopment ofÂWeb Catalogues forÂRare Diseases. Lecture Notes in Computer Science, 2023, , 165-179.	1.0	0
1504	Network Pharmacology for Drug Repositioning in Anti-Alzheimerâ€™s Drug Development. Neuromethods, 2023, , 433-463.	0.2	0
1520	The Nexus Between Chromosomal Abnormalities and Single Gene Disorders. , 2023, , 25-56.		0
1526	Genomic approaches to rare disorder diagnosis. , 2024, , 225-239.		0
1540	Identification of potential inhibitor(s) against phospholipase A2 using a network pharmacology-based approach. , 2023, , 15-38.		0
1572	Molecular Investigation of Proteinâ€“Protein Interaction Candidates Related to the Mammalian Brain. , 2023, , 81-107.		0
1646	Ontology Matching Using Multi-head Attention Graph Isomorphism Network. Lecture Notes in Computer Science, 2024, , 200-213.	1.0	0
1668	Hierarchical Semantic Augmentation Graph Neural Network for Drug-Disease Association Prediction. , 2023, , .		0
1693	The comparison of local context collection systems and methods. , 2024, , .		0