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The **STRING** database in 2011: functional interaction networks of proteins, globally integrated and scored

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2238	Detection and characterization of interleukin-6 gene variants in <i>Canis familiaris</i> : association studies with periodontal disease. 2011 , 485, 139-45		7
2237	Matrix vesicles isolated from mineralization-competent Saos-2 cells are selectively enriched with annexins and S100 proteins. 2011 , 412, 683-7		19
2236	ANAT: a tool for constructing and analyzing functional protein networks. 2011 , 4, pl1		68
2235	Global cellular changes induced by <i>Legionella pneumophila</i> infection of bone marrow-derived macrophages. 2011 , 216, 1274-85		10
2234	ERK-associated changes of AP-1 proteins during fear extinction. 2011 , 47, 137-44		27
2233	A differential proteomic approach identifies structural and functional components that contribute to the differentiation of brain capillary endothelial cells. 2011 , 75, 628-41		21
2232	Interaction databases on the same page. 2011 , 29, 391-3		33

2231	Targeting protein-protein interactions and fragment-based drug discovery. 2012 , 317, 145-79	79
2230	Proteomics Analysis of the Effects of Cyanate on <i>Chromobacterium violaceum</i> Metabolism. 2011 , 2, 736-47	4
2229	The Prediction and Analysis of Inter- and Intra-Species Protein-Protein Interaction. 2011 ,	
2228	Protein domain of unknown function 3233 is a translocation domain of autotransporter secretory mechanism in gamma proteobacteria. 2011 , 6, e25570	10
2227	Mesodermal progenitor cells (MPCs) differentiate into mesenchymal stromal cells (MSCs) by activation of Wnt5/calmodulin signalling pathway. 2011 , 6, e25600	24
2226	Revealing the functions of the transketolase enzyme isoforms in <i>Rhodospseudomonas palustris</i> using a systems biology approach. 2011 , 6, e28329	9
2225	3DSwap: curated knowledgebase of proteins involved in 3D domain swapping. 2011 , 2011, bar042	23
2224	Proteases in malaria parasites - a phylogenomic perspective. 2011 , 12, 417-27	12
2223	Challenges for the prediction of macromolecular interactions. 2011 , 21, 382-90	70
2222	Systematic prediction of gene function in <i>Arabidopsis thaliana</i> using a probabilistic functional gene network. 2011 , 6, 1429-42	38
2221	A proteome-wide, quantitative survey of in vivo ubiquitylation sites reveals widespread regulatory roles. 2011 , 10, M111.013284	644
2220	Integrative computational biology for cancer research. 2011 , 130, 465-81	21
2219	Beyond genome-wide association studies: new strategies for identifying genetic determinants of hypertension. 2011 , 13, 442-51	27
2218	Role of Bcl-3 in solid tumors. 2011 , 10, 152	60
2217	CREST--a large and diverse superfamily of putative transmembrane hydrolases. 2011 , 6, 37	51
2216	Predictive integration of gene functional similarity and co-expression defines treatment response of endothelial progenitor cells. 2011 , 5, 46	7
2215	GPS-Prot: a web-based visualization platform for integrating host-pathogen interaction data. 2011 , 12, 298	43
2214	ProPhylo: partial phylogenetic profiling to guide protein family construction and assignment of biological process. 2011 , 12, 434	13

2213	Network-based functional enrichment. 2011 , 12 Suppl 13, S14		10
2212	Genome-wide survey of yeast mutations leading to activation of the yeast cell integrity MAPK pathway: novel insights into diverse MAPK outcomes. 2011 , 12, 390		35
2211	Proteomic and biochemical analyses reveal the activation of unfolded protein response, ERK-1/2 and ribosomal protein S6 signaling in experimental autoimmune myocarditis rat model. 2011 , 12, 520		11
2210	Protease-associated cellular networks in malaria parasite <i>Plasmodium falciparum</i> . 2011 , 12 Suppl 5, S9		16
2209	Proteomic analysis of Col11a1-associated protein complexes. 2011 , 11, 4660-76		14
2208	Reactome pathway analysis to enrich biological discovery in proteomics data sets. 2011 , 11, 3598-613		71
2207	Links between genetics and pathophysiology in the autism spectrum disorders. 2011 , 3, 438-50		37
2206	A role for transcription factor E2F2 in hepatocyte proliferation and timely liver regeneration. 2011 , 301, G20-31		25
2205	Modeling metabolic networks for mammalian cell systems: general considerations, modeling strategies, and available tools. 2012 , 127, 71-108		6
2204	Pani. 2011 ,		4
2203	A hybrid framework for genome wide epistasis discovery. 2011 , 2011, 6479-82		
2202	Waves of early transcriptional activation and pluripotency program initiation during human preimplantation development. 2011 , 138, 3699-709		183
2201	The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2011 , 39, D1-6	20.1	60
2200	Functional and systems biology approaches to Huntington's disease. 2011 , 10, 109-14		3
2199	The universally conserved prokaryotic GTPases. 2011 , 75, 507-42, second and third pages of table of content		127
2198	'Sciencenet'--towards a global search and share engine for all scientific knowledge. 2011 , 27, 1734-5		3
2197	Identification of genes involved in radioresistance of nasopharyngeal carcinoma by integrating gene ontology and protein-protein interaction networks. 2012 , 40, 85-92		32
2196	The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation. 2011 , 7, 533		80

2195	GCView: the genomic context viewer for protein homology searches. <i>Nucleic Acids Research</i> , 2011 , 39, W353-6	20.1	18
2194	Tissue-specific subnetworks and characteristics of publicly available human protein interaction databases. 2011 , 27, 2414-21		41
2193	Network approaches to the functional analysis of microbial proteins. 2011 , 59, 101-33		4
2192	SH3 domain-based phototrapping in living cells reveals Rho family GAP signaling complexes. 2011 , 4, rs13		25
2191	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011 , 39, W412-5	20.1	244
2190	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. <i>Nucleic Acids Research</i> , 2011 , 39, 9473-97	20.1	102
2189	Mechanisms and evolutionary patterns of mammalian and avian dosage compensation. 2012 , 10, e1001328		139
2188	A discovery resource of rare copy number variations in individuals with autism spectrum disorder. 2012 , 2, 1665-85		132
2187	Evolution of the land plant exocyst complexes. 2012 , 3, 159		93
2186	Visual analysis of transcriptome data in the context of anatomical structures and biological networks. 2012 , 3, 252		5
2185	Reverse engineering: a key component of systems biology to unravel global abiotic stress cross-talk. 2012 , 3, 294		29
2184	The chordate proteome history database. 2012 , 8, 437-47		5
2183	Quantitative phosphoproteomics in nuclei of vasopressin-sensitive renal collecting duct cells. 2012 , 303, C1006-20		20
2182	RsfA (YbeB) proteins are conserved ribosomal silencing factors. 2012 , 8, e1002815		65
2181	Predicting the fission yeast protein interaction network. 2012 , 2, 453-67		20
2180	The induction of serine/threonine protein phosphorylations by a PDGFR/TrkA chimera in stably transfected PC12 cells. 2012 , 11, 15-30		12
2179	The core regulation module of stress-responsive regulatory networks in yeast. <i>Nucleic Acids Research</i> , 2012 , 40, 8793-802	20.1	16
2178	Large-scale phosphotyrosine proteomic profiling of rat renal collecting duct epithelium reveals predominance of proteins involved in cell polarity determination. 2012 , 302, C27-45		10

2177	BioContext: an integrated text mining system for large-scale extraction and contextualization of biomolecular events. 2012 , 28, 2154-61		38
2176	The CanOE strategy: integrating genomic and metabolic contexts across multiple prokaryote genomes to find candidate genes for orphan enzymes. 2012 , 8, e1002540		26
2175	Genomic context analysis reveals dense interaction network between vertebrate ultraconserved non-coding elements. 2012 , 28, i395-i401		16
2174	The non-classical ArsR-family repressor PyeR (PA4354) modulates biofilm formation in <i>Pseudomonas aeruginosa</i> . 2012 , 158, 2598-2609		14
2173	Exposure of rats to environmental tobacco smoke during cerebellar development alters behavior and perturbs mitochondrial energetics. 2012 , 120, 1684-91		16
2172	Proteomic characterization of a mouse model of familial Danish dementia. 2012 , 2012, 728178		8
2171	Proteomic cornerstones of hematopoietic stem cell differentiation: distinct signatures of multipotent progenitors and myeloid committed cells. 2012 , 11, 286-302		52
2170	The identification of short linear motif-mediated interfaces within the human interactome. 2012 , 28, 976-82		50
2169	iELM--a web server to explore short linear motif-mediated interactions. <i>Nucleic Acids Research</i> , 2012 , 40, W364-9	20.1	26
2168	Expression quantitative trait Loci for extreme host response to influenza a in pre-collaborative cross mice. 2012 , 2, 213-21		68
2167	Proteomic phenotyping of <i>Novosphingobium nitrogenifigens</i> reveals a robust capacity for simultaneous nitrogen fixation, polyhydroxyalkanoate production, and resistance to reactive oxygen species. 2012 , 78, 4802-15		18
2166	OGEE: an online gene essentiality database. <i>Nucleic Acids Research</i> , 2012 , 40, D901-6	20.1	140
2165	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, 60-76		130
2164	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012 , 40, D76-83	20.1	142
2163	Identification of critical host mitochondrion-associated genes during <i>Ehrlichia chaffeensis</i> infections. 2012 , 80, 3576-86		16
2162	Profiling lipid-protein interactions using nonquenched fluorescent liposomal nanovesicles and proteome microarrays. 2012 , 11, 1177-90		29
2161	Protein-protein interaction networks: unraveling the wiring of molecular machines within the cell. 2012 , 11, 489-96		53
2160	Selenium-dependent biogenesis of formate dehydrogenase in <i>Campylobacter jejuni</i> is controlled by the fdhTU accessory genes. 2012 , 194, 3814-23		33

2159	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. <i>Nucleic Acids Research</i> , 2012 , 40, 8818-34	20.1	64
2158	Vesicular signalling and immune modulation as hedonic fingerprints: proteomic profiling in the chronic mild stress depression model. 2012 , 26, 1569-83		22
2157	A Resource of Quantitative Functional Annotation for Homo sapiens Genes. 2012 , 2, 223-33		6
2156	ChromoHub: a data hub for navigators of chromatin-mediated signalling. 2012 , 28, 2205-6		66
2155	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012 , 40, D284-9	20.1	387
2154	Integrative proteomic profiling of protein activity and interactions using protein arrays. 2012 , 11, 1167-76		12
2153	First insights into the unexplored two-component system YehU/YehT in Escherichia coli. 2012 , 194, 4272-84		36
2152	Genome-wide transcriptomic variations of human lymphoblastoid cell lines: insights from pairwise gene-expression correlations. 2012 , 13, 1893-904		8
2151	Protein interactions with piALU RNA indicates putative participation of retroRNA in the cell cycle, DNA repair and chromatin assembly. 2012 , 2, 26-35		17
2150	Integration of stress-related and reactive oxygen species-mediated signals by Topoisomerase VI in Arabidopsis thaliana. 2012 , 109, 16360-5		40
2149	A FOXO3-IRF7 gene regulatory circuit limits inflammatory sequelae of antiviral responses. 2012 , 490, 421-5		112
2148	Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. <i>Nucleic Acids Research</i> , 2012 , 40, D465-71	20.1	66
2147	How much can we learn about the function of bacterial rRNA modification by mining large-scale experimental datasets?. <i>Nucleic Acids Research</i> , 2012 , 40, 5694-705	20.1	15
2146	Uncertain interactions affect degree distribution of biological networks. 2012 ,		4
2145	Prediction of novel systems components in cell cycle regulation in malaria parasite by subnetwork alignments. 2012 ,		
2144	An S-System Parameter Estimation Method (SPEM) for biological networks. 2012 , 19, 175-87		12
2143	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2013 , 41, D808-15	20.1	3033
2142	The BioGRID interaction database: 2013 update. <i>Nucleic Acids Research</i> , 2013 , 41, D816-23	20.1	534

2141	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. 2012 , 9, 345-50		375
2140	Robustness and accuracy of functional modules in integrated network analysis. 2012 , 28, 1887-94		18
2139	Proteomic assessment shows that many endoplasmic reticulum (ER)-resident proteins are targeted by N(epsilon)-lysine acetylation in the lumen of the organelle and predicts broad biological impact. 2012 , 287, 22436-40		38
2138	Biophysical and computational fragment-based approaches to targeting protein-protein interactions: applications in structure-guided drug discovery. 2012 , 45, 383-426		74
2137	Clinical proteomics: getting to the heart of the matter. 2012 , 5, 377		3
2136	Comparative expression profiling identifies differential roles for Myogenin and p38MAPK signaling in myogenesis. 2012 , 4, 386-97		44
2135	Extending signaling pathways with protein-interaction networks. Application to apoptosis. 2012 , 16, 245-56		5
2134	Core module network construction for breast cancer metastasis. 2012 ,		
2133	A comprehensive manually curated protein-protein interaction database for the Death Domain superfamily. <i>Nucleic Acids Research</i> , 2012 , 40, D331-6	20.1	35
2132	Molecular pathways: rodent parvoviruses--mechanisms of oncolysis and prospects for clinical cancer treatment. 2012 , 18, 3516-23		68
2131	Glioblastoma multiforme: novel therapeutic approaches. 2012 , 2012, 642345		13
2130	Virtual interactomics of proteins from biochemical standpoint. 2012 , 2012, 976385		5
2129	Mining the unknown: a systems approach to metabolite identification combining genetic and metabolic information. 2012 , 8, e1003005		126
2128	SMART 7: recent updates to the protein domain annotation resource. <i>Nucleic Acids Research</i> , 2012 , 40, D302-5	20.1	1226
2127	GENIES: gene network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2012 , 40, W162-7	20.1	33
2126	Evolution of the human-specific microRNA miR-941. 2012 , 3, 1145		85
2125	ProOpDB: Prokaryotic Operon DataBase. <i>Nucleic Acids Research</i> , 2012 , 40, D627-31	20.1	130
2124	Comparative interactomics with Funcoup 2.0. <i>Nucleic Acids Research</i> , 2012 , 40, D821-8	20.1	41

2123	COXPRESdb: a database of comparative gene coexpression networks of eleven species for mammals. <i>Nucleic Acids Research</i> , 2013 , 41, D1014-20	20.1	66
2122	ASEB: a web server for KAT-specific acetylation site prediction. <i>Nucleic Acids Research</i> , 2012 , 40, W376-9	20.1	58
2121	Structure and function of von Willebrand factor. 2012 , 23, 11-22		36
2120	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. 2012 , 21, 5385-94		162
2119	Comparison of tear protein levels in breast cancer patients and healthy controls using a de novo proteomic approach. 2012 , 28, 429-38		68
2118	Proteome-wide analysis of lysine acetylation suggests its broad regulatory scope in <i>Saccharomyces cerevisiae</i> . 2012 , 11, 1510-22		200
2117	PaxDb, a database of protein abundance averages across all three domains of life. 2012 , 11, 492-500		351
2116	Chaperones divide yeast proteins into classes of expression level and evolutionary rate. 2012 , 4, 618-25		16
2115	C7orf30 specifically associates with the large subunit of the mitochondrial ribosome and is involved in translation. <i>Nucleic Acids Research</i> , 2012 , 40, 4040-51	20.1	42
2114	Network systems biology for targeted cancer therapies. 2012 , 31, 134-41		20
2113	Computational analysis for functional and evolutionary aspects of BACE-1 and associated Alzheimer's related proteins. 2012 , 1, 322		5
2112	Longitudinal characterization of the brain proteomes for the tg2576 amyloid mouse model using shotgun based mass spectrometry. 2012 , 11, 6159-74		22
2111	A cohesin-RAD21 interactome. 2012 , 442, 661-70		14
2110	Glutamate decarboxylase-dependent acid resistance in orally acquired bacteria: function, distribution and biomedical implications of the gadBC operon. 2012 , 86, 770-86		96
2109	Genome-wide association analyses identify 13 new susceptibility loci for generalized vitiligo. 2012 , 44, 676-80		239
2108	Vertebrate nucleoplasmin and NASP: egg histone storage proteins with multiple chaperone activities. 2012 , 26, 4788-804		35
2107	Protein aggregation caused by aminoglycoside action is prevented by a hydrogen peroxide scavenger. 2012 , 48, 713-22		75
2106	Online tools for bioinformatics analyses in nutrition sciences. 2012 , 3, 654-65		12

2105	Proteomic evaluation of inflammatory proteins in rat spleen interstitial fluid and lymph during LPS-induced systemic inflammation reveals increased levels of ADAMST1. 2012 , 11, 5338-49	27
2104	Identification of retinoblastoma related genes with shortest path in a protein-protein interaction network. 2012 , 94, 1910-7	24
2103	Quantitative proteomic analysis of mouse embryonic fibroblasts and induced pluripotent stem cells using 16O/18O labeling. 2012 , 11, 2091-102	9
2102	Suite of activity-based probes for cellulose-degrading enzymes. 2012 , 134, 20521-32	52
2101	Temporal changes in milk proteomes reveal developing milk functions. 2012 , 11, 3897-907	74
2100	Emerging techniques in proteomics for probing nano-bio interactions. 2012 , 6, 10438-48	94
2099	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012 , 40, D876-80	20.1 219
2098	TranscriptomeBrowser 3.0: introducing a new compendium of molecular interactions and a new visualization tool for the study of gene regulatory networks. 2012 , 13, 19	16
2097	Data mining for microbiologists. 2012 , 39, 27-79	7
2096	Detergent selection for enhanced extraction of membrane proteins. 2012 , 86, 12-20	100
2095	Systems analysis of plant functional, transcriptional, physical interaction, and metabolic networks. 2012 , 24, 3859-75	76
2094	Divalent metal transporter 1 regulates iron-mediated ROS and pancreatic β cell fate in response to cytokines. 2012 , 16, 449-61	101
2093	Identity and function of a large gene network underlying mutagenic repair of DNA breaks. 2012 , 338, 1344-8	150
2092	Improving the description of metabolic networks: the TCA cycle as example. 2012 , 26, 3625-36	21
2091	Current methods for global proteome identification. 2012 , 9, 519-32	41
2090	Iterative orthology prediction uncovers new mitochondrial proteins and identifies C12orf62 as the human ortholog of COX14, a protein involved in the assembly of cytochrome c oxidase. 2012 , 13, R12	75
2089	Endosomal crosstalk: meeting points for signaling pathways. 2012 , 22, 447-56	84
2088	Comprehensive mapping of the bull sperm surface proteome. 2012 , 12, 3559-79	70

2087	TIP30 directly binds p53 tumor suppressor protein in vitro. 2012 , 34, 495-500	7
2086	Motif analysis unveils the possible co-regulation of chloroplast genes and nuclear genes encoding chloroplast proteins. 2012 , 80, 177-87	2
2085	Proteomic analysis of lysine acetylation sites in rat tissues reveals organ specificity and subcellular patterns. 2012 , 2, 419-31	405
2084	RNAi screening reveals proteasome- and Cullin3-dependent stages in vaccinia virus infection. 2012 , 2, 1036-47	105
2083	Characterizing the neurite outgrowth inhibitory effect of Mani. 2012 , 586, 3018-23	3
2082	A new family of bacterial DNA repair proteins annotated by the integration of non-homology, distant homology and structural bioinformatic methods. 2012 , 586, 3908-13	3
2081	Proteomic analysis of liver development of lean Pekin duck (<i>Anas platyrhynchos domestica</i>). 2012 , 75, 5396-413	15
2080	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , 2013 , 41, D306-11	20.1 99
2079	Rewiring the dynamic interactome. 2012 , 8, 2054-66, 2013	24
2078	ANAP: an integrated knowledge base for Arabidopsis protein interaction network analysis. 2012 , 158, 1523-33	26
2077	SAMNet: a network-based approach to integrate multi-dimensional high throughput datasets. 2012 , 4, 1415-27	19
2076	Large-scale signaling network reconstruction. 2012 , 9, 1696-708	13
2075	Construction and analysis of human phosphorylation network. 2012 ,	
2074	Quantitative proteome analysis reveals RNA processing factors as modulators of ionizing radiation-induced apoptosis in the <i>C. elegans</i> germline. 2012 , 11, 4277-88	8
2073	Potential for phosphite and phosphonate utilization by <i>Prochlorococcus</i> . 2012 , 6, 827-34	53
2072	In silico evidence of signaling pathways of notch mediated networks in leukemia. 2012 , 1, e201207005	3
2071	Integrated proteomic, transcriptomic, and biological network analysis of breast carcinoma reveals molecular features of tumorigenesis and clinical relapse. 2012 , 11, M111.014910	38
2070	Quantitative phosphoproteome profiling of iron-deficient Arabidopsis roots. 2012 , 159, 403-17	65

2069	Strategies beyond genome-wide association studies for atherosclerosis. 2012 , 32, 170-81	32
2068	Computational approaches for analyzing information flow in biological networks. 2012 , 5, re1	134
2067	Proteomic study and marker protein identification of <i>Caenorhabditis elegans</i> lipid droplets. 2012 , 11, 317-28	117
2066	Exome sequencing identifies a novel multiple sclerosis susceptibility variant in the <i>TYK2</i> gene. 2012 , 79, 406-11	42
2065	Uncovering the co-evolutionary network among prokaryotic genes. 2012 , 28, i389-i394	23
2064	A strategy based on protein-protein interface motifs may help in identifying drug off-targets. 2012 , 52, 2273-86	22
2063	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. 2012 , 14, 1089-98	195
2062	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, M111.015156	29
2061	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. 2012 , 46, 212-25	239
2060	Tianma modulates proteins with various neuro-regenerative modalities in differentiated human neuronal SH-SY5Y cells. 2012 , 60, 827-36	20
2059	Neuronal porosome proteome: Molecular dynamics and architecture. 2012 , 75, 3952-62	25
2058	Domain-mediated protein interaction prediction: From genome to network. 2012 , 586, 2751-63	35
2057	RACK1 research - ships passing in the night?. 2012 , 586, 2787-9	34
2056	A systems genetics approach identifies genes and pathways for type 2 diabetes in human islets. 2012 , 16, 122-34	266
2055	In silico structural, functional and pathogenicity evaluation of a novel mutation: an overview of HSD3B2 gene mutations. 2012 , 503, 215-21	22
2054	Understanding cancer mechanisms through network dynamics. 2012 , 11, 543-60	24
2053	ZO-1 regulates Erk, Smad1/5/8, Smad2, and RhoA activities to modulate self-renewal and differentiation of mouse embryonic stem cells. 2012 , 30, 1885-900	18
2052	Core module biomarker identification with network exploration for breast cancer metastasis. 2012 , 13, 12	31

2051	Genes2FANs: connecting genes through functional association networks. 2012 , 13, 156	23
2050	Network enrichment analysis: extension of gene-set enrichment analysis to gene networks. 2012 , 13, 226	86
2049	PhenoLink--a web-tool for linking phenotype to ~omics data for bacteria: application to gene-trait matching for <i>Lactobacillus plantarum</i> strains. 2012 , 13, 170	41
2048	The transcriptional landscape of the deep-sea bacterium <i>Photobacterium profundum</i> in both a <i>toxR</i> mutant and its parental strain. 2012 , 13, 567	24
2047	Expression of <i>Shigella flexneri</i> <i>gluQ-rs</i> gene is linked to <i>dksA</i> and controlled by a transcriptional terminator. 2012 , 12, 226	9
2046	A three-dimensional topology of complex I inferred from evolutionary correlations. 2012 , 12, 19	9
2045	Proteomic analysis of plasma membranes isolated from undifferentiated and differentiated HepaRG cells. 2012 , 10, 47	50
2044	Determination of minimal transcriptional signatures of compounds for target prediction. 2012 , 2012, 2	7
2043	MESSA: MEta-Server for protein Sequence Analysis. 2012 , 10, 82	33
2042	Ethanolamine utilization in <i>Vibrio alginolyticus</i> . 2012 , 7, 45; discussion 45	7
2041	Multiple biomarker tissue arrays: A computational approach to identifying protein-protein interactions in the EGFR/ERK signalling pathway. 2012 , 7, 14	1
2040	HINT: High-quality protein interactomes and their applications in understanding human disease. 2012 , 6, 92	268
2039	Autworks: a cross-disease network biology application for Autism and related disorders. 2012 , 5, 56	16
2038	A comparison and evaluation of five biclustering algorithms by quantifying goodness of biclusters for gene expression data. 2012 , 5, 8	18
2037	Human gene correlation analysis (HGCA): a tool for the identification of transcriptionally co-expressed genes. 2012 , 5, 265	20
2036	Schizophrenia shows a unique metabolomics signature in plasma. 2012 , 2, e149	111
2035	Loss of the tumor suppressor BAP1 causes myeloid transformation. 2012 , 337, 1541-6	290
2034	Archaeal JAB1/MPN/MOV34 metalloenzyme (HvJAMM1) cleaves ubiquitin-like small archaeal modifier proteins (SAMPs) from protein-conjugates. 2012 , 86, 971-87	36

2033	Using genome-wide expression profiling to define gene networks relevant to the study of complex traits: from RNA integrity to network topology. 2012 , 104, 91-133	12
2032	CINPER: an interactive web system for pathway prediction for prokaryotes. 2012 , 7, e51252	4
2031	Molecular mechanisms regulating the establishment of hepatocyte polarity during human hepatic progenitor cell differentiation into a functional hepatocyte-like phenotype. 2012 , 125, 5800-10	11
2030	Integrated inference and analysis of regulatory networks from multi-level measurements. 2012 , 110, 19-56	15
2029	Studies on <i>Shigella boydii</i> infection in <i>Caenorhabditis elegans</i> and bioinformatics analysis of immune regulatory protein interactions. 2012 , 1824, 1449-56	15
2028	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. 2012 , 23, 609-16	71
2027	Minority of mammalian orthologs can be regarded as physiologically closest genes. 2012 , 509, 201-5	
2026	Sequence of <i>Leptospira santarosai</i> serovar Shermani genome and prediction of virulence-associated genes. 2012 , 511, 364-70	36
2025	Quantitative phosphoproteomics to characterize signaling networks. 2012 , 23, 863-71	50
2024	Identification of the pathogenic pathways in osteoarthritic hip cartilage: commonality and discord between hip and knee OA. 2012 , 20, 1029-38	71
2023	Inferring Gene Interaction Networks. 2012 , 31-68	
2022	Using functional genomics to identify drug targets: a Dupuytren's disease example. 2012 , 910, 15-31	1
2021	Bioinformatical and in vitro approaches to essential oil-induced matrix metalloproteinase inhibition. 2012 , 50, 675-86	20
2020	The <i>Plasmodium falciparum</i> schizont phosphoproteome reveals extensive phosphatidylinositol and cAMP-protein kinase A signaling. 2012 , 11, 5323-37	110
2019	Differential expressions of nuclear proteomes between honeybee (<i>Apis mellifera</i> L.) Queen and Worker Larvae: a deep insight into caste pathway decisions. 2012 , 11, 1317-29	30
2018	Next generation sequencing in clinical medicine: Challenges and lessons for pathology and biomedical informatics. 2012 , 3, 40	106
2017	Novel biomarkers for pre-diabetes identified by metabolomics. 2012 , 8, 615	468
2016	Phosphoproteomic analysis of <i>Rhodospseudomonas palustris</i> reveals the role of pyruvate phosphate dikinase phosphorylation in lipid production. 2012 , 11, 5362-75	27

2015	Increased structural disorder of proteins encoded on human sex chromosomes. 2012 , 8, 229-36	22
2014	Application of MapMan and RiceNet drives systematic analyses of the early heat stress transcriptome in rice seedlings. 2012 , 55, 436-449	39
2013	Single nucleotide polymorphism microarray analysis in cortisol-secreting adrenocortical adenomas identifies new candidate genes and pathways. 2012 , 14, 206-18	28
2012	On a fundamental structure of gene networks in living cells. 2012 , 109, 4702-7	42
2011	Keystone Species of Molecular Interaction Networks. 2012 , 25, 73-88	
2010	A comprehensive differential proteomic study of nitrate deprivation in Arabidopsis reveals complex regulatory networks of plant nitrogen responses. 2012 , 11, 2301-15	58
2009	Time-resolved quantitative phosphoproteomics: new insights into Angiotensin-(1-7) signaling networks in human endothelial cells. 2012 , 11, 3370-81	62
2008	DNA methylation in amphioxus: from ancestral functions to new roles in vertebrates. 2012 , 11, 142-55	36
2007	Identifying functional links between genes by evolutionary transcriptomics. 2012 , 8, 2585-92	2
2006	Interactive cellular proteins related to classical swine fever virus non-structure protein 2 by yeast two-hybrid analysis. 2012 , 39, 10515-24	15
2005	Large scale of human duplicate genes divergence. 2012 , 75, 25-33	5
2004	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. 2012 , 13, 628	30
2003	Reconstructing differentially co-expressed gene modules and regulatory networks of soybean cells. 2012 , 13, 437	18
2002	Gene, pathway and network frameworks to identify epistatic interactions of single nucleotide polymorphisms derived from GWAS data. 2012 , 6 Suppl 3, S15	34
2001	Module-based subnetwork alignments reveal novel transcriptional regulators in malaria parasite Plasmodium falciparum. 2012 , 6 Suppl 3, S5	10
2000	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. 2012 , 6 Suppl 2, S13	23
1999	PCDq: human protein complex database with quality index which summarizes different levels of evidences of protein complexes predicted from h-invitational protein-protein interactions integrative dataset. 2012 , 6 Suppl 2, S7	50
1998	GraphAlignment: Bayesian pairwise alignment of biological networks. 2012 , 6, 144	6

1997	Protein expression in the midgut of sugar-fed <i>Aedes albopictus</i> females. 2012 , 5, 290	9
1996	An integrated Bayesian framework for identifying phosphorylation networks in stimulated cells. 2012 , 736, 59-80	5
1995	Identification of colorectal cancer related genes with mRMR and shortest path in protein-protein interaction network. 2012 , 7, e33393	128
1994	Annotation of the <i>M. tuberculosis</i> hypothetical orfeome: adding functional information to more than half of the uncharacterized proteins. 2012 , 7, e34302	47
1993	Context-specific protein network miner--an online system for exploring context-specific protein interaction networks from the literature. 2012 , 7, e34480	16
1992	Hub-centered gene network reconstruction using automatic relevance determination. 2012 , 7, e35077	18
1991	Proteome-wide analysis of single-nucleotide variations in the N-glycosylation sequon of human genes. 2012 , 7, e36212	30
1990	Peptide array X-linking (PAX): a new peptide-protein identification approach. 2012 , 7, e37035	14
1989	Phenotypic and transcriptomic response of auxotrophic <i>Mycobacterium avium</i> subsp. paratuberculosis leuD mutant under environmental stress. 2012 , 7, e37884	13
1988	High confidence prediction of essential genes in <i>Burkholderia cenocepacia</i> . 2012 , 7, e40064	48
1987	The transcription profile of Tax-3 is more similar to Tax-1 than Tax-2: insights into HTLV-3 potential leukemogenic properties. 2012 , 7, e41003	26
1986	Prediction and analysis of the protein interactome in <i>Pseudomonas aeruginosa</i> to enable network-based drug target selection. 2012 , 7, e41202	29
1985	A comparison of computational methods for identifying virulence factors. 2012 , 7, e42517	22
1984	Effects of psychological stress on innate immunity and metabolism in humans: a systematic analysis. 2012 , 7, e43232	38
1983	Topological and functional properties of the small GTPases protein interaction network. 2012 , 7, e44882	27
1982	Temporal differential proteomes of <i>Clostridium difficile</i> in the pig ileal-ligated loop model. 2012 , 7, e45608	12
1981	Benzoxazinoids in root exudates of maize attract <i>Pseudomonas putida</i> to the rhizosphere. 2012 , 7, e35498	292
1980	Global identification of prokaryotic glycoproteins based on an <i>Escherichia coli</i> proteome microarray. 2012 , 7, e49080	6

1979	MSH3-deficiency initiates EMAST without oncogenic transformation of human colon epithelial cells. 2012 , 7, e50541	48
1978	Screening the budding yeast genome reveals unique factors affecting K2 toxin susceptibility. 2012 , 7, e50779	16
1977	Computational prediction of protein-protein interactions in Leishmania predicted proteomes. 2012 , 7, e51304	26
1976	Protein-protein-interaction network organization of the hypusine modification system. 2012 , 11, 1289-305	12
1975	Whole Genome Sequencing and a New Bioinformatics Platform Allow for Rapid Gene Identification in <i>D. melanogaster</i> EMS Screens. 2012 , 1, 766-77	9
1974	The impact of classification of interest on predictive toxicogenomics. 2012 , 3, 14	6
1973	Proteomic analysis of HIV-T cell interaction: an update. 2012 , 3, 240	8
1972	Factors influencing the diversity of iron uptake systems in aquatic microorganisms. 2012 , 3, 362	19
1971	Candidate genes in ocular dominance plasticity. 2012 , 6, 11	9
1970	Dynamic Proteomics: Methodologies and Analysis. 2012 ,	1
1969	Tianma modulates blood vessel tonicity. 2012 , 6, 56-65	16
1968	Data Graphs for Linking Clinical Phenotype and Molecular Feature Space. 2012 , 1, 11-25	3
1967	Analysis of Protein Interaction Networks to Prioritize Drug Targets of Neglected-Diseases Pathogens. 2012 ,	2
1966	Protein-Protein Interactions and Disease. 2012 ,	1
1965	Fast and accurate modeling of protein-protein interactions by combining template-interface-based docking with flexible refinement. 2012 , 80, 1239-49	35
1964	Mass spectrometry-based proteomics: qualitative identification to activity-based protein profiling. 2012 , 4, 141-62	10
1963	How advancement in biological network analysis methods empowers proteomics. 2012 , 12, 550-63	48
1962	Quantitative proteomic analysis of exosomes from HIV-1-infected lymphocytic cells. 2012 , 12, 2203-11	37

1961	Combining many interaction networks to predict gene function and analyze gene lists. 2012 , 12, 1687-96	39
1960	Systems biology analysis of protein-drug interactions. 2012 , 6, 102-16	19
1959	The ABC transporters in <i>Candidatus Liberibacter asiaticus</i> . 2012 , 80, 2614-28	28
1958	Analyzing protein-protein interaction networks. 2012 , 11, 2014-31	103
1957	Microbial interactions: from networks to models. 2012 , 10, 538-50	1607
1956	Combinatorial drug therapy for cancer in the post-genomic era. 2012 , 30, 679-92	670
1955	Transcriptome analysis in tardigrade species reveals specific molecular pathways for stress adaptations. 2012 , 6, 69-96	25
1954	The last rRNA methyltransferase of <i>E. coli</i> revealed: the yhiR gene encodes adenine-N6 methyltransferase specific for modification of A2030 of 23S ribosomal RNA. 2012 , 18, 1725-34	45
1953	Networks of Protein-Protein Interactions: From Uncertainty to Molecular Details. 2012 , 31, 342-62	18
1952	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. 2012 , 14, 764-74	141
1951	Assessing relative bioactivity of chemical substances using quantitative molecular network topology analysis. 2012 , 52, 1238-49	5
1950	Topology of functional networks predicts physical binding of proteins. 2012 , 28, 2137-45	4
1949	A frontier in the understanding of synaptic plasticity: solving the structure of the postsynaptic density. 2012 , 34, 599-608	17
1948	Predicting drug targets based on protein domains. 2012 , 8, 1528-34	28
1947	Whole-genome sequencing of rifampicin-resistant <i>Mycobacterium tuberculosis</i> strains identifies compensatory mutations in RNA polymerase genes. 2011 , 44, 106-10	376
1946	<i>Mycobacterium tuberculosis</i> and <i>Clostridium difficile</i> interactomes: demonstration of rapid development of computational system for bacterial interactome prediction. 2012 , 2, 4	6
1945	Computational tools for prioritizing candidate genes: boosting disease gene discovery. 2012 , 13, 523-36	313
1944	System approaches reveal the molecular networks involved in neural stem cell differentiation. 2012 , 3, 213-24	8

1943	Effects of fluctuating glucose levels on neuronal cells in vitro. 2012 , 37, 1768-82	42
1942	From RNAi screens to molecular function in embryonic stem cells. 2012 , 8, 32-42	10
1941	Genotype-phenotype correlation in interstitial 6q deletions: a report of 12 new cases. 2012 , 13, 31-47	40
1940	Analysis of altered proteins related to blast crisis in chronic myeloid leukemia by proteomic study. 2012 , 34, 267-73	12
1939	Unraveling the human dendritic cell phagosome proteome by organellar enrichment ranking. 2012 , 75, 1547-62	24
1938	Neuronal p60TRP expression modulates cardiac capacity. 2012 , 75, 1600-17	9
1937	New insights into the brain protein metabolism of <i>Gastrodia elata</i> -treated rats by quantitative proteomics. 2012 , 75, 2468-79	23
1936	A potential in silico antibody-antigen based diagnostic test for precise identification of <i>Acinetobacter baumannii</i> . 2012 , 294, 29-39	23
1935	Precise detection of <i>L. monocytogenes</i> hitting its highly conserved region possessing several specific antibody binding sites. 2012 , 305, 15-23	23
1934	Immune and stress response 'cross-talk' in the <i>Drosophila</i> Malpighian tubule. 2012 , 58, 488-97	46
1933	A 15q24 microdeletion in transient myeloproliferative disease (TMD) and acute megakaryoblastic leukaemia (AMKL) implicates PML and SUMO3 in the leukaemogenesis of TMD/AMKL. 2012 , 157, 180-7	6
1932	Crystallization of an atypical short-chain dehydrogenase from <i>Vibrio vulnificus</i> lacking the conserved catalytic tetrad. 2012 , 68, 771-4	3
1931	Tracing dynamic biological processes during phase transition. 2012 , 6 Suppl 1, S12	5
1930	Data mining in the Life Sciences with Random Forest: a walk in the park or lost in the jungle?. 2013 , 14, 315-26	228
1929	Comparative modeling and docking studies of p16ink4/cyclin D1/Rb pathway genes in lung cancer revealed functionally interactive residue of RB1 and its functional partner E2F1. 2013 , 10, 1	30
1928	Differential proteomic analysis of drought stress response in leaves of common bean (<i>Phaseolus vulgaris</i> L.). 2013 , 78, 254-72	111
1927	Gene Ontology consistent protein function prediction: the FALCON algorithm applied to six eukaryotic genomes. 2013 , 8, 10	7
1926	Combinatorial targeting of FGF and ErbB receptors blocks growth and metastatic spread of breast cancer models. 2013 , 15, R8	56

1925	Salmonella enterica Typhimurium infection causes metabolic changes in chicken muscle involving AMPK, fatty acid and insulin/mTOR signaling. 2013 , 44, 35	44
1924	Proteomics as a tool to explore human milk in health and disease. 2013 , 88, 47-57	32
1923	The effects of non-synonymous single nucleotide polymorphisms (nsSNPs) on protein-protein interactions. 2013 , 425, 3949-63	133
1922	Genetic association and gene-gene interaction analyses suggest likely involvement of ITGB3 and TPH2 with autism spectrum disorder (ASD) in the Indian population. 2013 , 45, 131-43	17
1921	Mass spectrometry-based identification and characterisation of lysine and arginine methylation in the human proteome. 2013 , 9, 2231-47	122
1920	Discovery of functional protein groups by clustering community links and integration of ontological knowledge. 2013 , 40, 5101-5112	10
1919	Recent advances in cardiovascular proteomics. 2013 , 81, 3-14	25
1918	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. 2013 , 1828, 2937-43	23
1917	Exome sequencing analysis: a guide to disease variant detection. 2013 , 1038, 137-58	16
1916	Neighbor-favoring weight reinforcement to improve random walk-based disease gene prioritization. 2013 , 44, 1-8	36
1915	A subgraph isomorphism algorithm and its application to biochemical data. 2013 , 14 Suppl 7, S13	77
1914	The KUPNetViz: a biological network viewer for multiple -omics datasets in kidney diseases. 2013 , 14, 235	12
1913	Predicting PDZ domain mediated protein interactions from structure. 2013 , 14, 27	25
1912	SyntTax: a web server linking synteny to prokaryotic taxonomy. 2013 , 14, 4	105
1911	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . 2013 , 14, 75	181
1910	Microarray analysis of microRNA expression in peripheral blood mononuclear cells of critically ill patients with influenza A (H1N1). 2013 , 13, 257	61
1909	Effects of smoking and smoking cessation on human serum metabolite profile: results from the KORA cohort study. 2013 , 11, 60	77
1908	Novel semantic similarity measure improves an integrative approach to predicting gene functional associations. 2013 , 7, 22	12

1907	Multilevel omic data integration in cancer cell lines: advanced annotation and emergent properties. 2013 , 7, 14	47
1906	Pivotal role of the muscle-contraction pathway in cryptorchidism and evidence for genomic connections with cardiomyopathy pathways in RASopathies. 2013 , 6, 5	27
1905	Expression and sub-cellular localization of an epigenetic regulator, co-activator arginine methyltransferase 1 (CARM1), is associated with specific breast cancer subtypes and ethnicity. 2013 , 12, 40	18
1904	Phosphoproteomics study on the activated PKC-induced cell death. 2013 , 12, 4280-301	7
1903	Long-term effects of acute low-dose ionizing radiation on the neonatal mouse heart: a proteomic study. 2013 , 52, 451-61	23
1902	Microtubule affinity-regulating kinase 4: structure, function, and regulation. 2013 , 67, 485-99	67
1901	A new insight into structural and functional impact of single-nucleotide polymorphisms in PTEN gene. 2013 , 66, 249-63	20
1900	Transcriptional abundance is not the single force driving the evolution of bacterial proteins. 2013 , 13, 162	5
1899	Making sense of OMICS data in population-based environmental health studies. 2013 , 54, 468-79	14
1898	Proteomic comparison of historic and recently emerged hypervirulent Clostridium difficile strains. 2013 , 12, 1151-61	32
1897	Computational studies on Alzheimer's disease associated pathways and regulatory patterns using microarray gene expression and network data: revealed association with aging and other diseases. 2013 , 334, 109-21	27
1896	Quantitative proteomic profiling of tumor cell response to telomere dysfunction using isotope-coded protein labeling (ICPL) reveals interaction network of candidate senescence markers. 2013 , 91, 515-35	12
1895	Comparative study and meta-analysis of meta-analysis studies for the correlation of genomic markers with early cancer detection. 2013 , 7, 14	12
1894	Crowdsourcing in proteomics: public resources lead to better experiments. 2013 , 44, 1129-37	24
1893	Unraveling the function of paralogs of the aldehyde dehydrogenase super family from Sulfolobus solfataricus. 2013 , 17, 205-16	17
1892	Kaposi's sarcoma: a computational approach through protein-protein interaction and gene regulatory networks analysis. 2013 , 46, 242-54	6
1891	Screening biomarkers of prostate cancer by integrating microRNA and mRNA microarrays. 2013 , 17, 807-13	17
1890	Cell-type-specific profiling of gene expression and chromatin binding without cell isolation: assaying RNA Pol II occupancy in neural stem cells. 2013 , 26, 101-12	149

1889	PainNetworks: a web-based resource for the visualisation of pain-related genes in the context of their network associations. 2013 , 154, 2586e1-2586e12	27
1888	The sarcoplasmic fish proteome: pathways, metabolic networks and potential bioactive peptides for nutritional inferences. 2013 , 78, 211-20	30
1887	Functional assignment of Mycobacterium tuberculosis proteome revealed by genome-scale fold-recognition. 2013 , 93, 40-6	13
1886	Teaching the bioinformatics of signaling networks: an integrated approach to facilitate multi-disciplinary learning. 2013 , 14, 618-32	12
1885	Evaluating the performance of fibronectin 1 (FN1), integrin $\alpha 4$ (ITGA4), syndecan-2 (SDC2), and glycoprotein CD44 as the potential biomarkers of oral squamous cell carcinoma (OSCC). 2013 , 18, 63-72	43
1884	Dispersion and domestication shaped the genome of bread wheat. 2013 , 11, 564-71	55
1883	Exploitation of genetic interaction network topology for the prediction of epistatic behavior. 2013 , 102, 202-8	13
1882	Microproteomics by liquid extraction surface analysis: application to FFPE tissue to study the fimbria region of tubo-ovarian cancer. 2013 , 7, 234-40	33
1881	Proteins and domains vary in their tolerance of non-synonymous single nucleotide polymorphisms (nsSNPs). 2013 , 425, 1274-86	25
1880	Predicting the host protein interactors of Chandipura virus using a structural similarity-based approach. 2013 , 69, 29-35	12
1879	Effects of bisphosphonate treatment on DNA methylation in osteonecrosis of the jaw. 2013 , 757, 104-13	9
1878	Evolutionarily conserved motifs and modules in mitochondrial protein-protein interaction networks. 2013 , 13, 668-75	11
1877	Image-based transcriptomics in thousands of single human cells at single-molecule resolution. 2013 , 10, 1127-33	194
1876	Predicting functional gene interactions with the hierarchical interaction score. 2013 , 10, 1089-92	21
1875	Exploring the role of post-translational modifications on protein-protein interactions with survivin. 2013 , 538, 64-70	21
1874	Proteome profiling of exosomes derived from human primary and metastatic colorectal cancer cells reveal differential expression of key metastatic factors and signal transduction components. 2013 , 13, 1672-86	255
1873	Systemes analysis of interactions between microRNAs and genes in hepatocellular carcinoma. 2013 , 2013, 600-3	
1872	Rule-based modeling and simulations of the inner kinetochore structure. 2013 , 113, 33-45	24

1871	Comparison of SILAC and mTRAQ quantification for phosphoproteomics on a quadrupole orbitrap mass spectrometer. 2013 , 12, 4089-100	28
1870	Proteomic analysis of the SIRT6 interactome: novel links to genome maintenance and cellular stress signaling. 2013 , 3, 3085	32
1869	Analysis of serum metabolites for the discovery of amino acid biomarkers and the effect of galangin on cerebral ischemia. 2013 , 9, 2311-21	28
1868	Systems-level overview of host protein phosphorylation during <i>Shigella flexneri</i> infection revealed by phosphoproteomics. 2013 , 12, 2952-68	41
1867	Human β -glucuronidase: structure, function, and application in enzyme replacement therapy. 2013 , 16, 352-63	43
1866	Quantitative interaction screen of telomeric repeat-containing RNA reveals novel TERRA regulators. 2013 , 23, 2149-57	52
1865	Peptides presented by HLA class I molecules in the human thymus. 2013 , 94, 23-36	11
1864	Quantitative proteomics of protein complexes and their implications for cell reprogramming and pluripotency. 2013 , 12, 5878-90	5
1863	Network-based stratification of tumor mutations. 2013 , 10, 1108-15	546
1862	Circulating miRNA profile in HCV infected serum: novel insight into pathogenesis. 2013 , 3, 1555	66
1861	Pattern recognition in bioinformatics. 2013 , 14, 633-47	46
1860	Submergence confers immunity mediated by the WRKY22 transcription factor in <i>Arabidopsis</i> . 2013 , 25, 2699-713	111
1859	Predicting effective drug combinations via network propagation. 2013 ,	1
1858	Production of bulk chemicals via novel metabolic pathways in microorganisms. 2013 , 31, 925-35	57
1857	Topology of molecular interaction networks. 2013 , 7, 90	65
1856	Predicting gene regulatory networks of soybean nodulation from RNA-Seq transcriptome data. 2013 , 14, 278	20
1855	VarRanker: rapid prioritization of sequence variations associated with human disease. 2013 , 14 Suppl 13, S1	5
1854	HeLa cell response proteome alterations induced by mammalian reovirus T3D infection. 2013 , 10, 202	5

1853	Protein function prediction by collective classification with explicit and implicit edges in protein-protein interaction networks. 2013 , 14 Suppl 12, S4	13
1852	A novel subnetwork alignment approach predicts new components of the cell cycle regulatory apparatus in <i>Plasmodium falciparum</i> . 2013 , 14 Suppl 12, S2	5
1851	Epigenetic coordination of signaling pathways during the epithelial-mesenchymal transition. 2013 , 6, 28	34
1850	Core modular blood and brain biomarkers in social defeat mouse model for post traumatic stress disorder. 2013 , 7, 80	19
1849	Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). 2013 , 14, 573	136
1848	Highly precise protein-protein interaction prediction based on consensus between template-based and de novo docking methods. 2013 , 7, S6	20
1847	In silico prediction of structure and functions for some proteins of male-specific region of the human Y chromosome. 2013 , 5, 258-69	1
1846	A new computational strategy for predicting essential genes. 2013 , 14, 910	23
1845	A multi-level multi-scale approach to study essential genes in <i>Mycobacterium tuberculosis</i> . 2013 , 7, 132	14
1844	Comparative transcriptome analysis of tomato (<i>Solanum lycopersicum</i>) in response to exogenous abscisic acid. 2013 , 14, 841	67
1843	Inferring protein-protein interaction complexes from immunoprecipitation data. 2013 , 6, 468	5
1842	CellFateScout - a bioinformatics tool for elucidating small molecule signaling pathways that drive cells in a specific direction. 2013 , 11, 85	2
1841	SNPs of MYPN and TTN genes are associated to meat and carcass traits in Italian Large White and Italian Duroc pigs. 2013 , 40, 6927-33	9
1840	The periodontal pathogen <i>Porphyromonas gingivalis</i> changes the gene expression in vascular smooth muscle cells involving the TGFbeta/Notch signalling pathway and increased cell proliferation. 2013 , 14, 770	22
1839	Association of potentially functional genetic variants of PLCE1 with gallbladder cancer susceptibility in north Indian population. 2013 , 44, 436-43	14
1838	Screening of key genes in gastric cancer with DNA microarray analysis. 2013 , 18, 37	13
1837	A patient tumor transplant model of squamous cell cancer identifies PI3K inhibitors as candidate therapeutics in defined molecular bins. 2013 , 7, 776-90	116
1836	Artemisinin rewires the protein interaction network in cancer cells: network analysis, pathway identification, and target prediction. 2013 , 9, 3091-100	24

1835	Combined CpG and poly I:C stimulation of monocytes results in unique signaling activation not observed with the individual ligands. 2013 , 25, 2246-54	44
1834	A Gro/TLE-NuRD corepressor complex facilitates Tbx20-dependent transcriptional repression. 2013 , 12, 5395-409	24
1833	TIMP-1 increases expression and phosphorylation of proteins associated with drug resistance in breast cancer cells. 2013 , 12, 4136-51	26
1832	A functional siRNA screen identifies genes modulating angiotensin II-mediated EGFR transactivation. 2013 , 126, 5377-90	27
1831	Gender bias in autoimmunity is influenced by microbiota. 2013 , 39, 400-12	537
1830	The nebulin SH3 domain is dispensable for normal skeletal muscle structure but is required for effective active load bearing in mouse. 2013 , 126, 5477-89	28
1829	Acinetobacter baylyi long-term stationary-phase protein StiP is a protease required for normal cell morphology and resistance to tellurite. 2013 , 59, 726-36	1
1828	Computationally identifying virulence factors based on KEGG pathways. 2013 , 9, 1447-52	19
1827	Atopic dermatitis-associated protein interaction network lead to new insights in chronic sulfur mustard skin lesion mechanisms. 2013 , 10, 449-60	12
1826	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. 2013 , 9, 662	86
1825	The functional interactome landscape of the human histone deacetylase family. 2013 , 9, 672	204
1824	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein-protein interaction network. 2013 , 9, 2720-8	37
1823	Stress induces remodelling of yeast interaction and co-expression networks. 2013 , 9, 1697-707	18
1822	A system based approach to construct a Kaposi sarcoma-associated herpesvirus (KSHV) specific pathway crosstalk network. 2013 ,	
1821	PodNet, a protein-protein interaction network of the podocyte. 2013 , 84, 104-15	16
1820	Integrating multiple biomedical resources for protein complex prediction. 2013 ,	2
1819	Systems biology of pathogen-host interaction: networks of protein-protein interaction within pathogens and pathogen-human interactions in the post-genomic era. 2013 , 8, 85-96	27
1818	Ripples in the pond--using a systems approach to decipher the cellular functions of membrane microdomains. 2013 , 9, 330-8	11

1817	A genome-wide siRNA screen reveals positive and negative regulators of the NOD2 and NF- κ B signaling pathways. 2013 , 6, rs3	49
1816	Genome-wide analysis shows association of epigenetic changes in regulators of Rab and Rho GTPases with spinal muscular atrophy severity. 2013 , 21, 988-93	22
1815	Human diseases through the lens of network biology. 2013 , 29, 150-9	138
1814	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. 2013 , 78, 486-98	79
1813	Plant protein interactomes. 2013 , 64, 161-87	83
1812	Network approaches to drug discovery. 2013 , 8, 7-20	28
1811	Opportunities for protein interaction network-guided cellular engineering. 2013 , 65, 17-27	3
1810	The ToxBank Data Warehouse: Supporting the Replacement of In Vivo Repeated Dose Systemic Toxicity Testing. 2013 , 32, 47-63	33
1809	Host response to intravenous injection of epsilon toxin in mouse model: a proteomic view. 2013 , 13, 89-107	20
1808	Co-expression network with protein-protein interaction and transcription regulation in malaria parasite Plasmodium falciparum. 2013 , 518, 7-16	7
1807	Daxx is a key downstream component of receptor interacting protein kinase 3 mediating retinal ischemic cell death. 2013 , 587, 266-71	17
1806	Expression profiling of Mycobacterium tuberculosis H37Rv and Mycobacterium smegmatis in acid-nitrosative multi-stress displays defined regulatory networks. 2013 , 65, 89-96	17
1805	Progress in detecting genetic alterations and their association with human disease. 2013 , 425, 3914-8	6
1804	Nucleosome assembly proteins and their interacting proteins in neuronal differentiation. 2013 , 534, 20-6	23
1803	Quantitative proteomics of auditory fear conditioning. 2013 , 434, 87-94	12
1802	Characterization of carbonic anhydrase IX interactome reveals proteins assisting its nuclear localization in hypoxic cells. 2013 , 12, 282-92	37
1801	Letter to the editor: authors' response. 2013 , 84, 276-7	
1800	Natural selection and population genetic structure of domain-I of Plasmodium falciparum apical membrane antigen-1 in India. 2013 , 18, 247-56	8

1799	MicroRNA expression following activated protein C treatment during septic shock. 2013 , 182, 116-26	21
1798	Two-dimensional liquid chromatography-tandem mass spectrometry coupled with isobaric tags for relative and absolute quantification (iTRAQ) labeling approach revealed first proteome profiles of pulmonary alveolar macrophages infected with porcine circovirus type 2. 2013 , 79, 72-86	34
1797	PRASA: an integrated web server that analyzes protein interaction types. 2013 , 518, 78-83	1
1796	An effective, practical and low computational cost framework for the integration of heterogeneous data to predict functional associations between proteins by means of Artificial Neural Networks. 2013 , 121, 64-78	3
1795	Moving H5N1 studies into the era of systems biology. 2013 , 178, 151-67	12
1794	Identifying targets of the Sox domain protein Dichaete in the Drosophila CNS via targeted expression of dominant negative proteins. 2013 , 13, 1	19
1793	Structural, phylogenetic and docking studies of D-amino acid oxidase activator (DAOA), a candidate schizophrenia gene. 2013 , 10, 3	24
1792	A brief primer on microRNAs and their roles in angiogenesis. 2013 , 5, 2	37
1791	Characterization of thymosin α in mammals' saliva. 2013 , 40, 1-7	6
1790	Genetic requirements for <i>Moraxella catarrhalis</i> growth under iron-limiting conditions. 2013 , 87, 14-29	15
1789	Increased anaerobic metabolism is a distinctive signature in a colorectal cancer cellular model of resistance to anti-epidermal growth factor receptor antibody. 2013 , 13, 866-77	20
1788	Quantitative analysis of chaperone network throughput in budding yeast. 2013 , 13, 1276-91	26
1787	Structure and dynamics of molecular networks: a novel paradigm of drug discovery: a comprehensive review. 2013 , 138, 333-408	604
1786	Finding the targets of a drug by integration of gene expression data with a protein interaction network. 2013 , 9, 1676-85	47
1785	In vivo SILAC-based proteomics reveals phosphoproteome changes during mouse skin carcinogenesis. 2013 , 3, 552-66	82
1784	A network of genes connects polyglutamine toxicity to ploidy control in yeast. 2013 , 4, 1571	17
1783	Current trends in modeling host-pathogen interactions. 2013 , 3, 109-128	7
1782	Bioinformatics tools for secretome analysis. 2013 , 1834, 2442-53	68

1781	Understanding protein-protein interactions using local structural features. 2013 , 425, 1210-24	34
1780	<i>Klebsiella pneumoniae</i> targets an EGF receptor-dependent pathway to subvert inflammation. 2013 , 15, 1212-33	34
1779	MicroRNA-regulated networks: the perfect storm for classical molecular biology, the ideal scenario for systems biology. 2013 , 774, 55-76	41
1778	The α -crystallin domain of small heat shock protein b8 (Hspb8) acts as survival and differentiation factor in adult hippocampal neurogenesis. 2013 , 33, 5785-96	17
1777	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. 2013 , 9, 732-49	8
1776	Proteomic profiling and interactome analysis of ER-positive/HER2/neu negative invasive ductal carcinoma of the breast: towards proteomics biomarkers. 2013 , 17, 27-40	13
1775	Integrin-mediated signaling induced by simian virus 40 leads to transient uncoupling of cortical actin and the plasma membrane. 2013 , 8, e55799	21
1774	Secretome analyses of A β (1-42) stimulated hippocampal astrocytes reveal that CXCL10 is involved in astrocyte migration. 2013 , 12, 832-43	18
1773	Proteomic analyses of serous and endometrioid epithelial ovarian cancers - cases studies - molecular insights of a possible histological etiology of serous ovarian cancer. 2013 , 7, 337-54	17
1772	Yeast Systems Biology. 2013 , 343-365	6
1771	Protein complexes are under evolutionary selection to assemble via ordered pathways. 2013 , 153, 461-70	153
1770	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . 2013 , 101, 249-55	6
1769	The parkinson's disease-associated LRRK2 mutation R1441G inhibits neuronal differentiation of neural stem cells. 2013 , 22, 2487-96	29
1768	Punctuated evolution of prostate cancer genomes. 2013 , 153, 666-77	862
1767	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. 2013 , 15, 363-72	221
1766	Fibroblast growth factor-1 is a mesenchymal stromal cell-secreted factor stimulating proliferation of osteoarthritic chondrocytes in co-culture. 2013 , 22, 2356-67	54
1765	From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks. 2013 , 3, 1613	217
1764	The effect of starvation stress on <i>Lactobacillus brevis</i> L62 protein profile determined by de novo sequencing in positive and negative mass spectrometry ion mode. 2013 , 27, 1045-54	6

1763	Social networks to biological networks: systems biology of Mycobacterium tuberculosis. 2013 , 9, 1584-93	5
1762	Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. 2013 , 13, 559-72	123
1761	Neuron enriched nuclear proteome isolated from human brain. 2013 , 12, 3193-206	52
1760	PKC signaling prevents irradiation-induced apoptosis of primary human fibroblasts. 2013 , 4, e498	33
1759	Identification and expression levels of pig miRNAs in skeletal muscle. 2013 , 154, 45-54	6
1758	Exploring the multifactorial nature of autism through computational systems biology: calcium and the Rho GTPase RAC1 under the spotlight. 2013 , 15, 364-83	47
1757	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. 2013 , 31, 533-8	869
1756	A general molecular affinity strategy for global detection and proteomic analysis of lysine methylation. 2013 , 50, 444-56	122
1755	Resilience of death: intrinsic disorder in proteins involved in the programmed cell death. 2013 , 20, 1257-67	62
1754	RNA-binding proteins in Mendelian disease. 2013 , 29, 318-27	171
1753	A review of potassium channels in bipolar disorder. 2013 , 4, 105	14
1752	MicroRNA profiling in lymphocytes and serum of tyrosinemia type-I patients. 2013 , 40, 4619-23	4
1751	"Omics" of HER2-positive breast cancer. 2013 , 17, 119-29	18
1750	Assessment of high-confidence protein-protein interactome in yeast. 2013 , 45, 1-8	11
1749	Vascular proteomics. 2013 , 1000, 1-20	9
1748	Proteomic profile of carbonylated proteins in rat liver: exercise attenuated oxidative stress may be involved in fatty liver improvement. 2013 , 13, 1755-64	19
1747	A method for systematic mapping of protein lysine methylation identifies functions for HP1 in DNA damage response. 2013 , 50, 723-35	77
1746	Comparative proteomics and correlated signaling network of kidney in ApoE deficient mouse. 2013 , 7, 829-38	1

1745	Paleoproteomic study of the Iceman's brain tissue. 2013 , 70, 3709-22	33
1744	Systematic characterization of hypothetical proteins in <i>Synechocystis</i> sp. PCC 6803 reveals proteins functionally relevant to stress responses. 2013 , 512, 6-15	25
1743	Interaction analysis identifies semenogelin I fragments as new binding partners of PIP in human seminal plasma. 2013 , 52, 296-9	16
1742	Potential translational targets revealed by linking mouse grooming behavioral phenotypes to gene expression using public databases. 2013 , 40, 312-25	10
1741	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. 2013 , 11, S3	25
1740	Comparative analysis of differential network modularity in tissue specific normal and cancer protein interaction networks. 2013 , 3, 19	16
1739	Probabilistic biological network alignment. 2013 , 10, 109-21	23
1738	Subcellular proteomics reveals a role for nucleo-cytoplasmic trafficking at the DNA replication origin activation checkpoint. 2013 , 12, 1436-53	13
1737	Phosphoinositide-specific phospholipase C β (PI-PLC β) interactome: affinity purification-mass spectrometry analysis of PI-PLC β with nuclear protein. 2013 , 12, 2220-35	16
1736	The heparin-binding protein interactome in pancreatic diseases. 2013 , 13, 598-604	12
1735	Integrated gene co-expression network analysis in the growth phase of <i>Mycobacterium tuberculosis</i> reveals new potential drug targets. 2013 , 9, 2798-815	19
1734	Network biomarkers reveal dysfunctional gene regulations during disease progression. 2013 , 280, 5682-95	49
1733	Integrative transcriptome and proteome study to identify the signaling network regulated by POPX2 phosphatase. 2013 , 12, 2525-36	17
1732	Selective targeting capability acquired with a protein corona adsorbed on the surface of 1,2-dioleoyl-3-trimethylammonium propane/DNA nanoparticles. 2013 , 5, 13171-9	119
1731	Unraveling toxicological mechanisms and predicting toxicity classes with gene dysregulation networks. 2013 , 33, 1407-15	6
1730	Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. 2013 , 31, 115-24	1
1729	Aurora A kinase (AURKA) in normal and pathological cell division. 2013 , 70, 661-87	273
1728	Identification of novel in vivo MAP kinase substrates in <i>Arabidopsis thaliana</i> through use of tandem metal oxide affinity chromatography. 2013 , 12, 369-80	97

1727	A chemical proteomics approach to profiling the ATP-binding proteome of Mycobacterium tuberculosis. 2013 , 12, 1644-60	32
1726	Cell cycle regulation of microtubule interactomes: multi-layered regulation is critical for the interphase/mitosis transition. 2013 , 12, 3135-47	18
1725	AtFH1 formin mutation affects actin filament and microtubule dynamics in Arabidopsis thaliana. 2013 , 64, 585-97	49
1724	PReach. 2013 ,	4
1723	Characterization of native protein complexes and protein isoform variation using size-fractionation-based quantitative proteomics. 2013 , 12, 3851-73	104
1722	Thiouracil cross-linking mass spectrometry: a cell-based method to identify host factors involved in viral amplification. 2013 , 87, 8697-712	35
1721	Proteomic profiling and pathway analysis of the response of rat renal proximal convoluted tubules to metabolic acidosis. 2013 , 305, F628-40	15
1720	Autoantibody profiling in multiple sclerosis using arrays of human protein fragments. 2013 , 12, 2657-72	62
1719	A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. 2013 , 23, 1839-51	27
1718	Automated QuantMap for rapid quantitative molecular network topology analysis. 2013 , 29, 2369-70	6
1717	Prediction and analysis of retinoblastoma related genes through gene ontology and KEGG. 2013 , 2013, 304029	13
1716	Polymorphisms in inflammation pathway genes and endometrial cancer risk. 2013 , 22, 216-23	22
1715	PCorral--interactive mining of protein interactions from MEDLINE. 2013 , 2013, bat030	12
1714	HitWalker: variant prioritization for personalized functional cancer genomics. 2013 , 29, 509-10	8
1713	A genome-wide association study reveals ARL15, a novel non-HLA susceptibility gene for rheumatoid arthritis in North Indians. 2013 , 65, 3026-35	22
1712	A systems' biology approach to study microRNA-mediated gene regulatory networks. 2013 , 2013, 703849	28
1711	Minimum curvilinearity to enhance topological prediction of protein interactions by network embedding. 2013 , 29, i199-209	78
1710	Phylogeny, functional annotation, and protein interaction network analyses of the Xenopus tropicalis basic helix-loop-helix transcription factors. 2013 , 2013, 145037	2

1709	Identification of lung-cancer-related genes with the shortest path approach in a protein-protein interaction network. 2013 , 2013, 267375		19
1708	A systemic transcriptome analysis reveals the regulation of neural stem cell maintenance by an E2F1-miRNA feedback loop. <i>Nucleic Acids Research</i> , 2013 , 41, 3699-712	20.1	22
1707	Atypical protein kinases of the RIO family in archaea. 2013 , 41, 399-404		17
1706	Towards systematic discovery of signaling networks in budding yeast filamentous growth stress response using interventional phosphorylation data. 2013 , 9, e1003077		13
1705	How microRNA and transcription factor co-regulatory networks affect osteosarcoma cell proliferation. 2013 , 9, e1003210		62
1704	Impact of natural genetic variation on gene expression dynamics. 2013 , 9, e1003514		30
1703	Immunomodulatory impact of leishmania-induced macrophage exosomes: a comparative proteomic and functional analysis. 2013 , 7, e2185		89
1702	PhosphoChain: a novel algorithm to predict kinase and phosphatase networks from high-throughput expression data. 2013 , 29, 2435-44		6
1701	A kinome-wide RNAi screen in <i>Drosophila</i> Glia reveals that the RIO kinases mediate cell proliferation and survival through TORC2-Akt signaling in glioblastoma. 2013 , 9, e1003253		77
1700	Phosphoproteomic analyses reveal signaling pathways that facilitate lytic gammaherpesvirus replication. 2013 , 9, e1003583		19
1699	Structural disorder provides increased adaptability for vesicle trafficking pathways. 2013 , 9, e1003144		29
1698	Genetic modification of the association between peripubertal dioxin exposure and pubertal onset in a cohort of Russian boys. 2013 , 121, 111-7		4
1697	SpermatogenesisOnline 1.0: a resource for spermatogenesis based on manual literature curation and genome-wide data mining. <i>Nucleic Acids Research</i> , 2013 , 41, D1055-62	20.1	25
1696	Human monogenic disease genes have frequently functionally redundant paralogs. 2013 , 9, e1003073		34
1695	BioGranat-IG: a network analysis tool to suggest mechanisms of genetic heterogeneity from exome-sequencing data. 2013 , 29, 733-41		5
1694	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. 2013 , 29, i210-6		7
1693	Network analysis identifies an HSP90-central hub susceptible in ovarian cancer. 2013 , 19, 5053-67		42
1692	X-linked dystonia parkinsonism syndrome (XDP, lubag): disease-specific sequence change DSC3 in TAF1/DYT3 affects genes in vesicular transport and dopamine metabolism. 2013 , 22, 941-51		27

1691	Positive selection in nucleoporins challenges constraints on early expressed genes in <i>Drosophila</i> development. 2013 , 5, 2231-41		10
1690	Identification of the nature of reading frame transitions observed in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2013 , 41, 6514-30	20.1	22
1689	Unconventional secretion is a major contributor of cancer cell line secretomes. 2013 , 12, 1046-60		59
1688	Low-copy piggyBac transposon mutagenesis in mice identifies genes driving melanoma. 2013 , 110, E3640-9		24
1687	iLoops: a protein-protein interaction prediction server based on structural features. 2013 , 29, 2360-2		30
1686	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. 2013 , 12, 366-80		38
1685	Wnt3a-dependent and -independent protein interaction networks of chromatin-bound Ectenin in mouse embryonic stem cells. 2013 , 12, 1980-94		14
1684	Proteomics of genetically engineered mouse mammary tumors identifies fatty acid metabolism members as potential predictive markers for cisplatin resistance. 2013 , 12, 1319-34		19
1683	Exome sequencing identification of a GJB1 missense mutation in a kindred with X-linked spinocerebellar ataxia (SCA-X1). 2013 , 22, 4329-38		20
1682	Gene <i>ercA</i> , encoding a putative iron-containing alcohol dehydrogenase, is involved in regulation of ethanol utilization in <i>Pseudomonas aeruginosa</i> . 2013 , 195, 3925-32		10
1681	Proteome and metabolome profiling of cytokinin action in <i>Arabidopsis</i> identifying both distinct and similar responses to cytokinin down- and up-regulation. 2013 , 64, 4193-206		47
1680	GoSynthetic database tool to analyse natural and engineered molecular processes. 2013 , 2013, bat043		3
1679	Global subcellular characterization of protein degradation using quantitative proteomics. 2013 , 12, 638-50		91
1678	Transcription factor and chromatin features predict genes associated with eQTLs. <i>Nucleic Acids Research</i> , 2013 , 41, 1450-63	20.1	22
1677	The presence of HIV-1 Tat protein second exon delays fas protein-mediated apoptosis in CD4+ T lymphocytes: a potential mechanism for persistent viral production. 2013 , 288, 7626-7644		39
1676	BioGPS and MyGene.info: organizing online, gene-centric information. <i>Nucleic Acids Research</i> , 2013 , 41, D561-5	20.1	228
1675	The impact of trans-regulation on the evolutionary rates of metazoan proteins. <i>Nucleic Acids Research</i> , 2013 , 41, 6371-80	20.1	6
1674	In-depth characterization of the secretome of colorectal cancer metastatic cells identifies key proteins in cell adhesion, migration, and invasion. 2013 , 12, 1602-20		82

1673	Popular computational methods to assess multiprotein complexes derived from label-free affinity purification and mass spectrometry (AP-MS) experiments. 2013 , 12, 1-13		39
1672	Trichoderma-plant root colonization: escaping early plant defense responses and activation of the antioxidant machinery for saline stress tolerance. 2013 , 9, e1003221		205
1671	A genomic-scale artificial microRNA library as a tool to investigate the functionally redundant gene space in Arabidopsis. 2013 , 25, 2848-63		43
1670	Computational Pharmacogenomics. 2013 , 163-186		
1669	The UCSC Interaction Browser: multidimensional data views in pathway context. <i>Nucleic Acids Research</i> , 2013 , 41, W218-24	20.1	20
1668	ValidNESs: a database of validated leucine-rich nuclear export signals. <i>Nucleic Acids Research</i> , 2013 , 41, D338-43	20.1	58
1667	The relationship between long-range chromatin occupancy and polymerization of the Drosophila ETS family transcriptional repressor Yan. 2013 , 193, 633-49		22
1666	RhesusBase: a knowledgebase for the monkey research community. <i>Nucleic Acids Research</i> , 2013 , 41, D892-905	20.1	23
1665	Identification of a target gene and activating stimulus for the YpdA/YpdB histidine kinase/response regulator system in Escherichia coli. 2013 , 195, 807-15		30
1664	yApoptosis: yeast apoptosis database. 2013 , 2013, bat068		3
1663	L-form bacteria, cell walls and the origins of life. 2013 , 3, 120143		130
1662	The human gene connectome as a map of short cuts for morbid allele discovery. 2013 , 110, 5558-63		59
1661	Protein kinase PKN1 represses Wnt/ β -catenin signaling in human melanoma cells. 2013 , 288, 34658-70		28
1660	Advanced proteomic analyses yield a deep catalog of ubiquitylation targets in Arabidopsis. 2013 , 25, 1523-40		180
1659	Cloning, expression, purification, crystallization and preliminary crystallographic analysis of the kinase domain of AtMAP4Kalpha2 from Arabidopsis thaliana. 2013 , 69, 788-91		
1658	In vivo phosphoproteomics analysis reveals the cardiac targets of β adrenergic receptor signaling. 2013 , 6, rs11		129
1657	In silico discovery of mitosis regulation networks associated with early distant metastases in estrogen receptor positive breast cancers. 2013 , 12, 31-51		13
1656	Genes involved in host-parasite interactions can be revealed by their correlated expression. <i>Nucleic Acids Research</i> , 2013 , 41, 1508-18	20.1	20

1655	Proteomics analysis of UV-irradiated <i>Lonicera japonica</i> Thunb. with bioactive metabolites enhancement. 2013 , 13, 3508-22		18
1654	Mutations in <i>CCDC39</i> and <i>CCDC40</i> are the major cause of primary ciliary dyskinesia with axonemal disorganization and absent inner dynein arms. 2013 , 34, 462-72		129
1653	PRIMOS: an integrated database of reassessed protein-protein interactions providing web-based access to in silico validation of experimentally derived data. 2013 , 11, 333-46		9
1652	MMP?REDOX/NO interplay in periodontitis and its inhibition with <i>Satureja hortensis</i> L. essential oil. 2013 , 10, 507-23		16
1651	Characterizing the topology of probabilistic biological networks. 2013 , 10, 970-83		9
1650	Fly cryptochrome and the visual system. 2013 , 110, 6163-8		48
1649	Quantitative measurement of phosphoproteome response to osmotic stress in arabidopsis based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). 2013 , 12, 2354-69		55
1648	Computational construction of specialized biological networks. 2013 , 11, 1340003		1
1647	Multiple myeloma is affected by multiple and heterogeneous somatic mutations in adhesion- and receptor tyrosine kinase signaling molecules. 2013 , 3, e102		44
1646	Identification of CRM1-dependent Nuclear Export Cargos Using Quantitative Mass Spectrometry. 2013 , 12, 664-78		69
1645	GenomeRNAi: a database for cell-based and in vivo RNAi phenotypes, 2013 update. <i>Nucleic Acids Research</i> , 2013 , 41, D1021-6	20.1	111
1644	Missense mutation in the <i>MEN1</i> gene discovered through whole exome sequencing co-segregates with familial hyperparathyroidism. 2013 , 95, 114-20		10
1643	Proteome variations in pancreatic stellate cells upon stimulation with proinflammatory factors. 2013 , 288, 32517-32527		12
1642	Heterogeneous nuclear ribonucleoprotein (HnRNP) K genome-wide binding survey reveals its role in regulating 3'-end RNA processing and transcription termination at the early growth response 1 (<i>EGR1</i>) gene through <i>XRN2</i> exonuclease. 2013 , 288, 24788-98		23
1641	CluePedia Cytoscape plugin: pathway insights using integrated experimental and in silico data. 2013 , 29, 661-3		650
1640	Linker histone H1.0 interacts with an extensive network of proteins found in the nucleolus. <i>Nucleic Acids Research</i> , 2013 , 41, 4026-35	20.1	60
1639	Mining Graph Topological Patterns: Finding Covariations among Vertex Descriptors. 2013 , 25, 2090-2104		30
1638	Mining large-scale response networks reveals 'topmost activities' in <i>Mycobacterium tuberculosis</i> infection. 2013 , 3, 2302		25

1637	Global expression profiling reveals genetic programs underlying the developmental divergence between mouse and human embryogenesis. 2013 , 14, 568	24
1636	Host-Mycobacterium avium subsp. paratuberculosis interactome reveals a novel iron assimilation mechanism linked to nitric oxide stress during early infection. 2013 , 14, 694	28
1635	Re-annotation of the Saccharopolyspora erythraea genome using a systems biology approach. 2013 , 14, 699	18
1634	Hsp70s and J proteins of Plasmodium parasites infecting rodents and primates: structure, function, clinical relevance, and drug targets. 2013 , 19, 387-403	36
1633	Comparative analysis of resistant and susceptible macrophage gene expression response to Leishmania major parasite. 2013 , 14, 723	15
1632	Computational approaches for discovery of common immunomodulators in fungal infections: towards broad-spectrum immunotherapeutic interventions. 2013 , 13, 224	7
1631	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of β -synuclein. 2013 , 14, 136	13
1630	NGX6 expression improves the sensitivity of tamoxifen-resistant MCF-7 cells through modulation of the Smad signaling pathway. 2013 , 42, 2060-8	6
1629	Identifying potential cancer driver genes by genomic data integration. 2013 , 3, 3538	45
1628	P-Biblio-MetReS, a parallel data mining tool for the reconstruction of molecular networks. 2013 ,	
1627	Protein-protein interaction network prediction by using rigid-body docking tools: application to bacterial chemotaxis. 2014 , 21, 790-8	11
1626	Comparison of gene expression profile of epiretinal membranes obtained from eyes with proliferative vitreoretinopathy to that of secondary epiretinal membranes. 2013 , 8, e54191	23
1625	Dual coordination of post translational modifications in human protein networks. 2013 , 9, e1002933	61
1624	Distinct protein classes in human red cell proteome revealed by similarity of phylogenetic profiles. 2013 , 8, e54471	3
1623	Statistical assessment of crosstalk enrichment between gene groups in biological networks. 2013 , 8, e54945	28
1622	Large-scale event extraction from literature with multi-level gene normalization. 2013 , 8, e55814	69
1621	The evolutionary dynamics of protein-protein interaction networks inferred from the reconstruction of ancient networks. 2013 , 8, e58134	38
1620	Gene expression changes associated with the airway wall response to injury. 2013 , 8, e58930	2

1619	Identification and characterization of potential therapeutic candidates in emerging human pathogen <i>Mycobacterium abscessus</i> : a novel hierarchical in silico approach. 2013 , 8, e59126	65
1618	Genome-wide microarray analysis reveals roles for the REF-1 family member HLH-29 in ferritin synthesis and peroxide stress response. 2013 , 8, e59719	8
1617	Systematic analysis of experimental phenotype data reveals gene functions. 2013 , 8, e60847	16
1616	Proteomic profiling in <i>Drosophila</i> reveals potential Dube3a regulation of the actin cytoskeleton and neuronal homeostasis. 2013 , 8, e61952	30
1615	An ensemble prognostic model for colorectal cancer. 2013 , 8, e63494	12
1614	Detecting loci under recent positive selection in dairy and beef cattle by combining different genome-wide scan methods. 2013 , 8, e64280	65
1613	Functional diversity and structural disorder in the human ubiquitination pathway. 2013 , 8, e65443	22
1612	An information-theoretic machine learning approach to expression QTL analysis. 2013 , 8, e67899	24
1611	SMETANA: accurate and scalable algorithm for probabilistic alignment of large-scale biological networks. 2013 , 8, e67995	66
1610	Whole genome SNP genotyping and exome sequencing reveal novel genetic variants and putative causative genes in congenital hyperinsulinism. 2013 , 8, e68740	21
1609	Simplified method for predicting a functional class of proteins in transcription factor complexes. 2013 , 8, e68857	1
1608	Reconstruction of cellular signal transduction networks using perturbation assays and linear programming. 2013 , 8, e69220	8
1607	Comparative proteomics reveals novel components at the plasma membrane of differentiated HepaRG cells and different distribution in hepatocyte- and biliary-like cells. 2013 , 8, e71859	14
1606	Dynamics of DNA damage induced pathways to cancer. 2013 , 8, e72303	19
1605	Geptop: a gene essentiality prediction tool for sequenced bacterial genomes based on orthology and phylogeny. 2013 , 8, e72343	48
1604	Measles contributes to rheumatoid arthritis: evidence from pathway and network analyses of genome-wide association studies. 2013 , 8, e75951	24
1603	Identifying genes relevant to specific biological conditions in time course microarray experiments. 2013 , 8, e76561	1
1602	Evolutionary origin of the mitochondrial cholesterol transport machinery reveals a universal mechanism of steroid hormone biosynthesis in animals. 2013 , 8, e76701	33

1601	Novel factors in the pathogenesis of psoriasis and potential drug candidates are found with systems biology approach. 2013 , 8, e80751	16
1600	Interaction network of proteins associated with human cytomegalovirus IE2-p86 protein during infection: a proteomic analysis. 2013 , 8, e81583	9
1599	Differential network analysis applied to preoperative breast cancer chemotherapy response. 2013 , 8, e81784	13
1598	Exoproteome and secretome derived broad spectrum novel drug and vaccine candidates in <i>Vibrio cholerae</i> targeted by Piper betel derived compounds. 2013 , 8, e52773	51
1597	Genes associated with disc degeneration identified using microarray gene expression profiling and bioinformatics analysis. 2013 , 12, 1431-9	5
1596	Gene expression profile analysis of human intervertebral disc degeneration. 2013 , 36, 448-54	19
1595	From protein-protein interactions to rational drug design: are computational methods up to the challenge?. 2013 , 13, 602-18	15
1594	eQTL Epistasis - Challenges and Computational Approaches. 2013 , 4, 51	20
1593	Converging Evidence for Epistasis between ANK3 and Potassium Channel Gene KCNQ2 in Bipolar Disorder. 2013 , 4, 87	27
1592	Maternal-fetal unit interactions and eutherian neocortical development and evolution. 2013 , 7, 22	15
1591	Protein-Protein Interactions: Gene Acronym Redundancies and Current Limitations Precluding Automated Data Integration. 2013 , 1, 3-24	1
1590	Quantitative Analysis of the Human Milk Whey Proteome Reveals Developing Milk and Mammary-Gland Functions across the First Year of Lactation. 2013 , 1, 128-158	24
1589	Bioinformatic Analysis of Differential Protein Expression in Calu-3 Cells Exposed to Carbon Nanotubes. 2013 , 1, 219-239	7
1588	Major components of energy drinks (caffeine, taurine, and guarana) exert cytotoxic effects on human neuronal SH-SY5Y cells by decreasing reactive oxygen species production. 2013 , 2013, 791795	52
1587	Construction and Analysis of the Cell Surface's Protein Network for Human Sperm-Egg Interaction. 2013 , 2013, 962760	6
1586	Profiling of concanavalin A-binding glycoproteins in human hepatic stellate cells activated with transforming growth factor- β . 2014 , 19, 19845-67	11
1585	Bioinformatic analysis of endothelial progenitor cells exposed to folic acid in type 1 diabetes mellitus. 2014 , 13, 1-10	3
1584	Identification and analysis of potential targets in <i>Streptococcus sanguinis</i> using computer aided protein data analysis. 2014 , 7, 45-54	2

1583	Screening of key genes of unruptured intracranial aneurysms by using DNA microarray data analysis techniques. 2014 , 13, 758-67	6
1582	Whole-genome pathway analysis on 132,497 individuals identifies novel gene-sets associated with body mass index. 2014 , 9, e78546	3
1581	Training set selection for the prediction of essential genes. 2014 , 9, e86805	26
1580	Whole genome analyses of a well-differentiated liposarcoma reveals novel SYT1 and DDR2 rearrangements. 2014 , 9, e87113	13
1579	Identification of thyroid carcinoma related genes with mRMR and shortest path approaches. 2014 , 9, e94022	15
1578	Phase variation in <i>Myxococcus xanthus</i> yields cells specialized for iron sequestration. 2014 , 9, e95189	8
1577	IIS--Integrated Interactome System: a web-based platform for the annotation, analysis and visualization of protein-metabolite-gene-drug interactions by integrating a variety of data sources and tools. 2014 , 9, e100385	37
1576	Population distribution analyses reveal a hierarchy of molecular players underlying parallel endocytic pathways. 2014 , 9, e100554	13
1575	Harnessing gene expression networks to prioritize candidate epileptic encephalopathy genes. 2014 , 9, e102079	22
1574	Genes involved in the osteoarthritis process identified through genome wide expression analysis in articular cartilage; the RAAK study. 2014 , 9, e103056	103
1573	Identification of essential proteins based on ranking edge-weights in protein-protein interaction networks. 2014 , 9, e108716	12
1572	Bioinformatic prediction of WSSV-host protein-protein interaction. 2014 , 2014, 416543	12
1571	Database constraints applied to metabolic pathway reconstruction tools. 2014 , 2014, 967294	1
1570	De novo assembly and characterization of <i>Sophora japonica</i> transcriptome using RNA-seq. 2014 , 2014, 750961	15
1569	Exploring the miRNA-mRNA regulatory network in clear cell renal cell carcinomas by next-generation sequencing expression profiles. 2014 , 2014, 948408	32
1568	Identification of therapeutic target genes with DNA microarray in multiple myeloma cell line treated by IKK/NF- κ B inhibitor. 2014 , 29, 696-702	2
1567	The shape of the human language-ready brain. 2014 , 5, 282	82
1566	Globularity and language-readiness: generating new predictions by expanding the set of genes of interest. 2014 , 5, 1324	47

1565	Critical Role of Glycogen Synthase Kinase-3β in Regulating the Avian Heterophil Response to Salmonella enterica Serovar Enteritidis. 2014 , 1, 10	2
1564	A bayesian framework that integrates heterogeneous data for inferring gene regulatory networks. 2014 , 2, 13	11
1563	Analysis pipeline for the epistasis search - statistical versus biological filtering. 2014 , 5, 106	47
1562	Schizophrenia and cortical blindness: protective effects and implications for language. 2014 , 8, 940	13
1561	Functional analysis of differentially expressed genes associated with glaucoma from DNA microarray data. 2014 , 13, 9421-8	4
1560	Bioinformatic analysis of miRNA expression patterns in TFF2 knock-out mice. 2014 , 13, 8502-10	3
1559	Analysis of differentially expressed genes in malignant biliary strictures. 2014 , 13, 2674-82	4
1558	Screening for key genes associated with invasive ductal carcinoma of the breast via microarray data analysis. 2014 , 13, 7919-25	5
1557	The triple power of D ₁ protein intrinsic disorder in degenerative diseases. 2014 , 19, 181-258	62
1556	Quantitative proteomic analysis reveals potential diagnostic markers and pathways involved in pathogenesis of renal cell carcinoma. 2014 , 5, 506-18	72
1555	Identification of Influenza A/H7N9 virus infection-related human genes based on shortest paths in a virus-human protein interaction network. 2014 , 2014, 239462	11
1554	. 2014 ,	1
1553	Circulating levels of GDF15, MMP7 and miR-200c as a poor prognostic signature in gastric cancer. 2014 , 10, 1187-202	32
1552	Biological process annotation of proteins across the plant kingdom. 2014 , 1, 73-82	6
1551	Exploiting the power of OMICS approaches to produce E. coli O157 vaccines. 2014 , 5, 770-4	6
1550	Molecular Genetics of Coronary Artery Disease and Myocardial Infarction. 2014 , 217-250	1
1549	Global phylogenomic analysis disentangles the complex evolutionary history of DNA replication in archaea. 2014 , 6, 192-212	58
1548	PhenUMA: a tool for integrating the biomedical relationships among genes and diseases. 2014 , 15, 375	6

1547	Mutated in colorectal cancer (MCC) is a novel oncogene in B lymphocytes. 2014 , 7, 56	13
1546	Deciphering miRNA transcription factor feed-forward loops to identify drug repurposing candidates for cystic fibrosis. 2014 , 6, 94	16
1545	Systems biology approaches to enhance our understanding of drug hypersensitivity reactions. 2014 , 44, 1461-72	8
1544	A random set scoring model for prioritization of disease candidate genes using protein complexes and data-mining of GeneRIF, OMIM and PubMed records. 2014 , 15, 315	7
1543	Elucidation of a protein-protein interaction network involved in <i>Corynebacterium glutamicum</i> cell wall biosynthesis as determined by bacterial two-hybrid analysis. 2014 , 31, 475-83	9
1542	Reconstruction of metabolic pathways by combining probabilistic graphical model-based and knowledge-based methods. 2014 , 8, S5	10
1541	Revisiting topological properties of protein-protein interaction networks from the perspective of dataset evolution. 2014 ,	
1540	Screening miRNA and their target genes related to tetralogy of Fallot with microarray. 2014 , 24, 442-6	9
1539	Therapeutic expression of hairpins targeting apolipoprotein B100 induces phenotypic and transcriptome changes in murine liver. 2014 , 21, 60-70	10
1538	Whole-exome sequencing reveals TopBP1 as a novel gene in idiopathic pulmonary arterial hypertension. 2014 , 189, 1260-72	58
1537	Early targets of lithium in rat kidney inner medullary collecting duct include p38 and ERK1/2. 2014 , 86, 757-67	32
1536	Post-acute brain injury urinary signature: a new resource for molecular diagnostics. 2014 , 31, 782-8	19
1535	Unbiased functional clustering of gene variants with a phenotypic-linkage network. 2014 , 10, e1003815	41
1534	Navigating the multilayered organization of eukaryotic signaling: a new trend in data integration. 2014 , 10, e1003385	7
1533	Regulation of Sucrose non-Fermenting Related Kinase 1 genes in <i>Arabidopsis thaliana</i> . 2014 , 5, 324	43
1532	Definition of a Family of Tissue-Protective Cytokines Using Functional Cluster Analysis: A Proof-of-Concept Study. 2014 , 5, 115	5
1531	Ras-mediated deregulation of the circadian clock in cancer. 2014 , 10, e1004338	93
1530	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014 , 42, D401-7	20.1 290

1529	Salivary Peptidomics Targeting Clinical Applications. 2014 , 64, 223-245	2
1528	<i>Gleditsia sinensis</i> : transcriptome sequencing, construction, and application of its protein-protein interaction network. 2014 , 2014, 404578	7
1527	Computational biophysical, biochemical, and evolutionary signature of human R-spondin family proteins, the member of canonical Wnt/ β -catenin signaling pathway. 2014 , 2014, 974316	6
1526	Characterizing protein interactions employing a genome-wide siRNA cellular phenotyping screen. 2014 , 10, e1003814	7
1525	Systematic expression profiling analysis identifies specific microRNA-gene interactions that may differentiate between active and latent tuberculosis infection. 2014 , 2014, 895179	19
1524	In-vivo quantitative proteomics reveals a key contribution of post-transcriptional mechanisms to the circadian regulation of liver metabolism. 2014 , 10, e1004047	260
1523	Large scale RNAi reveals the requirement of nuclear envelope breakdown for nuclear import of human papillomaviruses. 2014 , 10, e1004162	107
1522	Large scale analysis of signal reachability. 2014 , 30, i96-104	5
1521	Coiled-coil proteins facilitated the functional expansion of the centrosome. 2014 , 10, e1003657	23
1520	Protein flexibility facilitates quaternary structure assembly and evolution. 2014 , 12, e1001870	56
1519	Functional association networks as priors for gene regulatory network inference. 2014 , 30, i130-8	30
1518	Network based integrated analysis of phenotype-genotype data for prioritization of candidate symptom genes. 2014 , 2014, 435853	8
1517	Keratin 19: a key role player in the invasion of human hepatocellular carcinomas. 2014 , 63, 674-85	182
1516	HGV&TB: a comprehensive online resource on human genes and genetic variants associated with tuberculosis. 2014 , 2014, bau112	3
1515	Physiological and genomic basis of mechanical-functional trade-off in plant vasculature. 2014 , 5, 224	10
1514	Genome-wide analysis of the distribution of AP2/ERF transcription factors reveals duplication and CBFs genes elucidate their potential function in <i>Brassica oleracea</i> . 2014 , 15, 422	40
1513	Overelaborated synaptic architecture and reduced synaptomatrix glycosylation in a <i>Drosophila</i> classic galactosemia disease model. 2014 , 7, 1365-78	29
1512	Deciphering kinase-substrate relationships by analysis of domain-specific phosphorylation network. 2014 , 30, 1730-8	15

1511	Degree-adjusted algorithm for prioritisation of candidate disease genes from gene expression and protein interactome. 2014 , 8, 41-6	1
1510	Proteomics of muscle chronological ageing in post-menopausal women. 2014 , 15, 1165	53
1509	Beyond genomic variation--comparison and functional annotation of three Brassica rapa genomes: a turnip, a rapid cycling and a Chinese cabbage. 2014 , 15, 250	70
1508	Actinous enigma or enigmatic actin: Folding, structure, and functions of the most abundant eukaryotic protein. 2014 , 2, e34500	10
1507	Differential skeletal muscle proteome of high- and low-active mice. 2014 , 116, 1057-67	13
1506	Three-dimensional eukaryotic genomic organization is strongly correlated with codon usage expression and function. 2014 , 5, 5876	19
1505	Unreported intrinsic disorder in proteins: Building connections to the literature on IDPs. 2014 , 2, e970499	7
1504	Proteome and phosphoproteome characterization reveals new response and defense mechanisms of Brachypodium distachyon leaves under salt stress. 2014 , 13, 632-52	103
1503	How does altering the resolution of chromosomal microarray analysis in the prenatal setting affect the rates of pathological and uncertain findings?. 2014 , 27, 649-57	22
1502	Protter: interactive protein feature visualization and integration with experimental proteomic data. 2014 , 30, 884-6	666
1501	Comprehensive quantitative comparison of the membrane proteome, phosphoproteome, and sialome of human embryonic and neural stem cells. 2014 , 13, 311-28	52
1500	Genes expressed in blood link osteoarthritis with apoptotic pathways. 2014 , 73, 1844-53	47
1499	Shifts in the vascular endothelial growth factor isoforms result in transcriptome changes correlated with early neural stem cell proliferation and differentiation in mouse forebrain. 2014 , 74, 63-81	6
1498	Quantitative proteome analyses identify PrfA-responsive proteins and phosphoproteins in Listeria monocytogenes. 2014 , 13, 6046-57	21
1497	Comparison of transcriptional profiles between CD4+ and CD8+ T cells in HIV type 1-infected patients. 2014 , 30, 134-41	10
1496	Profiling human protein degradome delineates cellular responses to proteasomal inhibition and reveals a feedback mechanism in regulating proteasome homeostasis. 2014 , 24, 1214-30	12
1495	Representation of the Protein Universe using Classifications, Maps, and Networks. 2014 , 54, 1286-1292	9
1494	Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. 2014 , 3, 858-75	25

1493	Alterations in the cerebellar (Phospho)proteome of a cyclic guanosine monophosphate (cGMP)-dependent protein kinase knockout mouse. 2014 , 13, 2004-16	11
1492	Proteomics, genomics and transcriptomics: their emerging roles in the discovery and validation of colorectal cancer biomarkers. 2014 , 11, 179-205	21
1491	Simultaneous analysis of large-scale RNAi screens for pathogen entry. 2014 , 15, 1162	28
1490	Proteome changes underpin improved meat quality and yield of chickens (<i>Gallus gallus</i>) fed the probiotic <i>Enterococcus faecium</i> . 2014 , 15, 1167	40
1489	Papillomavirus binding factor (PBF) is an intrinsically disordered protein with potential participation in osteosarcoma genesis, in silico evidence. 2014 , 11, 51	1
1488	Integration of heterogeneous molecular networks to unravel gene-regulation in <i>Mycobacterium tuberculosis</i> . 2014 , 8, 111	12
1487	The study of severe cutaneous drug hypersensitivity reactions from a systems biology perspective. 2014 , 14, 301-6	5
1486	Functional network pipeline reveals genetic determinants associated with in situ lymphocyte proliferation and survival of cancer patients. 2014 , 6, 228ra37	141
1485	Proteomic Approach to the Reprogramming Machinery of the Mouse Oocyte. 2014 , 407-417	
1484	Overrepresentation of glutamate signaling in Alzheimer's disease: network-based pathway enrichment using meta-analysis of genome-wide association studies. 2014 , 9, e95413	42
1483	Proteomic analysis of <i>Synechocystis</i> sp. PCC6803 responses to low-temperature and high light conditions. 2014 , 19, 629-640	2
1482	Detecting Dysregulated Processes and Pathways. 2014 , 309-334	
1481	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. 2014 , 7, rs6	26
1480	Impacts of pretranscriptional DNA methylation, transcriptional transcription factor, and posttranscriptional microRNA regulations on protein evolutionary rate. 2014 , 6, 1530-41	20
1479	A survey of computational intelligence techniques in protein function prediction. 2014 , 2014, 845479	25
1478	First comprehensive in silico analysis of the functional and structural consequences of SNPs in human GalNAc-T1 gene. 2014 , 2014, 904052	18
1477	Probing the Unknowns in Cytokinin-Mediated Immune Defense in <i>Arabidopsis</i> with Systems Biology Approaches. 2014 , 8, BBI.S13462	11
1476	In Silico Molecular Characterization of Cysteine Protease YopT from <i>Yersinia pestis</i> by Homology Modeling and Binding Site Identification. 2014 , 8, 1-9	15

1475	Integrated analysis of gene network in childhood leukemia from microarray and pathway databases. 2014 , 2014, 278748	7
1474	MetReS: A Metabolic Reconstruction Database for Cloud Computing. 2014 ,	
1473	Protein domains of unknown function are essential in bacteria. 2013 , 5, e00744-13	77
1472	Colorectal cancer derived organotypic spheroids maintain essential tissue characteristics but adapt their metabolism in culture. 2014 , 12, 39	30
1471	Inferring gene function from evolutionary change in signatures of translation efficiency. 2014 , 15, R44	37
1470	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. 2014 , 6, 17	21
1469	TOPOISOMERASE 6B is involved in chromatin remodelling associated with control of carbon partitioning into secondary metabolites and cell walls, and epidermal morphogenesis in Arabidopsis. 2014 , 65, 4217-39	4
1468	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014 , 42, D23129.1	387
1467	SuSPect: enhanced prediction of single amino acid variant (SAV) phenotype using network features. 2014 , 426, 2692-701	140
1466	Neuronal -The Secretory Portal at the Nerve Terminal: It's Structure-Function, Composition, and Reconstitution. 2014 , 1073, 187-195	4
1465	Unraveling molecular mechanistic differences in liver metabolism between lean and fat lines of Pekin duck (<i>Anas platyrhynchos domestica</i>): a proteomic study. 2014 , 98, 271-88	15
1464	2DGE and DIGE based proteomic study of malignant B-cells in B-cell acute lymphoblastic leukemia. 2014 , 3, 13-26	10
1463	Global analysis of induced transcription factors and cofactors identifies Tfdp2 as an essential coregulator during terminal erythropoiesis. 2014 , 42, 464-76.e5	12
1462	Structural network analysis of biological networks for assessment of potential disease model organisms. 2014 , 47, 178-91	5
1461	Biomarkers of coordinate metabolic reprogramming in colorectal tumors in mice and humans. 2014 , 146, 1313-24	63
1460	Expression of the mevalonate pathway enzymes in the <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) sex pheromone gland demonstrated by an integrated proteomic approach. 2014 , 96, 117-32	11
1459	An integrated immunoproteomics and bioinformatics approach for the analysis of <i>Schistosoma japonicum</i> tegument proteins. 2014 , 98, 289-99	23
1458	Double deficiency of cathepsins B and L results in massive secretome alterations and suggests a degradative cathepsin-MMP axis. 2014 , 71, 899-916	30

1457	The organisational structure of protein networks: revisiting the centrality-lethality hypothesis. 2014 , 8, 73-81	59
1456	The Human Interactome Knowledge Base (HINT-KB): an integrative human protein interaction database enriched with predicted protein-protein interaction scores using a novel hybrid technique. 2014 , 42, 427-443	4
1455	Activating transcription factor 4 links metabolic stress to interleukin-6 expression in macrophages. 2014 , 63, 152-61	69
1454	Exploiting human CD34+ stem cell-conditioned medium for tissue repair. 2014 , 22, 149-59	7
1453	Integrating microRNA target predictions for the discovery of gene regulatory networks: a semi-supervised ensemble learning approach. 2014 , 15 Suppl 1, S4	37
1452	DnaK protein interaction of phage marked Bradyrhizobium of soybean. 2014 , 64, 1535-1542	
1451	Differential gene expression in Acidithiobacillus ferrooxidans LR planktonic and attached cells in the presence of chalcopyrite. 2014 , 54, 650-7	1
1450	Identification of Disease Genes Using Gene Expression and Protein-Protein Interaction Data. 2014 , 155-170	
1449	Pathogens and host immunity in the ancient human oral cavity. 2014 , 46, 336-44	353
1448	DDGni: dynamic delay gene-network inference from high-temporal data using gapped local alignment. 2014 , 30, 377-83	21
1447	Leucine-rich repeat kinase 2 binds to neuronal vesicles through protein interactions mediated by its C-terminal WD40 domain. 2014 , 34, 2147-61	72
1446	Thymosin β 4 gene silencing decreases stemness and invasiveness in glioblastoma. 2014 , 137, 433-48	29
1445	Experimental and computational tools for analysis of signaling networks in primary cells. 2014 , 104, 11.11.1-11.11.1.23	
1444	Screening of cellular proteins that interact with the classical swine fever virus non-structural protein 5A by yeast two-hybrid analysis. 2014 , 39, 63-74	18
1443	Construction of Geobacillus thermoglucosidasius cDNA library and analysis of genes expressed in response to heat stress. 2014 , 41, 1639-44	3
1442	Integration of transcription and flux data reveals molecular paths associated with differences in oxygen-dependent phenotypes of Saccharomyces cerevisiae. 2014 , 8, 16	2
1441	Global secretome characterization of A549 human alveolar epithelial carcinoma cells during Mycoplasma pneumoniae infection. 2014 , 14, 27	15
1440	Research on the typical miRNA and target genes in squamous cell carcinoma and adenocarcinoma of esophagus cancer with DNA microarray. 2014 , 20, 245-52	12

1439	Stage-specific quantitative changes in renal and urinary proteome during the progression and development of streptozotocin-induced diabetic nephropathy in rats. 2014 , 388, 95-111	10
1438	Application of a subtractive genomics approach for in silico identification and characterization of novel drug targets in <i>Mycobacterium tuberculosis</i> F11. 2014 , 6, 48-56	34
1437	Prediction of novel drug indications using network driven biological data prioritization and integration. 2014 , 6, 1	48
1436	ISAAC - InterSpecies Analysing Application using Containers. 2014 , 15, 18	4
1435	Mitochondrial-related proteomic changes during obesity and fasting in mice are greater in the liver than skeletal muscles. 2014 , 14, 245-59	19
1434	Exome sequencing links corticospinal motor neuron disease to common neurodegenerative disorders. 2014 , 343, 506-511	374
1433	Secretome profiling reveals the signaling molecules of apoptotic HCT116 cells induced by the dietary polyacetylene gymnasterkoreayne B. 2014 , 62, 2353-63	6
1432	Computational gene network study on antibiotic resistance genes of <i>Acinetobacter baumannii</i> . 2014 , 48, 17-27	24
1431	Feature selection and classification of protein-protein complexes based on their binding affinities using machine learning approaches. 2014 , 82, 2088-96	26
1430	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. 2014 , 123, e68-78	58
1429	A distance measure for large graphs based on prime graphs. 2014 , 47, 2993-3005	10
1428	Structural and functional analysis of hypothetical and conserved proteins of <i>Clostridium tetani</i> . 2014 , 7, 296-307	15
1427	Resources for systems biology in rice. 2014 , 57, 80-92	29
1426	Global identification of O-GlcNAc transferase (OGT) interactors by a human proteome microarray and the construction of an OGT interactome. 2014 , 14, 1020-30	23
1425	The role of apolipoprotein E in neurodegeneration and cardiovascular disease. 2014 , 11, 371-81	20
1424	Docking and Pharmacophore Modelling for Virtual Screening. 2014 , 195-269	1
1423	Comparative analysis of viral protein interaction networks in Hepatitis B virus and Hepatitis C virus infected HCC. 2014 , 1844, 271-9	5
1422	Kinome-wide functional analysis highlights the role of cytoskeletal remodeling in somatic cell reprogramming. 2014 , 14, 523-34	51

1421	The role of low-grade inflammation and metabolic flexibility in aging and nutritional modulation thereof: a systems biology approach. 2014 , 136-137, 138-47	64
1420	Cytokinin modulates proteomic, transcriptomic and growth responses to temperature shocks in Arabidopsis. 2014 , 37, 1641-55	60
1419	Potential biomarkers and latent pathways for vasculitis based on latent pathway identification analysis. 2014 , 17, 671-8	2
1418	Functional clustering of immunoglobulin superfamily proteins with protein-protein interaction information calibrated hidden Markov model sequence profiles. 2014 , 426, 945-61	19
1417	Label-free quantitative proteomics analysis of antibiotic response in Staphylococcus aureus to oxacillin. 2014 , 13, 1223-33	59
1416	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. 2014 , 1844, 12-20	24
1415	Identification and validation of dysregulated metabolic pathways in metastatic renal cell carcinoma. 2014 , 35, 1833-46	25
1414	OMICS in ecology: systems level analyses of Halobacterium salinarum reveal large-scale temperature-mediated changes and a requirement of CctA for thermotolerance. 2014 , 18, 65-80	7
1413	Expression levels of DNA replication and repair genes predict regional somatic repeat instability in the brain but are not altered by polyglutamine disease protein expression or age. 2014 , 23, 1606-18	37
1412	Structural insights from GRP78-NF- κ B binding interactions: a computational approach to understand a possible neuroprotective pathway in brain injuries. 2014 , 345, 43-51	7
1411	Sirtuin 7 plays a role in ribosome biogenesis and protein synthesis. 2014 , 13, 73-83	81
1410	A generally applicable translational strategy identifies S100A4 as a candidate gene in allergy. 2014 , 6, 218ra4	37
1409	A perspective on proteomics in cell biology. 2014 , 24, 257-64	38
1408	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. 2014 , 30, 540-8	42
1407	Colorectal cancer candidate biomarkers identified by tissue secretome proteome profiling. 2014 , 99, 26-39	74
1406	Integrative approaches for predicting protein function and prioritizing genes for complex phenotypes using protein interaction networks. 2014 , 15, 685-98	17
1405	Integrating in silico resources to map a signaling network. 2014 , 1101, 197-245	17
1404	Transcription and enhancer profiling in human monocyte subsets. 2014 , 123, e90-9	101

1403	Comparisons of gene expression in normal, lesional, and non-lesional psoriatic skin using DNA microarray techniques. 2014 , 53, 1213-20	9
1402	Analyzing time-series microarray data reveals key genes in spinal cord injury. 2014 , 41, 6827-35	4
1401	Genomewide RNAi screen identifies protein kinase C β and new members of mitogen-activated protein kinase pathway as regulators of melanoma cell growth and metastasis. 2014 , 27, 418-30	8
1400	Comparative proteomic analysis of outer membrane vesicles from <i>Shigella flexneri</i> under different culture conditions. 2014 , 453, 696-702	12
1399	Identification of the PKR nuclear interactome reveals roles in ribosome biogenesis, mRNA processing and cell division. 2014 , 229, 1047-60	14
1398	Stress response of <i>Pseudomonas</i> species to silver nanoparticles at the molecular level. 2014 , 33, 2126-32	17
1397	Identifying the potential extracellular electron transfer pathways from a c-type cytochrome network. 2014 , 10, 3138-46	7
1396	Identification of inflammatory bowel disease-related proteins using a reverse k-nearest neighbor search. 2014 , 12, 1450017	10
1395	BioTextQuest(+): a knowledge integration platform for literature mining and concept discovery. 2014 , 30, 3249-56	14
1394	Discovery of an integrative network of microRNAs and transcriptomics changes for acute kidney injury. 2014 , 86, 943-53	71
1393	mRNA Transcript abundance during plant growth and the influence of Li(+) exposure. 2014 , 229, 262-279	6
1392	Time course label-free quantitative analysis of cardiac muscles of rats after myocardial infarction. 2014 , 10, 505-13	11
1391	Improving the performance of protein kinase identification via high dimensional protein-protein interactions and substrate structure data. 2014 , 10, 694-702	20
1390	Systematic identification of hypothetical bacteriophage proteins targeting key protein complexes of <i>Pseudomonas aeruginosa</i> . 2014 , 13, 4446-56	38
1389	Label-free quantitative protein profiling of vastus lateralis muscle during human aging. 2014 , 13, 283-94	37
1388	Characterization of probabilistic signaling networks through signal propagation. 2014 ,	4
1387	Global transcriptional response to heat shock of the legume symbiont <i>Mesorhizobium loti</i> MAFF303099 comprises extensive gene downregulation. 2014 , 21, 195-206	20
1386	Primary cilium-associated genes mediate bone marrow stromal cell response to hypoxia. 2014 , 13, 284-99	13

1385	Knockdown of a zebrafish aryl hydrocarbon receptor repressor (AHRRa) affects expression of genes related to photoreceptor development and hematopoiesis. 2014 , 139, 381-95	17
1384	Metabolic programming of mesenchymal stromal cells by oxygen tension directs chondrogenic cell fate. 2014 , 111, 13954-9	85
1383	Interactive host cells related to <i>Mycoplasma suis</i> hemolase by yeast two-hybrid analysis. 2014 , 97, 282-7	2
1382	Global identification of CobB interactors by an <i>Escherichia coli</i> proteome microarray. 2014 , 46, 548-55	11
1381	Unraveling novel broad-spectrum antibacterial targets in food and waterborne pathogens using comparative genomics and protein interaction network analysis. 2014 , 27, 300-8	19
1380	Bioinformatic and biochemical characterizations of C-S bond formation and cleavage enzymes in the fungus <i>Neurospora crassa</i> ergothioneine biosynthetic pathway. 2014 , 16, 5382-5	50
1379	Identification of putative fertility markers in seminal plasma of crossbred bulls through differential proteomics. 2014 , 82, 1254-62.e1	33
1378	Genetic diversity and natural selection of three blood-stage 6-Cys proteins in <i>Plasmodium vivax</i> populations from the China-Myanmar endemic border. 2014 , 28, 167-74	11
1377	Proteomic analysis of arginine methylation sites in human cells reveals dynamic regulation during transcriptional arrest. 2014 , 13, 2072-88	61
1376	Quantitative proteomics in cardiovascular research: global and targeted strategies. 2014 , 8, 488-505	17
1375	LCK: a new biomarker candidate for the early diagnosis of acute myocardial infarction. 2014 , 41, 8047-53	4
1374	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies. 2014 , 93-131	1
1373	A high-throughput siRNA screen identifies genes that regulate mannose 6-phosphate receptor trafficking. 2014 , 127, 5079-92	12
1372	Comparative proteomic analysis of different developmental stages of the edible mushroom <i>Termitomyces heimii</i> . 2014 , 47, 30	25
1371	Dynamic probabilistic threshold networks to infer signaling pathways from time-course perturbation data. 2014 , 15, 250	9
1370	Inferring the perturbed microRNA regulatory networks from gene expression data using a network propagation based method. 2014 , 15, 255	8
1369	Elucidation of the evolutionary expansion of phosphorylation signaling networks using comparative phosphomotif analysis. 2014 , 15, 546	6
1368	Inspecting the potential physiological and biomedical value of 44 conserved uncharacterised proteins of <i>Streptococcus pneumoniae</i> . 2014 , 15, 652	4

1367	A network-based approach to dissect the cilia/centrosome complex interactome. 2014 , 15, 658	14
1366	Molecularly and clinically related drugs and diseases are enriched in phenotypically similar drug-disease pairs. 2014 , 6, 52	14
1365	Immunoproteasomes shape the transcriptome and regulate the function of dendritic cells. 2014 , 193, 1121-32	22
1364	Single-step enrichment by Ti4+-IMAC and label-free quantitation enables in-depth monitoring of phosphorylation dynamics with high reproducibility and temporal resolution. 2014 , 13, 2426-34	80
1363	Temporal gene expression analysis of Sjögren's syndrome in C57BL/6.NOD-Aec1Aec2 mice based on microarray time-series data using an improved empirical Bayes approach. 2014 , 41, 5953-60	3
1362	Genes commonly involved in acid tolerance are not overexpressed in the plant micro symbiont <i>Mesorhizobium loti</i> MAFF303099 upon acidic shock. 2014 , 98, 7137-47	11
1361	Protein-protein interaction network analysis in chronic obstructive pulmonary disease. 2014 , 192, 87-93	5
1360	Plant systems biology: insights, advances and challenges. 2014 , 240, 33-54	55
1359	Combination use of protein-protein interaction network topological features improves the predictive scores of deleterious non-synonymous single-nucleotide polymorphisms. 2014 , 46, 2025-35	17
1358	Identifying gene expression profile of spinal cord injury in rat by bioinformatics strategy. 2014 , 41, 3169-77	21
1357	Immune-related chemotactic factors were found in acute coronary syndromes by bioinformatics. 2014 , 41, 4389-95	2
1356	APC/C is an essential regulator of centrosome clustering. 2014 , 5, 3686	50
1355	Targeted protein quantification using sparse reference labeling. 2014 , 11, 301-4	8
1354	Docosahexaenoic acid modulates the enterocyte Caco-2 cell expression of microRNAs involved in lipid metabolism. 2014 , 144, 575-85	51
1353	Proteome-driven elucidation of adaptive responses to combined vitamin E and C deficiency in zebrafish. 2014 , 13, 1647-56	6
1352	Identification of candidate biomarkers for the early detection of nasopharyngeal carcinoma by quantitative proteomic analysis. 2014 , 109, 162-75	22
1351	Comprehensive profiling of lysine acetylome in <i>Staphylococcus aureus</i> . 2014 , 57, 732-738	16
1350	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. 2014 , 15, 232	31

1349	A network-based approach to identify substrate classes of bacterial glycosyltransferases. 2014 , 15, 349	99
1348	Stringent homology-based prediction of <i>H. sapiens</i> - <i>M. tuberculosis</i> H37Rv protein-protein interactions. 2014 , 9, 5	55
1347	Computational prediction of the human-microbial oral interactome. 2014 , 8, 24	27
1346	RUNX1T1/MTG8/ETO gene expression status in human t(8;21)(q22;q22)-positive acute myeloid leukemia cells. 2014 , 38, 1102-10	7
1345	Combination of a discovery LC-MS/MS analysis and a label-free quantification for the characterization of an epithelial-mesenchymal transition signature. 2014 , 110, 183-94	9
1344	Active learning for protein function prediction in protein-protein interaction networks. 2014 , 145, 44-52	16
1343	Identification of hypoxia-regulated proteins using MALDI-mass spectrometry imaging combined with quantitative proteomics. 2014 , 13, 2297-313	26
1342	Nuclear cytoplasmic trafficking of proteins is a major response of human fibroblasts to oxidative stress. 2014 , 13, 4398-423	11
1341	Neuronal process structure and growth proteins are targets of heavy PTM regulation during brain development. 2014 , 101, 77-87	10
1340	Gene expression profiles during short-term heat stress in the red sea coral <i>Stylophora pistillata</i> . 2014 , 20, 3026-35	53
1339	Prediction of gene-based drug indications using compendia of public gene expression data and PubMed abstracts. 2014 , 12, 1450007	1
1338	Wnt signaling directs a metabolic program of glycolysis and angiogenesis in colon cancer. 2014 , 33, 1454-73	256
1337	Insights into the cellular response triggered by silver nanoparticles using quantitative proteomics. 2014 , 8, 2161-75	153
1336	CloudNMF: a MapReduce implementation of nonnegative matrix factorization for large-scale biological datasets. 2014 , 12, 48-51	30
1335	Intrinsic disorder in proteins involved in the innate antiviral immunity: another flexible side of a molecular arms race. 2014 , 426, 1322-50	27
1334	Prioritizing drug targets in <i>Clostridium botulinum</i> with a computational systems biology approach. 2014 , 104, 24-35	22
1333	Deciphering early development of complex diseases by progressive module network. 2014 , 67, 334-43	36
1332	Global phosphoproteomic profiling reveals distinct signatures in B-cell non-Hodgkin lymphomas. 2014 , 184, 1331-42	23

1331	Peroxiredoxin 2 nuclear levels are regulated by circadian clock synchronization in human keratinocytes. 2014 , 53, 24-34	22
1330	Current status and future prospects of toxicogenomics in drug discovery. 2014 , 19, 562-78	26
1329	Suppression mechanism of the calcium sensitivity in <i>Saccharomyces cerevisiae</i> ptp2hsg5 double disruptant involves a novel HOG-independent function of Ssk2, transcription factor Msn2 and the protein kinase A component Bcy1. 2014 , 117, 135-141	5
1328	Proteomics of differential extraction fractions enriched for chromatin-binding proteins from colon adenoma and carcinoma tissues. 2014 , 1844, 1034-43	5
1327	Primary effusion lymphoma: secretome analysis reveals novel candidate biomarkers with potential pathogenetic significance. 2014 , 184, 618-30	10
1326	CELSR2-PSRC1-SORT1 gene expression and association with coronary artery disease and plasma lipid levels in an Asian Indian cohort. 2014 , 64, 339-46	40
1325	Ossification of the posterior longitudinal ligament related genes identification using microarray gene expression profiling and bioinformatics analysis. 2014 , 533, 515-9	8
1324	Methylomics analysis identifies epigenetically silenced genes and implies an activation of E-catenin signaling in cervical cancer. 2014 , 135, 117-27	52
1323	The highly conserved MraZ protein is a transcriptional regulator in <i>Escherichia coli</i> . 2014 , 196, 2053-66	46
1322	Quantitative proteomics identifies unanticipated regulators of nitrogen- and glucose starvation. 2014 , 10, 2176-88	3
1321	Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. 2014 , 3, 83-112	56
1320	A common atopy-associated variant in the Th2 cytokine locus control region impacts transcriptional regulation and alters SMAD3 and SP1 binding. 2014 , 69, 632-42	9
1319	Transcription factor cooperativity in early adipogenic hotspots and super-enhancers. 2014 , 7, 1443-1455	163
1318	Evolution of protein interactions: from interactomes to interfaces. 2014 , 554, 65-75	40
1317	Human cytochrome P450 epoxygenases: variability in expression and role in inflammation-related disorders. 2014 , 144, 134-61	66
1316	Human Dopamine Receptors Interaction Network (DRIN): a systems biology perspective on topology, stability and functionality of the network. 2014 , 357, 169-83	7
1315	Prediction of protein phenotype based on protein interaction network by coupling genetic algorithm and K-nearest neighbor algorithm. 2014 , 6, 5281	3
1314	SUMV-1 antagonizes the activity of synthetic multivulva genes in <i>Caenorhabditis elegans</i> . 2014 , 392, 266-82	3

1313	Protein-protein interactions and genetic diseases: The interactome. 2014 , 1842, 1971-1980	75
1312	Focussed microarray analysis of apoptosis in periodontitis and its potential pharmacological targeting by carvacrol. 2014 , 59, 461-9	20
1311	Biological network extraction from scientific literature: state of the art and challenges. 2014 , 15, 856-77	45
1310	Protein-protein interactions: switch from classical methods to proteomics and bioinformatics-based approaches. 2014 , 71, 205-28	84
1309	Nonconvex Proximal Splitting with Computational Errors Suvrit Sra. 2014 , 101-120	
1308	Drug Bioavailability and Gene Probing: Challenges and Opportunities for Pharmaceuticals and Personalized Medicine. 2014 , 179-228	
1307	Genetics of Peptidoglycan Biosynthesis. 2014 , 2, MGM2-0034-2013	19
1306	Identification of differentially expressed microRNAs in metastatic melanoma using next-generation sequencing technology. 2014 , 33, 1117-21	19
1305	Proteomic and bioinformatic analysis of differentially expressed proteins in denervated skeletal muscle. 2014 , 33, 1586-96	22
1304	Module-based functional pathway enrichment analysis of a protein-protein interaction network to study the effects of intestinal microbiota depletion in mice. 2014 , 9, 2205-12	6
1303	The centrality of cancer proteins in human protein-protein interaction network: a revisit. 2014 , 7, 146-56	7
1302	Unbiased RNAi screen for hepcidin regulators links hepcidin suppression to proliferative Ras/RAF and nutrient-dependent mTOR signaling. 2014 , 123, 1574-85	50
1301	Screening of diagnostic markers for osteosarcoma. 2014 , 10, 2415-20	28
1300	Screening of differentially expressed genes related to esophageal squamous cell carcinoma and functional analysis with DNA microarrays. 2014 , 44, 1163-70	5
1299	Bioinformatic analysis of Msx1 and Msx2 involved in craniofacial development. 2014 , 25, 129-34	9
1298	Analysis of signaling networks distributed over intracellular compartments based on protein-protein interactions. 2014 , 15 Suppl 12, S7	5
1297	Identifying disease associated genes by network propagation. 2014 , 8 Suppl 1, S6	20
1296	RASSF1A promotes apoptosis and suppresses the proliferation of ovarian cancer cells. 2014 , 33, 1153-60	13

1295	Identification of key genes and crucial modules associated with coronary artery disease by bioinformatics analysis. 2014 , 34, 863-9	10
1294	cDNA microarray and bioinformatic analysis for the identification of key genes in Alzheimer's disease. 2014 , 33, 457-61	5
1293	Identification of the typical miRNAs and target genes in hepatocellular carcinoma. 2014 , 10, 229-35	12
1292	Gene expression profiles of patients with cerebral hematoma following spontaneous intracerebral hemorrhage. 2014 , 10, 1671-8	6
1291	Participation of proteins binding both actin filaments and microtubules in higher plant cell growth. 2015 , 49, 270-278	
1290	Revisiting topological properties and models of protein-protein interaction networks from the perspective of dataset evolution. 2015 , 9, 113-9	3
1289	Extensive differential protein phosphorylation as intraerythrocytic Plasmodium falciparum schizonts develop into extracellular invasive merozoites. 2015 , 15, 2716-29	46
1288	Comparative two-dimensional polyacrylamide gel electrophoresis of the salivary proteome of children with autism spectrum disorder. 2015 , 19, 2664-78	34
1287	Vaccinia Virus Infection Requires Maturation of Macropinosomes. 2015 , 16, 814-31	34
1286	Identification of therapeutic targets for breast cancer using biological informatics methods. 2015 , 12, 1789-95	11
1285	A Systems Biology-Based Investigation into the Pharmacological Mechanisms of Sheng-ma-bie-jia-tang Acting on Systemic Lupus Erythematosus by Multi-Level Data Integration. 2015 , 5, 16401	17
1284	In silico analysis of the molecular mechanism of postmenopausal osteoporosis. 2015 , 12, 6584-90	12
1283	Microarray based analysis of gene regulation by microRNA in intervertebral disc degeneration. 2015 , 12, 4925-30	21
1282	Prognostic interaction patterns in diabetes mellitus II: A random-matrix-theory relation. 2015 , 92, 022806	5
1281	PALM-IST: Pathway Assembly from Literature Mining--an Information Search Tool. 2015 , 5, 10021	17
1280	A whole-genome RNAi screen uncovers a novel role for human potassium channels in cell killing by the parasite Entamoeba histolytica. 2015 , 5, 13613	21
1279	Influence of age on rat bone-marrow mesenchymal stem cells potential. 2015 , 5, 16765	48
1278	Microarray data analysis of neuroblastoma: Expression of SOX2 downregulates the expression of MYCN. 2015 , 12, 6867-72	0

1277	Research Resource: Androgen Receptor Activity Is Regulated Through the Mobilization of Cell Surface Receptor Networks. 2015 , 29, 1195-218	7
1276	Screening biomarkers of bladder cancer using combined miRNA and mRNA microarray analysis. 2015 , 12, 3170-6	8
1275	Gene discovery for facioscapulohumeral muscular dystrophy by machine learning techniques. 2016 , 90, 343-56	0
1274	Genetic interactions and network reliability. 51-64	
1273	Metagenomics: Assigning Functional Status to Community Gene Content. 2015 , 2.4.4-1-2.4.4-7	
1272	Exploring novel mechanistic insights in Alzheimer's disease by assessing reliability of protein interactions. 2015 , 5, 13634	8
1271	DATA MINING AND SYSTEMS BIOLOGY FOR IDENTIFYING KEY GENES INVOLVED IN CITRUS QUALITY. 2015 , 591-598	
1270	Condition-specific genetic interaction maps reveal crosstalk between the cAMP/PKA and the HOG MAPK pathways in the activation of the general stress response. 2015 , 11, 829	28
1269	Screening of biomarkers in cervical squamous cell carcinomas via gene expression profiling. 2015 , 12, 6985-9	3
1268	Counting motifs in probabilistic biological networks. 2015 ,	7
1267	The L1TD1 protein interactome reveals the importance of post-transcriptional regulation in human pluripotency. 2015 , 4, 519-28	18
1266	Protein-protein interaction network and mechanism analysis in ischemic stroke. 2015 , 11, 29-36	13
1265	Inference of gene interaction networks using conserved subsequential patterns from multiple time course gene expression datasets. 2015 , 16 Suppl 12, S4	0
1264	Signal reachability facilitates characterization of probabilistic signaling networks. 2015 , 16 Suppl 17, S6	2
1263	Alteration of intracellular protein expressions as a key mechanism of the deterioration of bacterial denitrification caused by copper oxide nanoparticles. 2015 , 5, 15824	64
1262	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. 2015 , 5, 17201	29
1261	eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs. 2015 , 58, 226-234	8
1260	Variants in the interleukin-1 alpha and beta genes, and the risk for periodontal disease in dogs. 2015 , 94, 651-9	3

1259	Intracellular expression of Tat alters mitochondrial functions in T cells: a potential mechanism to understand mitochondrial damage during HIV-1 replication. 2015 , 12, 78	23
1258	Integrative enrichment analysis: a new computational method to detect dysregulated pathways in heterogeneous samples. 2015 , 16, 918	12
1257	novPTMenzy: a database for enzymes involved in novel post-translational modifications. 2015 , 2015, bav039	3
1256	IIDB: a database for isoform-isoform interactions and isoform network modules. 2015 , 16 Suppl 2, S10	25
1255	Predicting and exploring network components involved in pathogenesis in the malaria parasite via novel subnetwork alignments. 2015 , 9 Suppl 4, S1	2
1254	Nanopublications for exposing experimental data in the life-sciences: a Huntington's Disease case study. 2015 , 6, 5	10
1253	Interlog protein network: an evolutionary benchmark of protein interaction networks for the evaluation of clustering algorithms. 2015 , 16, 319	11
1252	A bioinformatic survey of RNA-binding proteins in Plasmodium. 2015 , 16, 890	47
1251	Unravelling personalized dysfunctional gene network of complex diseases based on differential network model. 2015 , 13, 189	24
1250	Proteins interaction network and modeling of IGVH mutational status in chronic lymphocytic leukemia. 2015 , 12, 12	7
1249	On predicting regulatory genes by analysis of functional networks in C. elegans. 2015 , 8, 33	4
1248	A close look at protein function prediction evaluation protocols. 2015 , 4, 41	16
1247	Study of phosphorylation events for cancer diagnoses and treatment. 2015 , 4, 59	4
1246	Identification and functional analysis of the BIM interactome; new clues on its possible involvement in Epstein-Barr Virus-associated diseases. 2015 , 22, 14	
1245	Stereochemical Studies of the Karlotoxin Class Using NMR Spectroscopy and DP4 Chemical-Shift Analysis: Insights into their Mechanism of Action. 2015 , 127, 15931-15936	11
1244	Stereochemical Studies of the Karlotoxin Class Using NMR Spectroscopy and DP4 Chemical-Shift Analysis: Insights into their Mechanism of Action. 2015 , 54, 15705-10	28
1243	SlNCRE-structural interactome computational resource for Mycobacterium tuberculosis. 2015 , 2015, bav060	5
1242	Proteomic identification of mitochondrial carbonylated proteins in two maturation stages of pepper fruits. 2015 , 15, 2634-42	21

1241	Irf6-Related Gene Regulatory Network Involved in Palate and Lip Development. 2015 , 26, 1600-5	7
1240	A time course study about gene expression of post-thermal injury with DNA microarray. 2015 , 54, 757-64	6
1239	Whole Exome Sequencing Identifies Rare Protein-Coding Variants in Behçet's Disease. 2016 , 68, 1272-80	5
1238	HES-Mediated Repression of Pten in <i>Caenorhabditis elegans</i> . 2015 , 5, 2619-28	2
1237	Integrating herb effect similarity for network-based herb target prediction. 2015 ,	
1236	Classification of Enzymes Using Machine Learning Based Approaches: A Review. 2015 , 2, 30-49	7
1235	Prediction and Analysis of Hepatocellular Carcinoma Related Genes Using Gene Ontology and KEGG. 2015 , 10, 31-38	
1234	DDA: A Novel Network-Based Scoring Method to Identify Disease-Disease Associations. 2015 , 9, 175-86	17
1233	Clinical and genetic investigation of a multi-generational Chinese family afflicted with Von Hippel-Lindau disease. 2015 , 128, 32-8	3
1232	Comparative proteomic analyses demonstrate enhanced interferon and STAT-1 activation in reovirus T3D-infected HeLa cells. 2015 , 5, 30	6
1231	Data Mining of Gene Arrays for Biomarkers of Survival in Ovarian Cancer. 2015 , 4, 324-38	3
1230	Mining protein interactomes to improve their reliability and support the advancement of network medicine. 2015 , 6, 296	14
1229	Tetracycline hypersensitivity of an <i>ezaA</i> mutant links GalE and TseB (YpmB) to cell division. 2015 , 6, 346	9
1228	Further insight into molecular mechanism underlying thoracic spinal cord injury using bioinformatics methods. 2015 , 12, 7851-8	6
1227	Integrated annotation and analysis of in situ hybridization images using the ImAnno system: application to the ear and sensory organs of the fetal mouse. 2015 , 10, e0118024	
1226	Effect of Embryo Vitrification on Rabbit Foetal Placenta Proteome during Pregnancy. 2015 , 10, e0125157	6
1225	Synergistic antifungal activity of berberine derivative B-7b and fluconazole. 2015 , 10, e0126393	8
1224	Distinctive Behaviors of Druggable Proteins in Cellular Networks. 2015 , 11, e1004597	30

1223	A Network-Based Target Overlap Score for Characterizing Drug Combinations: High Correlation with Cancer Clinical Trial Results. 2015 , 10, e0129267	9
1222	Novel recA-Independent Horizontal Gene Transfer in Escherichia coli K-12. 2015 , 10, e0130813	8
1221	Network Topologies Decoding Cervical Cancer. 2015 , 10, e0135183	8
1220	Two of Them Do It Better: Novel Serum Biomarkers Improve Autoimmune Hepatitis Diagnosis. 2015 , 10, e0137927	7
1219	DNA Damage Response Checkpoint Activation Drives KP1019 Dependent Pre-Anaphase Cell Cycle Delay in <i>S. cerevisiae</i> . 2015 , 10, e0138085	7
1218	Interferon- γ Modulates the Innate Immune Response against Glioblastoma Initiating Cells. 2015 , 10, e0139603	9
1217	Towards a Hierarchical Strategy to Explore Multi-Scale IP/MS Data for Protein Complexes. 2015 , 10, e0139704	
1216	Global analysis of lysine acetylation in strawberry leaves. 2015 , 6, 739	46
1215	A Role for the Non-Canonical Wnt- β -Catenin and TGF- β Signaling Pathways in the Induction of Tolerance during the Establishment of a <i>Salmonella enterica</i> Serovar Enteritidis Persistent Cecal Infection in Chickens. 2015 , 2, 33	18
1214	Surfing the Protein-Protein Interaction Surface Using Docking Methods: Application to the Design of PPI Inhibitors. 2015 , 20, 11569-603	45
1213	Identification of potential therapeutic targets for melanoma using gene expression analysis. 2015 , 62, 733-9	4
1212	Pan-genome analysis of human gastric pathogen <i>H. pylori</i> : comparative genomics and pathogenomics approaches to identify regions associated with pathogenicity and prediction of potential core therapeutic targets. 2015 , 2015, 139580	35
1211	Protective Effects of Scutellarin on Human Cardiac Microvascular Endothelial Cells against Hypoxia-Reoxygenation Injury and Its Possible Target-Related Proteins. 2015 , 2015, 278014	6
1210	Label-free quantitative mass spectrometry reveals a panel of differentially expressed proteins in colorectal cancer. 2015 , 2015, 365068	14
1209	Implication of Caspase-3 as a Common Therapeutic Target for Multineurodegenerative Disorders and Its Inhibition Using Nonpeptidyl Natural Compounds. 2015 , 2015, 379817	36
1208	Identification of Gene Biomarkers for Distinguishing Small-Cell Lung Cancer from Non-Small-Cell Lung Cancer Using a Network-Based Approach. 2015 , 2015, 685303	11
1207	Temporal Identification of Dysregulated Genes and Pathways in Clear Cell Renal Cell Carcinoma Based on Systematic Tracking of Disrupted Modules. 2015 , 2015, 313740	3
1206	RecRWR: a recursive random walk method for improved identification of diseases. 2015 , 2015, 747156	1

1205	Estimating reachability in dense biological networks. 2015,	3
1204	Interactome analysis and design of inhibitors against selected protein targets of Ser/Thr protein kinase (STPK) signaling pathways in <i>Mycobacterium tuberculosis</i> H37Rv. 2015, 14, 10390-403	4
1203	Association study in Alzheimer's disease of single nucleotide polymorphisms implicated with coffee consumption. 2015, 42, 69-73	3
1202	Identification of Putative Major Space Genes Using Genome-Wide Literature Data. 2015,	3
1201	Characterizing and controlling the inflammatory network during influenza A virus infection. 2014, 4, 3799	45
1200	From raw data to biological discoveries: a computational analysis pipeline for mass spectrometry-based proteomics. 2015, 26, 1820-6	11
1199	cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism. <i>Nucleic Acids Research</i> , 2015, 43, e87	20.1 27
1198	Randomness and preserved patterns in cancer network. 2014, 4, 6368	19
1197	Analysis of gene expression profiles associated with glioma progression. 2015, 12, 1884-90	16
1196	<i>Plasmodium falciparum</i> complicated malaria: Modulation and connectivity between exportome and variant surface antigen gene families. 2015, 201, 31-46	10
1195	Whole-exome SNP array identifies 15 new susceptibility loci for psoriasis. 2015, 6, 6793	95
1194	Bioinformatics Analysis of Potential Candidates for Therapy of TDRD7 Deficiency-Induced Congenital Cataract. 2015, 54, 10-7	4
1193	The Protein Interactome of Mycobacteriophage Giles Predicts Functions for Unknown Proteins. 2015, 197, 2508-16	15
1192	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. 2015, 2015,	36
1191	Integration of gene expression and GWAS results supports involvement of calcium signaling in Schizophrenia. 2015, 164, 92-9	29
1190	Cellular proteome alterations in response to enterovirus 71 and coxsackievirus A16 infections in neuronal and intestinal cell lines. 2015, 125, 121-30	10
1189	The functional interactome of PYHIN immune regulators reveals IFIX is a sensor of viral DNA. 2015, 11, 787	59
1188	Transcriptomic profiles of aging in purified human immune cells. 2015, 16, 333	47

1187	Large-scale analysis of the evolutionary histories of phosphorylation motifs in the human genome. 2015 , 4, 21	5
1186	Transcriptional analysis of host responses to Marek's disease virus infection in chicken thymus. 2015 , 58, 95-105	7
1185	Visualization of module alignment discovery. 2015 ,	
1184	Identification of differential splicing genes in gliomas using exon expression profiling. 2015 , 11, 843-50	15
1183	Proteomic signatures of antiplatelet drugs: new approaches to exploring drug effects. 2015 , 13 Suppl 1, S323-31	17
1182	Proteomic analyses uncover a new function and mode of action for mouse homolog of Diaphanous 2 (mDia2). 2015 , 14, 1064-78	14
1181	PAGER: constructing PAGs and new PAG-PAG relationships for network biology. 2015 , 31, i250-7	14
1180	RPdb: a database of experimentally verified cellular reprogramming records. 2015 , 31, 3237-9	3
1179	MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. <i>Nucleic Acids Research</i> , 2015 , 43, W258-63	20.1 29
1178	Prediction of kinase-substrate relations based on heterogeneous networks. 2015 , 13, 1542003	7
1177	Comparative Genomics and Evolutionary Modularity of Prokaryotes. 2015 , 883, 77-96	1
1176	iTRAQ-based analysis of progerin expression reveals mitochondrial dysfunction, reactive oxygen species accumulation and altered proteostasis. 2015 , 6, 119	18
1175	Actions of Huangqi decoction against rat liver fibrosis: a gene expression profiling analysis. 2015 , 10, 39	20
1174	Is HNF4A a candidate to study zinc finger protein slug?. 2015 , 11, 366-73	
1173	Identification of genes associated with melanoma metastasis. 2015 , 31, 553-61	16
1172	Screening of potential biomarkers for chemoresistant ovarian carcinoma with miRNA expression profiling data by bioinformatics approach. 2015 , 10, 2427-2431	8
1171	Integrating GO and KEGG terms to characterize and predict acute myeloid leukemia-related genes. 2015 , 20, 336-42	13
1170	Application of gap-constraints given sequential frequent pattern mining for protein function prediction. 2015 , 6, 112-20	1

1169	Identification of biomarkers with a tumor stage-dependent expression and exploration of the mechanism involved in laryngeal squamous cell carcinoma. 2015 , 34, 2627-35	9
1168	Potential microRNA biomarkers for acute ischemic stroke. 2015 , 36, 1639-47	30
1167	Computational Modeling of miRNA Biogenesis. 2015 , 85-98	1
1166	Proteomes of host cell membranes modified by intracellular activities of <i>Salmonella enterica</i> . 2015 , 14, 81-92	38
1165	Identification of hepatocellular carcinoma-related genes with a machine learning and network analysis. 2015 , 22, 63-71	37
1164	Nocturnal to diurnal transition in the common ancestor of haplorrhines: evidence from genomic-scan for positively selected genes. 2015 , 42, 33-7	3
1163	Unc-51 like kinase 1 (ULK1) in silico analysis for biomarker identification: a vital component of autophagy. 2015 , 562, 40-9	15
1162	In silico identification of regulatory motifs in co-expressed genes under osmotic stress representing their co-regulation. 2015 , 1, 29-34	3
1161	Interactions of the Antiviral Factor Interferon Gamma-Inducible Protein 16 (IFI16) Mediate Immune Signaling and Herpes Simplex Virus-1 Immunosuppression. 2015 , 14, 2341-56	65
1160	Reachability Analysis in Probabilistic Biological Networks. 2015 , 12, 53-66	3
1159	Predicting of disease genes for gestational diabetes mellitus based on network and functional consistency. 2015 , 186, 91-6	5
1158	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. 2015 , 15, 1390-404	33
1157	Modified ribosome profiling reveals high abundance of ribosome protected mRNA fragments derived from 3' untranslated regions. <i>Nucleic Acids Research</i> , 2015 , 43, 1019-34	20.1 50
1156	Total body exposure to low-dose ionizing radiation induces long-term alterations to the liver proteome of neonatally exposed mice. 2015 , 14, 366-73	31
1155	MicroRNA let-7 modulates the immune response to <i>Mycobacterium tuberculosis</i> infection via control of A20, an inhibitor of the NF- κ B pathway. 2015 , 17, 345-356	170
1154	The proteomic 2D-DIGE approach reveals the protein voltage-dependent anion channel 2 as a potential therapeutic target in epithelial thyroid tumours. 2015 , 404, 37-45	11
1153	How the edaphic <i>Bacillus megaterium</i> strain Mes11 adapts its metabolism to the herbicide mesotrione pressure. 2015 , 199, 198-208	24
1152	Comparative computational analysis of pluripotency in human and mouse stem cells. 2015 , 5, 7927	14

1151	Proteome mining for drug target identification in <i>Listeria monocytogenes</i> strain EGD-e and structure-based virtual screening of a candidate drug target penicillin binding protein 4. 2015 , 111, 9-18		17
1150	Topological, functional, and dynamic properties of the protein interaction networks rewired by benzo(a)pyrene. 2015 , 283, 83-91		10
1149	A Similarity-Based Learning Algorithm Using Distance Transformation. 2015 , 27, 1452-1464		0
1148	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015 , 43, D447-52	20.1	6276
1147	PathPPI: an integrated dataset of human pathways and protein-protein interactions. 2015 , 58, 579-89		7
1146	Unravelling adverse reactions to NSAIDs using systems biology. 2015 , 36, 172-80		22
1145	Novel insights into the evolution and structural characterization of dyskerin using comprehensive bioinformatics analysis. 2015 , 14, 874-87		4
1144	AealRACK1 expression and localization in response to stress in C6/36 HT mosquito cells. 2015 , 119, 45-60		7
1143	Excess copper induced proteomic changes in the marine brown algae <i>Sargassum fusiforme</i> . 2015 , 111, 271-80		37
1142	Genome-wide identification, classification and functional analyses of the bHLH transcription factor family in the pig, <i>Sus scrofa</i> . 2015 , 290, 1415-33		3
1141	Mis-sense mutations in Tafazzin (TAZ) that escort to mild clinical symptoms of Barth syndrome is owed to the minimal inhibitory effect of the mutations on the enzyme function: In-silico evidence. 2015 , 7, 21-35		3
1140	A Pilot Proteomic Analysis of Salivary Biomarkers in Autism Spectrum Disorder. 2015 , 8, 338-50		57
1139	Transcriptome analysis of individual stromal cell populations identifies stroma-tumor crosstalk in mouse lung cancer model. 2015 , 10, 1187-201		73
1138	Revealing the Strong Functional Association of adipor2 and cdh13 with adipog: A Gene Network Study. 2015 , 71, 1445-56		5
1137	Galahad: a web server for drug effect analysis from gene expression. <i>Nucleic Acids Research</i> , 2015 , 43, W208-12	20.1	7
1136	Unreported intrinsic disorder in proteins: Disorder emergency room. 2015 , 3, e1010999		3
1135	Dynamic Proteomics: In Vivo Proteome-Wide Measurement of Protein Kinetics Using Metabolic Labeling. 2015 , 561, 219-76		34
1134	Towards New Drug Targets? Function Prediction of Putative Proteins of <i>Neisseria meningitidis</i> MC58 and Their Virulence Characterization. 2015 , 19, 416-34		17

1133	Agriproteomics of Bread Wheat: Comparative Proteomics and Network Analyses of Grain Size Variation. 2015 , 19, 372-82	1
1132	Detection of selection signatures in Piemontese and Marchigiana cattle, two breeds with similar production aptitudes but different selection histories. 2015 , 47, 52	24
1131	Human consensus interferons: Bridging the natural and artificial cytokines with intrinsic disorder. 2015 , 26, 637-45	4
1130	Genome-wide expression analyses of the stationary phase model of ageing in yeast. 2015 , 149, 65-74	6
1129	Analysis of dermal papilla cell interactome using STRING database to profile the ex vivo hair growth inhibition effect of a vinca alkaloid drug, colchicine. 2015 , 16, 3579-98	18
1128	A global network-based protocol for functional inference of hypothetical proteins in <i>Synechocystis</i> sp. PCC 6803. 2015 , 116, 44-52	5
1127	Comparative analysis of the role of CD4+ and CD8+ T cells in severe asthma development. 2015 , 49, 427-434	
1126	The prognostic landscape of genes and infiltrating immune cells across human cancers. 2015 , 21, 938-945	1541
1125	OMICS for Tumor Biomarker Research. 2015 , 3-30	1
1124	Tumor Cell Adhesion As a Risk Factor for Sentinel Lymph Node Metastasis in Primary Cutaneous Melanoma. 2015 , 33, 2509-15	45
1123	<i>Arabidopsis thaliana</i> : A Model for Plant Research. 2015 , 1-26	4
1122	DNA Methylation in Basal Metazoans: Insights from Ctenophores. 2015 , 55, 1096-110	30
1121	Dynamic Proteome Response of <i>Pseudomonas aeruginosa</i> to Tobramycin Antibiotic Treatment. 2015 , 14, 2126-37	29
1120	Identification and characterization of cellular proteins interacting with Hepatitis E virus untranslated regions. 2015 , 208, 98-109	14
1119	Identifying genes related with rheumatoid arthritis via system biology analysis. 2015 , 571, 97-106	7
1118	Transcriptome analysis of acetic-acid-treated yeast cells identifies a large set of genes whose overexpression or deletion enhances acetic acid tolerance. 2015 , 99, 6391-403	25
1117	Improving 3D Genome Reconstructions Using Orthologous and Functional Constraints. 2015 , 11, e1004298	9
1116	Recent coselection in human populations revealed by protein-protein interaction network. 2014 , 7, 136-53	11

1115	Evolutionary signatures amongst disease genes permit novel methods for gene prioritization and construction of informative gene-based networks. 2015 , 11, e1004967	16
1114	Multiscale characterization of ageing and cancer progression by a novel network entropy measure. 2015 , 11, 1824-31	14
1113	ZnO nanoparticles impose a panmetabolic toxic effect along with strong necrosis, inducing activation of the envelope stress response in Salmonella enterica serovar Enteritidis. 2015 , 59, 3317-28	39
1112	Structure-based function analysis of putative conserved proteins with isomerase activity from Haemophilus influenzae. 2015 , 5, 741-763	11
1111	cisPath: an R/Bioconductor package for cloud users for visualization and management of functional protein interaction networks. 2015 , 9 Suppl 1, S1	8
1110	A novel locus for mycelial aggregation forms a gateway to improved Streptomyces cell factories. 2015 , 14, 44	32
1109	Deeper insight into chronic kidney disease-related atherosclerosis: comparative proteomic studies of blood plasma using 2DE and mass spectrometry. 2015 , 13, 20	20
1108	An integrative approach for a network based meta-analysis of viral RNAi screens. 2015 , 10, 6	6
1107	Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). 2015 , 7, 3	48
1106	Identification of pivotal markers in vascular dementia based on proteomics data. 2015 , 39, 312-20	4
1105	Biological noise and H2A.Z: a promising connection for language. 2014 , 5, 463	2
1104	Systems biology approach reveals possible evolutionarily conserved moonlighting functions for enolase. 2015 , 58, 1-8	12
1103	Integrative analysis of kinase networks in TRAIL-induced apoptosis provides a source of potential targets for combination therapy. 2015 , 8, rs3	26
1102	Genome-wide identification of SSR and SNP markers from the non-heading Chinese cabbage for comparative genomic analyses. 2015 , 16, 328	33
1101	Latent Pathways Identification by Microarray Expression Profiles in Thyroid-Associated Ophthalmopathy Patients. 2015 , 26, 200-10	6
1100	Validation of a novel shotgun proteomic workflow for the discovery of protein-protein interactions: focus on ZNF521. 2015 , 14, 1888-99	15
1099	Acetylation site specificities of lysine deacetylase inhibitors in human cells. 2015 , 33, 415-23	186
1098	MicroRNA Levels as Prognostic Markers for the Differentiation Potential of Human Mesenchymal Stromal Cell Donors. 2015 , 24, 1946-55	5

1097	Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdRNAs and a piRNA in pancreatic cancer. 2015 , 14, 94	171
1096	Modelling the yeast interactome. 2014 , 4, 4273	10
1095	Identification of potential therapeutic target genes, key miRNAs and mechanisms in acute myeloid leukemia based on bioinformatics analysis. 2015 , 32, 152	8
1094	Proteomics profiling of ethylene-induced tomato flower pedicel abscission. 2015 , 121, 67-87	24
1093	Network-based proteomic approaches reveal the neurodegenerative, neuroprotective and pain-related mechanisms involved after retrograde axonal damage. 2015 , 5, 9185	23
1092	Identification of putative vaccine candidates against <i>Helicobacter pylori</i> exploiting exoproteome and secretome: a reverse vaccinology based approach. 2015 , 32, 280-91	121
1091	Disease gene prioritization using network and feature. 2015 , 22, 313-23	10
1090	KPC1-mediated ubiquitination and proteasomal processing of NF- κ B1 p105 to p50 restricts tumor growth. 2015 , 161, 333-47	66
1089	P-Finder: Reconstruction of Signaling Networks from Protein-Protein Interactions and GO Annotations. 2015 , 12, 309-21	4
1088	In silico approaches for the identification of virulence candidates amongst hypothetical proteins of <i>Mycoplasma pneumoniae</i> 309. 2015 , 59 Pt A, 67-80	22
1087	A mutation profile for top-k patient search exploiting Gene-Ontology and orthogonal non-negative matrix factorization. 2015 , 31, 3653-9	6
1086	Reveal genes functionally associated with ACADS by a network study. 2015 , 569, 294-302	5
1085	The outer mucus layer hosts a distinct intestinal microbial niche. 2015 , 6, 8292	273
1084	NeuCode Labeling in Nematodes: Proteomic and Phosphoproteomic Impact of Ascaroside Treatment in <i>Caenorhabditis elegans</i> . 2015 , 14, 2922-35	17
1083	AtRAV1 and AtRAV2 overexpression in cotton increases fiber length differentially under drought stress and delays flowering. 2015 , 241, 78-95	22
1082	Tumor characterization and stratification by integrated molecular profiles reveals essential pan-cancer features. 2015 , 16, 503	26
1081	KnowEnG: a knowledge engine for genomics. 2015 , 22, 1115-9	12
1080	Integrated web visualizations for protein-protein interaction databases. 2015 , 16, 195	41

1079	SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. 2015 , 12, 998-1009	12
1078	Expression quantitative trait locus analysis for translational medicine. 2015 , 7, 60	49
1077	Characterization of the hypothalamic transcriptome in response to food deprivation reveals global changes in long noncoding RNA, and cell cycle response genes. 2015 , 10, 48	14
1076	Quantitative proteomic analysis of formalin-fixed, paraffin-embedded clear cell renal cell carcinoma tissue using stable isotopic dimethylation of primary amines. 2015 , 16, 559	17
1075	MicroRNA-148a regulates LDL receptor and ABCA1 expression to control circulating lipoprotein levels. 2015 , 21, 1280-9	149
1074	Proteomic changes of the porcine small intestine in response to chronic heat stress. 2015 , 55, 277-93	21
1073	Identifying and characterising key alternative splicing events in Drosophila development. 2015 , 16, 608	9
1072	Integrative proteome analysis of Brachypodium distachyon roots and leaves reveals a synergetic responsive network under H2O2 stress. 2015 , 128, 388-402	22
1071	Bioinformatics analysis of transcription profiling of sepsis. 2015 , 13, 82-90	
1070	Network analysis of S. aureus response to ramoplanin reveals modules for virulence factors and resistance mechanisms and characteristic novel genes. 2015 , 574, 149-62	15
1069	YPED: an integrated bioinformatics suite and database for mass spectrometry-based proteomics research. 2015 , 13, 25-35	13
1068	Identifying new targets in leukemogenesis using computational approaches. 2015 , 22, 610-22	6
1067	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. 2015 , 12, 1519-30	44
1066	Applications of comparative evolution to human disease genetics. 2015 , 35, 16-24	6
1065	Intrinsically disordered proteins in the nucleus of human cells. 2015 , 1, 33-51	37
1064	Empowering biologists with multi-omics data: colorectal cancer as a paradigm. 2015 , 31, 1436-43	19
1063	Identification of recurrent regulated alternative splicing events across human solid tumors. <i>Nucleic Acids Research</i> , 2015 , 43, 5130-44	20.1 100
1062	Molecular Consequences of Proprotein Convertase 1/3 (PC1/3) Inhibition in Macrophages for Application to Cancer Immunotherapy: A Proteomic Study. 2015 , 14, 2857-77	18

1061	Effects of Phosphorylation of β Subunits of Phycocyanins on State Transition in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. 2015 , 56, 1997-2013	27
1060	The miR-199-dynamin regulatory axis controls receptor-mediated endocytosis. 2015 , 128, 3197-209	34
1059	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. 2015 , 112, 15084-9	82
1058	Loss of Dfg5 glycosylphosphatidylinositol-anchored membrane protein confers enhanced heat tolerance in <i>Saccharomyces cerevisiae</i> . 2015 , 17, 2721-34	10
1057	PhosphoPICK: modelling cellular context to map kinase-substrate phosphorylation events. 2015 , 31, 382-9	26
1056	Single-cell and multivariate approaches in genetic perturbation screens. 2015 , 16, 18-32	65
1055	Novel protein-protein interaction between spermidine synthase and S-adenosylmethionine decarboxylase from <i>Leishmania donovani</i> . 2015 , 456, 637-42	9
1054	Insights into the poliovirus-plant interactome revealed by coimmunoprecipitation and mass spectrometry. 2015 , 28, 467-81	32
1053	Graph similarity search on large uncertain graph databases. 2015 , 24, 271-296	22
1052	Quantitative proteomics of kinase inhibitor targets and mechanisms. 2015 , 10, 201-12	23
1051	MicroRNA expression profiling and bioinformatics analysis of dysregulated microRNAs in vinorelbine-resistant breast cancer cells. 2015 , 556, 113-8	13
1050	Integrating proteomics profiling data sets: a network perspective. 2015 , 1243, 237-53	4
1049	Proteome of the insulin-secreting Min6 cell porosome complex: involvement of Hsp90 in its assembly and function. 2015 , 114, 83-92	8
1048	Proteomic adaptations to starvation prepare <i>Escherichia coli</i> for disinfection tolerance. 2015 , 69, 110-119	22
1047	Exploring the Genomic Roadmap and Molecular Phylogenetics Associated with MODY Cascades Using Computational Biology. 2015 , 71, 1491-502	2
1046	Searching for repetitions in biological networks: methods, resources and tools. 2015 , 16, 118-36	21
1045	Amyloid-beta-activated human microglial cells through ER-resident proteins. 2015 , 14, 214-23	13
1044	Bioinformatic Analysis of GJB2 Gene Missense Mutations. 2015 , 71, 1623-42	14

1043	The discovery of integrated gene networks for autism and related disorders. 2015 , 25, 142-54	180
1042	Disease-targeted sequencing of ion channel genes identifies de novo mutations in patients with non-familial Brugada syndrome. 2014 , 4, 6733	40
1041	Label-free quantitative proteomic analysis reveals potential biomarkers and pathways in renal cell carcinoma. 2015 , 36, 939-51	33
1040	Gene and Protein Network Analysis of AmpC β -Lactamase. 2015 , 71, 1553-67	16
1039	Ecological roles of dominant and rare prokaryotes in acid mine drainage revealed by metagenomics and metatranscriptomics. 2015 , 9, 1280-94	131
1038	Gene expression analyses to explore the biomarkers and therapeutic targets for gliomas. 2015 , 36, 403-9	5
1037	Microbial communities evolve faster in extreme environments. 2014 , 4, 6205	76
1036	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. 2015 , 24, 397-409	43
1035	Making proteomics data accessible and reusable: current state of proteomics databases and repositories. 2015 , 15, 930-49	138
1034	Identifying hepatocellular carcinoma-related genes and pathways by system biology analysis. 2015 , 184, 357-64	7
1033	Structure-based functional annotation of putative conserved proteins having lyase activity from Haemophilus influenzae. 2015 , 5, 317-336	11
1032	fabp4 is central to eight obesity associated genes: a functional gene network-based polymorphic study. 2015 , 364, 344-54	24
1031	Predicting Diagnostic Gene Biomarkers for Non-Small-Cell Lung Cancer. 2016 , 2016, 3952494	4
1030	Drosophila Torsin Protein Regulates Motor Control and Stress Sensitivity and Forms a Complex with Fragile-X Mental Retardation Protein. 2016 , 2016, 6762086	2
1029	Identifying candidate agents for lung adenocarcinoma by walking the human interactome. 2016 , 9, 5439-5450	3
1028	Chicken-Specific Kinome Array Reveals that Salmonella enterica Serovar Enteritidis Modulates Host Immune Signaling Pathways in the Cecum to Establish a Persistence Infection. 2016 , 17,	30
1027	RNA Sequencing and Transcriptome Analyses for Cercis Gigantea. 2016 , 11, 32-39	
1026	An Empirical Study of Features Fusion Techniques for Protein-Protein Interaction Prediction. 2016 , 11, 4-12	44

1025	Prediction and Analysis of the Protein-Protein Interaction Networks for Chickens, Cattle, Dogs, Horses and Rabbits. 2016 , 11, 131-142	3
1024	Feature Classification and Analysis of Lung Cancer Related Genes through Gene Ontology and KEGG Pathways. 2016 , 11, 40-50	8
1023	Early Transcriptional Changes Induced by Wnt/-Catenin Signaling in Hippocampal Neurons. 2016 , 2016, 4672841	16
1022	Biomolecular Network-Based Synergistic Drug Combination Discovery. 2016 , 2016, 8518945	18
1021	Leaf Proteome Analysis Reveals Prospective Drought and Heat Stress Response Mechanisms in Soybean. 2016 , 2016, 6021047	80
1020	Impacts of Nonsynonymous Single Nucleotide Polymorphisms of Adiponectin Receptor 1 Gene on Corresponding Protein Stability: A Computational Approach. 2016 , 2016, 9142190	12
1019	Role of miRNAs in Epicardial Adipose Tissue in CAD Patients with T2DM. 2016 , 2016, 1629236	11
1018	A Systems Biology Approach to Reveal Putative Host-Derived Biomarkers of Periodontitis by Network Topology Characterization of MMP-REDOX/NO and Apoptosis Integrated Pathways. 2015 , 5, 102	13
1017	Systems Medicine as an Emerging Tool for Cardiovascular Genetics. 2016 , 3, 27	7
1016	Immunosenescence-Related Transcriptomic and Immunologic Changes in Older Individuals Following Influenza Vaccination. 2016 , 7, 450	25
1015	Dissection of the cis-2-decenoic acid signaling network in Pseudomonas aeruginosa using microarray technique. 2015 , 6, 383	17
1014	In silico Analysis Revealed High-risk Single Nucleotide Polymorphisms in Human Pentraxin-3 Gene and their Impact on Innate Immune Response against Microbial Pathogens. 2016 , 7, 192	14
1013	Finding Potential Therapeutic Targets against through Proteome Exploration. 2016 , 7, 1817	12
1012	Compartmentalization and Functionality of Nuclear Disorder: Intrinsic Disorder and Protein-Protein Interactions in Intra-Nuclear Compartments. 2015 , 17,	78
1011	Chronic Heat Stress Induces Immune Response, Oxidative Stress Response, and Apoptosis of Finishing Pig Liver: A Proteomic Approach. 2016 , 17,	57
1010	p53 Proteoforms and Intrinsic Disorder: An Illustration of the Protein Structure-Function Continuum Concept. 2016 , 17,	102
1009	Prediction of Protein-Protein Interactions by Evidence Combining Methods. 2016 , 17,	22
1008	Analysis of Potential Amino Acid Biomarkers in Brain Tissue and the Effect of Galangin on Cerebral Ischemia. 2016 , 21, 438	9

1007	A Novel Drug-Mouse Phenotypic Similarity Method Detects Molecular Determinants of Drug Effects. 2016 , 12, e1005111	5
1006	Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. 2016 , 12, e1005816	17
1005	Quantitative Phosphoproteomics Analysis of ERBB3/ERBB4 Signaling. 2016 , 11, e0146100	7
1004	Computational Characterization of Osteoporosis Associated SNPs and Genes Identified by Genome-Wide Association Studies. 2016 , 11, e0150070	24
1003	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. 2016 , 11, e0152034	33
1002	Prothymosin- α Variants Elicit Anti-HIV-1 Response via TLR4 Dependent and Independent Pathways. 2016 , 11, e0156486	7
1001	Proteomic Analysis of the Excretory and Secretory Proteins of <i>Haemonchus contortus</i> (HcESP) Binding to Goat PBMCs In Vivo Revealed Stage-Specific Binding Profiles. 2016 , 11, e0159796	52
1000	B Cell Receptor Activation Predominantly Regulates AKT-mTORC1/2 Substrates Functionally Related to RNA Processing. 2016 , 11, e0160255	2
999	Role of Hepatic-Specific Transcription Factors and Polycomb Repressive Complex 2 during Induction of Fibroblasts to Hepatic Fate. 2016 , 11, e0167081	3
998	Prediction of Possible Biomarkers and Novel Pathways Conferring Risk to Post-Traumatic Stress Disorder. 2016 , 11, e0168404	6
997	Coupling of Physiological and Proteomic Analysis to Understand the Ethylene- and Chilling-Induced Kiwifruit Ripening Syndrome. 2016 , 7, 120	37
996	Proteomic Responses of Switchgrass and Prairie Cordgrass to Senescence. 2016 , 7, 293	5
995	Genome-Wide Investigation of Hsf Genes in Sesame Reveals Their Segmental Duplication Expansion and Their Active Role in Drought Stress Response. 2016 , 7, 1522	50
994	Comparative Analysis of DNA Methyltransferase Gene Family in Fungi: A Focus on Basidiomycota. 2016 , 7, 1556	10
993	High-Throughput Sequencing Reveals HO Stress-Associated MicroRNAs and a Potential Regulatory Network in Seedlings. 2016 , 7, 1567	13
992	Comparative Physiological and Proteomic Analysis Reveal Distinct Regulation of Peach Skin Quality Traits by Altitude. 2016 , 7, 1689	34
991	Global Lysine Acetylome Analysis of Desiccated Somatic Embryos of. 2016 , 7, 1927	9
990	Prediction of genetic risk factors of atherosclerosis using various bioinformatic tools. 2016 , 15,	6

989	Identification of altered pathways in hypertrophic cardiomyopathy based on combined data of protein-protein interactions and molecular pathways. 2016 , 15,	2
988	Autophagy-related intrinsically disordered proteins in intra-nuclear compartments. 2016 , 12, 2798-817	24
987	Comparative transcriptome analysis of <i>Triticum aestivum</i> in response to nitrogen stress. 2016 , 63, 365-374	3
986	Biological function derived from predicted structures in CASP11. 2016 , 84 Suppl 1, 370-91	9
985	Plasma proteomics for the assessment of acute renal transplant rejection. 2016 , 158, 111-20	8
984	Transcriptional control of quorum sensing and associated metabolic interactions in <i>Pseudomonas syringae</i> strain B728a. 2016 , 99, 1080-98	5
983	SPATA2 links CYLD to the TNF- α receptor signaling complex and modulates the receptor signaling outcomes. 2016 , 35, 1868-84	98
982	Evaluating the effectiveness of a practical inquiry-based learning bioinformatics module on undergraduate student engagement and applied skills. 2016 , 44, 304-13	11
981	Gene Network Analysis of Metallo Beta Lactamase Family Proteins Indicates the Role of Gene Partners in Antibiotic Resistance and Reveals Important Drug Targets. 2016 , 117, 1330-9	19
980	Signaling and Gene Regulatory Networks Governing Definitive Endoderm Derivation From Pluripotent Stem Cells. 2016 , 231, 1994-2006	5
979	Ultrastructure of the liver microcirculation influences hepatic and systemic insulin activity and provides a mechanism for age-related insulin resistance. 2016 , 15, 706-15	42
978	DrugTargetInspector: An assistance tool for patient treatment stratification. 2016 , 138, 1765-76	8
977	Bioinformatics Analysis of microRNA Time-Course Expression in Brown Rat (<i>Rattus norvegicus</i>): Spinal Cord Injury Self-Repair. 2016 , 41, 97-103	10
976	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. 2016 , 7, 11607	36
975	Preimplantation factor is an anti-apoptotic effector in human trophoblasts involving p53 signaling pathway. 2016 , 7, e2504	19
974	ProtLID, a Residue-Based Pharmacophore Approach to Identify Cognate Protein Ligands in the Immunoglobulin Superfamily. 2016 , 24, 2217-2226	8
973	Modelling microbial metabolic rewiring during growth in a complex medium. 2016 , 17, 970	10
972	Intrinsic disorder in spondins and some of their interacting partners. 2016 , 4, e1255295	7

971	Systematic analysis of the lysine acetylome in <i>Fusarium graminearum</i> . 2016 , 17, 1019	31
970	A map of mobile DNA insertions in the NCI-60 human cancer cell panel. 2016 , 7, 20	3
969	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. 2016 , 17, 158	10
968	Understanding the roles of intrinsic disorder in subunits of hemoglobin and the disease process of sickle cell anemia. 2016 , 4, e1248273	4
967	Identification of candidate target genes of pituitary adenomas based on the DNA microarray. 2016 , 13, 2182-6	7
966	Surface energetics and protein-protein interactions: analysis and mechanistic implications. 2016 , 6, 24035	10
965	In Silico identification of SNP diversity in cultivated and wild tomato species: insight from molecular simulations. 2016 , 6, 38715	14
964	PhosD: inferring kinase-substrate interactions based on protein domains. 2017 , 33, 1197-1204	8
963	Dissecting the expression relationships between RNA-binding proteins and their cognate targets in eukaryotic post-transcriptional regulatory networks. 2016 , 6, 25711	10
962	Widespread occurrence of lysine methylation in <i>Plasmodium falciparum</i> proteins at asexual blood stages. 2016 , 6, 35432	14
961	Viral DNA Sensors IFI16 and Cyclic GMP-AMP Synthase Possess Distinct Functions in Regulating Viral Gene Expression, Immune Defenses, and Apoptotic Responses during Herpesvirus Infection. 2016 , 7,	105
960	The effects for PM2.5 exposure on non-small-cell lung cancer induced motility and proliferation. 2016 , 5, 2059	26
959	Modern Proteomics Sample Preparation, Analysis and Practical Applications. 2016 ,	10
958	Bioinformatics Tools for Proteomics Data Interpretation. 2016 , 919, 281-341	16
957	Gene markers of fracture healing in early stage and the regulatory mechanism during the process using microarray analysis. 2016 , 50, 681-685	3
956	Pangenome and immuno-proteomics analysis of <i>Acinetobacter baumannii</i> strains revealed the core peptide vaccine targets. 2016 , 17, 732	65
955	Establishment of MAGEC2-knockout cells and functional investigation of MAGEC2 in tumor cells. 2016 , 107, 1888-1897	11
954	Counting independent motifs in probabilistic networks. 2016 ,	2

953	PKC δ and HMGB1 antagonistically control hydrogen peroxide-induced poly-ADP-ribose formation. <i>Nucleic Acids Research</i> , 2016 , 44, 7630-45	20.1	12
952	Bioinformatics Based Approaches to Study Virus-Host Interactions During Chikungunya Virus Infection. 2016 , 1426, 195-200		
951	Chikungunya Virus. 2016 ,		2
950	Comprehensive quantification of N-glycoproteome in <i>Fusarium graminearum</i> reveals intensive glycosylation changes against fungicide. 2016 , 142, 82-90		11
949	Genetic and neuroendocrine regulation of the postpartum brain. 2016 , 42, 1-17		27
948	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. 2016 , 17 Suppl 1, 3		32
947	Bioinformatics identification of the methylerythritol phosphate pathway associated genes in <i>Arabidopsis thaliana</i> with <i>ceh1</i> mutant. 2016 , 63, 293-299		1
946	Gene expression profile analysis of pancreatic cancer based on microarray data. 2016 , 13, 3913-9		13
945	Condensin I and II behaviour in interphase nuclei and cells undergoing premature chromosome condensation. 2016 , 24, 243-69		20
944	The Bioinformatics Report of Mutation Outcome on NADPH Flavin Oxidoreductase Protein Sequence in Clinical Isolates of <i>H. pylori</i> . 2016 , 72, 596-605		1
943	Troponins, intrinsic disorder, and cardiomyopathy. 2016 , 397, 731-51		15
942	Small molecules, big targets: drug discovery faces the protein-protein interaction challenge. 2016 , 15, 533-50		555
941	Identification of potential therapeutic target genes and mechanisms in head and neck squamous cell carcinoma by bioinformatics analysis. 2016 , 11, 3009-3014		16
940	Unraveling molecular effects of ADAR1 overexpression in HEK293T cells by label-free quantitative proteomics. 2016 , 15, 1591-601		5
939	Claudin-7 indirectly regulates the integrin/FAK signaling pathway in human colon cancer tissue. 2016 , 61, 711-20		19
938	Coexpression of <i>Escherichia coli</i> <i>obgE</i> , Encoding the Evolutionarily Conserved Obg GTPase, with Ribosomal Proteins L21 and L27. 2016 , 198, 1857-1867		4
937	Proteomic and phosphoproteomic analysis reveals the response and defense mechanism in leaves of diploid wheat <i>T. monococcum</i> under salt stress and recovery. 2016 , 143, 93-105		51
936	Digestion of cooked meat proteins is slightly affected by age as assessed using the dynamic gastrointestinal TIM model and mass spectrometry. 2016 , 7, 2682-91		41

935	APPAGATO: an APproximate PARallel and stochastic GrAph querying TOol for biological networks. 2016 , 32, 2159-66	8
934	Identification of potential therapeutic targets for papillary thyroid carcinoma by bioinformatics analysis. 2016 , 11, 51-58	12
933	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. 2016 , 127, e12-23	35
932	Uterine flushing proteome of the tammar wallaby after reactivation from diapause. 2016 , 152, 491-505	10
931	Simultaneous discovery of cancer subtypes and subtype features by molecular data integration. 2016 , 32, i445-i454	21
930	Construction of protein interaction network involved in lung adenocarcinomas using a novel algorithm. 2016 , 12, 1792-1800	1
929	Integrative transcriptomic analysis of NAFLD animal model reveals dysregulated genes and pathways in metabolism. 2016 , 595, 99-108	8
928	The epichaperome is an integrated chaperome network that facilitates tumour survival. 2016 , 538, 397-401	148
927	An integrated approach to infer dynamic protein-gene interactions - A case study of the human P53 protein. 2016 , 110, 3-13	7
926	Yerba mate (<i>Ilex paraguariensis</i>) inhibits lymphocyte activation in vitro. 2016 , 7, 4556-4563	8
925	IDENTIFICATION OF NOVEL GENES RELATED TO DIABETIC RETINOPATHY USING PROTEIN-PROTEIN INTERACTION NETWORK AND GENE ONTOLOGIES. 2016 , 24, 117-127	5
924	Discovery of functional module alignment. 2016 , 206, 19-27	1
923	Finding lost genes in GWAS via integrative-omics analysis reveals novel sub-networks associated with preterm birth. 2016 , 25, 5254-5264	11
922	Caspase-related apoptosis genes in gliomas by RNA-seq and bioinformatics analysis. 2016 , 33, 259-263	2
921	Transcription Factors Involved in Plant Drought Tolerance Regulation. 2016 , 315-358	1
920	ModuleAlign: module-based global alignment of protein-protein interaction networks. 2016 , 32, i658-i664	27
919	Gene signatures associated with adaptive humoral immunity following seasonal influenza A/H1N1 vaccination. 2016 , 17, 371-379	16
918	HER2 expression identifies dynamic functional states within circulating breast cancer cells. 2016 , 537, 102-106	237

917	Systems Analysis of the Complement-Induced Priming Phase of Liver Regeneration. 2016 , 197, 2500-8	17
916	Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. 2016 , 6, 26362	5
915	HC StratoMiner: A Web-Based Tool for the Rapid Analysis of High-Content Datasets. 2016 , 14, 439-452	8
914	Nickel impact on human health: An intrinsic disorder perspective. 2016 , 1864, 1714-1731	98
913	A network-driven approach for genome-wide association mapping. 2016 , 32, i164-i173	6
912	Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. 2016 , 65, 3776-3785	30
911	An integrative approach predicted co-expression sub-networks regulating properties of stem cells and differentiation. 2016 , 64, 250-262	6
910	Joint Alignment of Multiple Protein-Protein Interaction Networks via Convex Optimization. 2016 , 23, 903-911	12
909	Heterodimer Autorepression Loop: A Robust and Flexible Pulse-Generating Genetic Module. 2016 , 117, 018102	0
908	Protein-protein interactions: detection, reliability assessment and applications. 2017 , 18, 798-819	43
907	Identification of potential therapeutic targets for lung cancer by bioinformatics analysis. 2016 , 13, 1975-82	12
906	Identification of molecular pathway changes after spinal cord injury by microarray analysis. 2016 , 11, 101	14
905	Menopause-induced uterine epithelium atrophy results from arachidonic acid/prostaglandin E2 axis inhibition-mediated autophagic cell death. 2016 , 6, 31408	16
904	THBS2 is a Potential Prognostic Biomarker in Colorectal Cancer. 2016 , 6, 33366	46
903	Proteomic and phosphoproteomic analysis of renal cortex in a salt-load rat model of advanced kidney damage. 2016 , 6, 35906	3
902	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. 2016 , 9, rs9	163
901	Analysis of the molecular mechanism of osteosarcoma using a bioinformatics approach. 2016 , 12, 3075-3080	11
900	LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. 2016 , 6, 18871	29

899	Genome-wide analysis of long intergenic non-coding RNAs in chickpea and their potential role in flower development. 2016 , 6, 33297	53
898	Differential pathway network analysis used to identify key pathways associated with pediatric pneumonia. 2016 , 101, 50-55	2
897	Human islets contain four distinct subtypes of β cells. 2016 , 7, 11756	211
896	SYVN1, NEDD8, and FBXO2 Proteins Regulate β 508 Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Ubiquitin-mediated Proteasomal Degradation. 2016 , 291, 25489-25504	23
895	Omics for prediction of environmental health effects: Blood leukocyte-based cross-omic profiling reliably predicts diseases associated with tobacco smoking. 2016 , 6, 20544	33
894	Identification potential biomarkers in pulmonary tuberculosis and latent infection based on bioinformatics analysis. 2016 , 16, 500	7
893	Quantitative Proteomics Illuminates a Functional Interaction between mDia2 and the Proteasome. 2016 , 15, 4624-4637	8
892	Crosstalk between miRNAs and their regulated genes network in stroke. 2016 , 6, 20429	8
891	RNA-seq analysis of the hypothalamic transcriptome reveals the networks regulating physiopathological progress in the diabetic GK rat. 2016 , 6, 34138	10
890	A critical role for the <i>Drosophila</i> dopamine D1-like receptor Dop1R2 at the onset of metamorphosis. 2016 , 16, 15	13
889	MicroRNA-378 promotes myogenic differentiation by targeting BMP4. 2016 , 13, 2194-200	9
888	CLIP-GENE: a web service of the condition specific context-laid integrative analysis for gene prioritization in mouse TF knockout experiments. 2016 , 11, 57	1
887	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. 2016 ,	4
886	A Hitchhiker's Guide to Metatranscriptomics. 2016 , 313-342	4
885	Intrinsic disorder in biomarkers of insulin resistance, hypoadiponectinemia, and endothelial dysfunction among the type 2 diabetic patients. 2016 , 4, e1171278	5
884	Tcof1-Related Molecular Networks in Treacher Collins Syndrome. 2016 , 27, 1420-6	9
883	Genetic heterogeneity in autism: From single gene to a pathway perspective. 2016 , 68, 442-453	30
882	Identification of key genes in glioblastoma-associated stromal cells using bioinformatics analysis. 2016 , 11, 3999-4007	8

881	Transcriptional signatures of influenza A/H1N1-specific IgG memory-like B cell response in older individuals. 2016 , 34, 3993-4002	25
880	Response and Defense Mechanisms of <i>Taxus chinensis</i> Leaves Under UV-A Radiation are Revealed Using Comparative Proteomics and Metabolomics Analyses. 2016 , 57, 1839-53	19
879	Interleukin-11: A Multifunctional Cytokine with Intrinsically Disordered Regions. 2016 , 74, 285-96	12
878	Increased intramuscular fat induced by reduced dietary protein in finishing pigs: effects on the longissimus lumborum muscle proteome. 2016 , 12, 2447-57	15
877	In silico analysis of deleterious single nucleotide polymorphisms in human BUB1 mitotic checkpoint serine/threonine kinase B gene. 2016 , 9, 142-50	9
876	An atlas of gene expression and gene co-regulation in the human retina. <i>Nucleic Acids Research</i> , 2016 , 44, 5773-84	20.1 44
875	PRELP (proline/arginine-rich end leucine-rich repeat protein) promotes osteoblastic differentiation of preosteoblastic MC3T3-E1 cells by regulating the Eatenin pathway. 2016 , 470, 558-562	11
874	Parkinson's disease and lactoferrin: Analysis of dependent protein networks. 2016 , 4, 177-183	7
873	NACE: A web-based tool for prediction of intercompartmental efficiency of human molecular genetic networks. 2016 , 218, 79-85	4
872	A Thermodynamic-Based Interpretation of Protein Expression Heterogeneity in Different Glioblastoma Multiforme Tumors Identifies Tumor-Specific Unbalanced Processes. 2016 , 120, 5990-7	8
871	Evolutionary patterns of Toll-like receptor signaling pathway genes in the Suidae. 2016 , 16, 33	4
870	Heterogeneity of transcription factor binding specificity models within and across cell lines. 2016 , 26, 1110-23	4
869	Physical activity delays hippocampal neurodegeneration and rescues memory deficits in an Alzheimer disease mouse model. 2016 , 6, e800	48
868	Analyzing ERK 1/2 signalling and targets. 2016 , 12, 2436-46	16
867	Identification of novel proliferative diabetic retinopathy related genes on protein-protein interaction network. 2016 , 217, 63-72	26
866	Proteomic Identification of Putative MicroRNA394 Target Genes in <i>Arabidopsis thaliana</i> Identifies Major Latex Protein Family Members Critical for Normal Development. 2016 , 15, 2033-47	26
865	The effect of forced exercise on knee joints in Dio2(-/-) mice: type II iodothyronine deiodinase-deficient mice are less prone to develop OA-like cartilage damage upon excessive mechanical stress. 2016 , 75, 571-7	19
864	Gene expression and protein-protein interaction data for identification of colon cancer related genes using f-information measures. 2016 , 15, 449-463	8

863	Exosomes Secreted by Apoptosis-Resistant Acute Myeloid Leukemia (AML) Blasts Harbor Regulatory Network Proteins Potentially Involved in Antagonism of Apoptosis. 2016 , 15, 1281-98	63
862	Protein kinase A signalling in <i>Schistosoma mansoni</i> cercariae and schistosomules. 2016 , 46, 425-37	13
861	Nuclear AURKA acquires kinase-independent transactivating function to enhance breast cancer stem cell phenotype. 2016 , 7, 10180	96
860	Analyses of Gingival Adhesion Molecules in Periodontitis: Theoretical In Silico, Comparative In Vivo, and Explanatory In Vitro Models. 2016 , 87, 193-202	10
859	Integrative Omics Analysis Reveals Post-Transcriptionally Enhanced Protective Host Response in Colorectal Cancers with Microsatellite Instability. 2016 , 15, 766-76	7
858	Characterization and refinement of growth related quantitative trait loci in European sea bass (<i>Dicentrarchus labrax</i>) using a comparative approach. 2016 , 455, 8-21	10
857	Pan-transcriptomic analysis identifies coordinated and orthologous functional modules in the diatoms <i>Thalassiosira pseudonana</i> and <i>Phaeodactylum tricornutum</i> . 2016 , 26, 21-8	15
856	Finding gastric cancer related genes and clinical biomarkers for detection based on gene-gene interaction network. 2016 , 276, 1-7	4
855	Quantification of peptides released during in vitro digestion of cooked meat. 2016 , 197 Pt B, 1311-23	46
854	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. 2015 , 8, 42-50	23
853	Comparative transcriptome analysis of atrial septal defect identifies dysregulated genes during heart septum morphogenesis. 2016 , 575, 303-12	13
852	Genomic, Lipidomic and Metabolomic Analysis of Cyclooxygenase-null Cells: Eicosanoid Storm, Cross Talk, and Compensation by COX-1. 2016 , 14, 81-93	10
851	The Kub5-Hera/RPRD1B interactome: a novel role in preserving genetic stability by regulating DNA mismatch repair. <i>Nucleic Acids Research</i> , 2016 , 44, 1718-31	20.1 15
850	Proteomic analysis reveals that the protective effects of ginsenoside Rb1 are associated with the actin cytoskeleton in β -amyloid-treated neuronal cells. 2016 , 40, 278-84	14
849	Double-layer clustering method to predict protein complexes based on power-law distribution and protein sublocalization. 2016 , 395, 186-193	7
848	Dynamics of Hippocampal Protein Expression During Long-term Spatial Memory Formation. 2016 , 15, 523-41	13
847	Function and regulation of TRPM7, as well as intracellular magnesium content, are altered in cells expressing E508-CFTR and G551D-CFTR. 2016 , 73, 3351-73	5
846	Genome-wide survey and characterization of the small heat shock protein gene family in <i>Bursaphelenchus xylophilus</i> . 2016 , 579, 153-61	4

845	Methylation and expression analyses of Pallister-Killian syndrome reveal partial dosage compensation of tetrasomy 12p and hypomethylation of gene-poor regions on 12p. 2016 , 11, 194-204	4
844	Identification of protein complexes of microsomes in rat adipocytes by native gel coupled with LC-ESI-QTOF. 2016 , 12, 1313-23	1
843	RNA sequencing identifies crucial genes in papillary thyroid carcinoma (PTC) progression. 2016 , 100, 151-9	20
842	Characterization and abiotic stress-responsive expression analysis of SGT1 genes in Brassica oleracea. 2016 , 59, 243-51	11
841	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. 2016 , 34, 663-686	27
840	TMT-based quantitative proteomics analyses reveal novel defense mechanisms of Brassica napus against the devastating necrotrophic pathogen Sclerotinia sclerotiorum. 2016 , 143, 265-277	20
839	Probiotic (Enterococcus faecium) induced responses of the hepatic proteome improves metabolic efficiency of broiler chickens (Gallus gallus). 2016 , 17, 89	34
838	An efficient exact algorithm for triangle listing in large graphs. 2016 , 30, 1350-1369	4
837	Identification of Viral and Host Proteins That Interact with Murine Gammaherpesvirus 68 Latency-Associated Nuclear Antigen during Lytic Replication: a Role for Hsc70 in Viral Replication. 2016 , 90, 1397-413	10
836	New Method for Joint Network Analysis Reveals Common and Different Coexpression Patterns among Genes and Proteins in Breast Cancer. 2016 , 15, 743-54	15
835	Chondrocytes Cocultured with Stromal Vascular Fraction of Adipose Tissue Present More Intense Chondrogenic Characteristics Than with Adipose Stem Cells. 2016 , 22, 336-48	19
834	HIV Protocols. 2016 ,	
833	Network-Assisted Disease Classification and Biomarker Discovery. 2016 , 1386, 353-74	8
832	Characterization and comparison of proteomes of albino sea cucumber Apostichopus japonicus (Selenka) by iTRAQ analysis. 2016 , 51, 229-239	15
831	Differential effects of metal ions on TCDD-induced cytotoxicity and cytochrome P4501A1 gene expression in a zebrafish liver (ZFL) cell-line. 2016 , 8, 236-51	8
830	canSAR: an updated cancer research and drug discovery knowledgebase. <i>Nucleic Acids Research</i> , 2016 , 44, D938-43	20.1 67
829	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. 2016 , 131, 205-213	11
828	PDCD2 and NCoR1 as putative tumor suppressors in gastric gastrointestinal stromal tumors. 2016 , 39, 129-37	13

827	Inferring Disease Associated Phosphorylation Sites via Random Walk on Multi-Layer Heterogeneous Network. 2016 , 13, 836-844	10
826	Pushing the annotation of cellular activities to a higher resolution: Predicting functions at the isoform level. 2016 , 93, 110-8	7
825	Mining for novel tumor suppressor genes using a shortest path approach. 2016 , 34, 664-75	24
824	Big-data-based edge biomarkers: study on dynamical drug sensitivity and resistance in individuals. 2016 , 17, 576-92	33
823	Global Alignment of Protein-Protein Interaction Networks: A Survey. 2016 , 13, 689-705	46
822	Proteomic comparison of the EWS-FLI1 expressing cells EF with NIH-3T3 and actin remodeling effect of (R/W) cell-penetrating peptide. 2016 , 10, 1-8	2
821	Human microRNAs profiling in response to influenza A viruses (subtypes pH1N1, H3N2, and H5N1). 2016 , 241, 409-20	33
820	Antimicrobial potentials and structural disorder of human and animal defensins. 2016 , 28, 95-111	45
819	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. 2016 , 17, 841-62	13
818	DNA damage-induced ephrin-B2 reverse signaling promotes chemoresistance and drives EMT in colorectal carcinoma harboring mutant p53. 2016 , 23, 707-22	53
817	Prediction of the engendering mechanism and specific genes of primary melanoma by bioinformatics analysis. 2016 , 34, 14-19	2
816	Orange proteomic fingerprinting: From fruit to commercial juices. 2016 , 196, 739-49	26
815	Gene network analysis reveals the association of important functional partners involved in antibiotic resistance: A report on an important pathogenic bacterium Staphylococcus aureus. 2016 , 575, 253-63	42
814	The neuronal porosome complex in health and disease. 2016 , 241, 115-30	1
813	Up-Regulation of Oligodendrocyte Lineage Markers in the Cerebellum of Autistic Patients: Evidence from Network Analysis of Gene Expression. 2016 , 53, 4019-4025	17
812	Identification of Biomarkers Associated With Alzheimer's Disease by Bioinformatics Analysis. 2016 , 31, 163-8	17
811	Identification of sequence motifs involved in Dengue virus-host interactions. 2016 , 34, 676-87	5
810	Interleukin-11 binds specific EF-hand proteins via their conserved structural motifs. 2017 , 35, 78-91	18

809	Abundance and functional roles of intrinsic disorder in the antimicrobial peptides of the NK-lysin family. 2017 , 35, 836-856	8
808	Identification of Novel Key Molecules Involved in Spatial Memory Impairment in Triple Transgenic Mice of Alzheimer's Disease. 2017 , 54, 3843-3858	14
807	Disrupted pathways associated with neonatal sepsis: Combination of protein-protein interactions and pathway data. 2017 , 11, 1-7	2
806	A bi-objective network design approach for discovering functional modules linking Golgi apparatus fragmentation and neuronal death. 2017 , 258, 5-30	1
805	-alpha -308G/A and -238G/A polymorphisms and its protein network associated with type 2 diabetes mellitus. 2017 , 24, 1195-1203	18
804	Proteomics offers insight to the mechanism behind <i>Pisum sativum</i> L. response to pea seed-borne mosaic virus (PSbMV). 2017 , 153, 78-88	23
803	Screening for potential genes associated with bone overgrowth after mid-shaft femur fracture in a rat model. 2017 , 12, 8	5
802	Mouse Models of Breast Cancer Share Amplification and Deletion Events with Human Breast Cancer. 2017 , 22, 71-84	11
801	Human Antiviral Protein IFIX Suppresses Viral Gene Expression during Herpes Simplex Virus 1 (HSV-1) Infection and Is Counteracted by Virus-induced Proteasomal Degradation. 2017 , 16, S200-S214	19
800	Crohn disease risk prediction-Best practices and pitfalls with exome data. 2017 , 38, 1193-1200	6
799	Studying hematopoiesis using single-cell technologies. 2017 , 10, 27	26
798	HAPPI-2: a Comprehensive and High-quality Map of Human Annotated and Predicted Protein Interactions. 2017 , 18, 182	30
797	Elucidating the biosynthetic pathways of volatile organic compounds in <i>Mycobacterium tuberculosis</i> through a computational approach. 2017 , 13, 750-755	4
796	Genomewide landscape of gene-metabolome associations in <i>Escherichia coli</i> . 2017 , 13, 907	72
795	Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier. 2017 , 83, 67-74	174
794	Gene expression profiles reveal key pathways and genes associated with neuropathic pain in patients with spinal cord injury. 2017 , 15, 2120-2128	8
793	Proteome mining for the identification and in-silico characterization of putative drug targets of multi-drug resistant <i>Clostridium difficile</i> strain 630. 2017 , 136, 6-10	3
792	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. 2017 , 8, 14364	131

791	A Shotgun Proteomics Approach Reveals a New Toxic Role for Alzheimer's Disease Aβ Peptide: Spliceosome Impairment. 2017 , 16, 1526-1541	17
790	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in Hevea species. 2017 , 7, 41457	60
789	Protein carbonylation linked to wheat seedling tolerance to water deficiency. 2017 , 137, 84-95	5
788	Bioinformatics Analysis of Epigenetics. 2017 , 247-273	0
787	A Systems Perspective of Signalling Networks in Host-Pathogen Interactions. 2017 , 97, 41-57	
786	Effect of age on pro-inflammatory miRNAs contained in mesenchymal stem cell-derived extracellular vesicles. 2017 , 7, 43923	44
785	Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases. 2017 , 49, 515-526	283
784	Structural and functional genomics analysis of methyltransferase genes and networks associate to understand antibiotic resistance inside the pangenome of Pseudomonas aeruginosa. 2017 , 702-705	1
783	ZK DrugResist 2.0: A TextMiner to extract semantic relations of drug resistance from PubMed. 2017 , 69, 93-98	3
782	Comprehensive Dissection of Transcriptome Data and Regulatory Factors in Pancreatic Cancer Cells. 2017 , 118, 3976-3985	1
781	Bioinformatics from a Big Data Perspective: Meeting the Challenge. 2017 , 349-359	
780	Mps1 Regulates Kinetochore-Microtubule Attachment Stability via the Ska Complex to Ensure Error-Free Chromosome Segregation. 2017 , 41, 143-156.e6	52
779	Summarizing Biological Networks. 2017 ,	
778	Integrated proteomic analysis of Brachypodium distachyon roots and leaves reveals a synergistic network in the response to drought stress and recovery. 2017 , 7, 46183	23
777	Identification of key genes associated with Schmid-type metaphyseal chondrodysplasia based on microarray data. 2017 , 39, 1428-1436	5
776	A Systemic Analysis of Transcriptomic and Epigenomic Data To Reveal Regulation Patterns for Complex Disease. 2017 , 7, 2271-2279	4
775	Effects of fine air particulates on gene expression in non-small-cell lung cancer. 2017 , 62, 295-301	10
774	Mediterranean versus Red sea corals facing climate change, a transcriptome analysis. 2017 , 7, 42405	17

773	Prediction of vaccine candidates against <i>Pseudomonas aeruginosa</i> : An integrated genomics and proteomics approach. 2017 , 109, 274-283	34
772	Effects of low dose ionizing radiation on DNA damage-caused pathways by reverse-phase protein array and Bayesian networks. 2017 , 15, 1750006	3
771	Differential proteome profiling in the hippocampus of amnesic mice. 2017 , 27, 845-859	5
770	In-depth analysis of the synaptic plasma membrane proteome of small hippocampal slices using an integrated approach. 2017 , 353, 119-132	13
769	Neuro-symbolic representation learning on biological knowledge graphs. 2017 , 33, 2723-2730	63
768	In silico characterization of Myogenic Factor 6 transcript of Hilsa, <i>Tenulosa ilisha</i> and putative role of its SNPs with differential growth. 2017 , 13, 140-148	2
767	Multi-omics analysis provides insight to the <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> association. 2017 , 1861, 2218-2227	4
766	Salt-induced phosphoproteomic changes in the hypothalamic paraventricular nucleus in rats with chronic renal failure. 2017 , 1669, 1-10	3
765	Structural annotation of Beta-1,4-N-acetyl galactosaminyltransferase 1 (B4GALNT1) causing Hereditary Spastic Paraplegia 26. 2017 , 626, 258-263	5
764	Bioinformatics analysis of gene expression profiles of esophageal squamous cell carcinoma. 2017 , 30, 1-8	19
763	Identification of critical genes in nucleus pulposus cells isolated from degenerated intervertebral discs using bioinformatics analysis. 2017 , 16, 553-564	9
762	Lysine Acetylome Analysis Reveals Photosystem II Manganese-stabilizing Protein Acetylation is Involved in Negative Regulation of Oxygen Evolution in Model Cyanobacterium sp. PCC 7002. 2017 , 16, 1297-1311	16
761	Molecular cloning and characterization of genes encoding FK506-binding proteins (FKBPs) in wheat (<i>Triticum aestivum</i> L.). 2017 , 26, 467-477	
760	Identification of gene markers associated with metastasis in clear cell renal cell carcinoma. 2017 , 13, 4755-4761	9
759	Melatonin ameliorates anxiety and depression-like behaviors and modulates proteomic changes in triple transgenic mice of Alzheimer's disease. 2017 , 43, 593-611	31
758	Inhibition of N-glycan processing modulates the network of EDEM3 interactors. 2017 , 486, 978-984	5
757	ERCC1-XPF cooperates with CTCF and cohesin to facilitate the developmental silencing of imprinted genes. 2017 , 19, 421-432	22
756	Label-free quantitative proteomics unravels the importance of RNA processing in glioma malignancy. 2017 , 351, 84-95	14

755	Machine Learning of Global Phosphoproteomic Profiles Enables Discrimination of Direct versus Indirect Kinase Substrates. 2017 , 16, 786-798	20
754	Mathematical models of cell phenotype regulation and reprogramming: Make cancer cells sensitive again!. 2017 , 1867, 167-175	13
753	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. 2017 , 7, 681	10
752	HUMAN KINASES DISPLAY MUTATIONAL HOTSPOTS AT COGNATE POSITIONS WITHIN CANCER. 2017 , 22, 414-425	0
751	GEAR: A database of Genomic Elements Associated with drug Resistance. 2017 , 7, 44085	15
750	iTRAQ-based quantitative proteomics reveals important host factors involved in the high pathogenicity of the H5N1 avian influenza virus in mice. 2017 , 206, 125-147	9
749	Evaluation of non-supervised MALDI mass spectrometry imaging combined with microproteomics for glioma grade III classification. 2017 , 1865, 875-890	27
748	Approaches for the integration of big data in translational medicine: single-cell and computational methods. 2021 , 1493, 3-28	4
747	Comprehensive analysis of lncRNA-miRNA-mRNA regulatory networks for microbiota-mediated colorectal cancer associated with immune cell infiltration. 2021 , 12, 3410-3425	8
746	Identification and validation of the miRNA-mRNA regulatory network in fetoplacental arterial endothelial cells of gestational diabetes mellitus. 2021 , 12, 3503-3515	3
745	High expression of MAPK-14 promoting the death of chondrocytes is an important signal of osteoarthritis process. 2021 , 9, e10656	5
744	Integrative analysis of miRNA-mRNA network in high altitude retinopathy by bioinformatics analysis. 2021 , 41,	4
743	DIVERSE: Bayesian Data IntegratiVE learning for precise drug ResponSE prediction. 2021 , PP,	1
742	MKL-GRNI: A parallel multiple kernel learning approach for supervised inference of large-scale gene regulatory networks. 2021 , 7, e363	3
741	A functional interaction between GRP78 and Zika virus E protein. 2021 , 11, 393	14
740	PKSPS: a novel method for predicting kinase of specific phosphorylation sites based on maximum weighted bipartite matching algorithm and phosphorylation sequence enrichment analysis. 2021 ,	2
739	Identification and validation of potential mRNA- microRNA- long-noncoding RNA (mRNA-miRNA-lncRNA) prognostic signature for cervical cancer. 2021 , 12, 898-913	13
738	Elevated Ras related GTP binding B (RRAGB) expression predicts poor overall survival and constructs a prognostic nomogram for colon adenocarcinoma. 2021 , 12, 4620-4632	0

737	BIRC5, GAJ5, and lncRNA NPHP3-AS1 Are Correlated with the Development of Atrial Fibrillation-Valvular Heart Disease. 2021 , 62, 153-161	0
736	Metabolic Response to the Mitochondrial Toxin 1-Methyl-4-phenylpyridinium (MPP+) in LDH-A/B Double-knockout LS174T Colon Cancer Cells. 2021 , 18, 385-405	0
735	Databases for Protein-Protein Interactions. 2021 , 2361, 229-248	2
734	Construction of an mRNA-miRNA-lncRNA network prognostic for triple-negative breast cancer. 2021 , 13, 1153-1175	7
733	Label-Free Mass Spectrometry-Based Plasma Proteomics Identified LY6D, DSC3, CDSN, SERPINB12, and SLURP1 as Novel Protein Biomarkers For Pulmonary Tuberculosis. 2021 , 18, 50-61	
732	Super enhancer-mediated transcription of miR146a-5p drives M2 polarization during Leishmania donovani infection. 2021 , 17, e1009343	7
731	Waves of sumoylation support transcription dynamics during adipocyte differentiation.	
730	A gene co-association network regulating gut microbial communities in a Duroc pig population. 2021 , 9, 52	6
729	Identification of potential biomarkers for abdominal pain in IBS patients by bioinformatics approach. 2021 , 21, 48	1
728	Protein kinase TgCDPK7 regulates vesicular trafficking and phospholipid synthesis in Toxoplasma gondii. 2021 , 17, e1009325	5
727	Mining prognostic markers of Asian hepatocellular carcinoma patients based on the apoptosis-related genes. 2021 , 21, 175	3
726	Genome-scale meta-analysis of breast cancer datasets identifies promising targets for drug development. 2021 , 28, 5	1
725	Path to drugging functional clones of luminal breast cancers using in-depth proteomics with spatially resolved mass spectrometry guided by MALDI imaging.	
724	A novel DNA methylation-based model that effectively predicts prognosis in hepatocellular carcinoma. 2021 , 41,	1
723	A proteomics approach for the identification of cullin-9 (CUL9) related signaling pathways in induced pluripotent stem cell models. 2021 , 16, e0248000	1
722	miRNA and mRNA expression profiling reveals potential biomarkers for metastatic cutaneous melanoma. 2021 , 21, 557-567	4
721	Identification of a ceRNA Network in Lung Adenocarcinoma Based on Integration Analysis of Tumor-Associated Macrophage Signature Genes. 2021 , 9, 629941	3
720	A gene module identification algorithm and its applications to identify gene modules and key genes of hepatocellular carcinoma. 2021 , 11, 5517	4

719	Comparative proteomics reveals mechanisms that underlie insecticide resistance in <i>Culex pipiens pallens</i> Coquillett. 2021 , 15, e0009237	0
718	Secreted midbody remnants are a class of extracellular vesicles molecularly distinct from exosomes and microparticles. 2021 , 4, 400	11
717	Identification of fibroblast activation-related genes in two acute kidney injury models. 2021 , 9, e10926	2
716	Transcriptome reveals the important role of metabolic imbalances, immune disorders and apoptosis in the treatment of <i>Procambarus clarkii</i> at super high temperature. 2021 , 37, 100781	1
715	IL-8, MSPa, MIF, FGF-9, ANG-2 and AgRP collection were identified for the diagnosis of colorectal cancer based on the support vector machine model. 2021 , 20, 781-791	0
714	A New Framework for Discovering Protein Complex and Disease Association via Mining Multiple Databases. 2021 , 13, 683-692	1
713	MicroRNA-29 is an essential regulator of brain maturation through regulation of CH methylation. 2021 , 35, 108946	7
712	Proteomic responses of maize roots to the combined stress of sulphur deficiency and chromium toxicity. 2021 , 76, 1887-1899	
711	Comprehensive analysis of lumbar disc degeneration and autophagy-related candidate genes, pathways, and targeting drugs. 2021 , 16, 252	2
710	SIGNAL: A web-based iterative analysis platform integrating pathway and network approaches optimizes hit selection from genome-scale assays. 2021 , 12, 338-352.e5	1
709	Parallel genome-wide RNAi screens identify lymphocyte-specific protein tyrosine kinase (LCK) as a targetable vulnerability of cell proliferation and chemoresistance in nasopharyngeal carcinoma. 2021 , 504, 81-90	5
708	Transcriptome profiling reveals response genes for downy mildew resistance in cucumber. 2021 , 253, 112	4
707	E2F2 inhibition induces autophagy via the PI3K/Akt/mTOR pathway in gastric cancer. 2021 , 13, 13626-13643	3
706	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. 2021 , 22, 209	
705	UBTD1 regulates ceramide balance and endolysosomal positioning to coordinate EGFR signaling. 2021 , 10,	3
704	Comprehensive analysis of IgA nephropathy expression profiles: identification of potential biomarkers and therapeutic agents. 2021 , 22, 137	3
703	Bioinformatic Analysis of Crosstalk Between circRNA, miRNA, and Target Gene Network in NAFLD. 2021 , 12, 671523	2
702	Identification of Key Pathways and Genes in Dementia via Integrated Bioinformatics Analysis.	

701	Identification of KEY lncRNAs and mRNAs Associated with Oral Squamous Cell Carcinoma Progression. 2021 , 16, 207-215	2
700	Based on Network Pharmacology and Molecular Docking to Explore the Underlying Mechanism of Huangqi Gegen Decoction for Treating Diabetic Nephropathy. 2021 , 2021, 9928282	4
699	A Prognostic DNA Damage Repair Genes Signature and Its Impact on Immune Cell Infiltration in Glioma. 2021 , 11, 682932	5
698	Construction and External Validation of a Ferroptosis-Related Gene Signature of Predictive Value for the Overall Survival in Bladder Cancer. 2021 , 8, 675651	13
697	Genetic network and gene set enrichment analyses identify MND1 as potential diagnostic and therapeutic target gene for lung adenocarcinoma. 2021 , 11, 9430	1
696	Construction of circRNA-miRNA-mRNA network in the pathogenesis of recurrent implantation failure using integrated bioinformatics study. 2021 ,	3
695	A comprehensive review of m6A/m6Am RNA methyltransferase structures. <i>Nucleic Acids Research</i> , 2021 , 49, 7239-7255	20.1 27
694	Effect of trachea stiffness on tumor distribution in papillary thyroid microcarcinoma. 2021 , 22, 518	
693	Network Protein Interaction in the Link between Stroke and Periodontitis Interplay: A Pilot Bioinformatic Analysis. 2021 , 12,	0
692	Neoisoliquiritin exerts tumor suppressive effects on prostate cancer by repressing androgen receptor activity. 2021 , 85, 153514	1
691	Study on Pathological Mechanism of Pneumonia Infected by Coronavirus Based on Time-Series Gene Co-expression Network Analysis. 2021 ,	
690	Upregulation of LIMK1 Is Correlated With Poor Prognosis and Immune Infiltrates in Lung Adenocarcinoma. 2021 , 12, 671585	4
689	Melatonin influences the early growth stage in <i>Zoysia japonica</i> Steud. by regulating plant oxidation and genes of hormones. 2021 , 11, 12381	1
688	Integrated systems biology approach using gene network analysis to identify the important pathways and new potential drug targets for Neuroblastoma. 2021 , 23, 101101	2
687	Identification of differently expressed mRNAs by peripheral blood mononuclear cells in Vogt-Koyanagi-Harada disease. 2021 ,	
686	In-depth proteomics analysis of sentinel lymph nodes from individuals with endometrial cancer. 2021 , 2, 100318	3
685	A New Prognostic Risk Signature of Eight Ferroptosis-Related Genes in the Clear Cell Renal Cell Carcinoma. 2021 , 11, 700084	1
684	Synergistic effects of methyl 2-cyano-3,11-dioxo-18beta-olean-1,-12-dien-30-oate and erlotinib on erlotinib-resistant non-small cell lung cancer cells.. 2021 , 11, 799-807	0

683	A Knowledge-guided Mechanistic Model of Synthetic Lethality in the HCT116 Vorinostat-resistant Colon Cancer Xenograft Model Cell-line.	
682	Integrated MicroRNA Expression Profile Reveals Dysregulated miR-20a-5p and miR-200a-3p in Liver Fibrosis. 2021 , 2021, 9583932	2
681	Screening of cervical cancer-related hub genes based on comprehensive bioinformatics analysis. 2021 , 32, 303-315	1
680	Quantitative Proteomics Reveals that Hsp90 Inhibition Dynamically Regulates Global Protein Synthesis in <i>Leishmania mexicana</i> . 2021 , 6,	3
679	StrongestPath: a Cytoscape application for protein-protein interaction analysis. 2021 , 22, 352	3
678	Multi-Omics Approach Reveals the Potential Core Vaccine Targets for the Emerging Foodborne Pathogen. 2021 , 12, 665858	1
677	Gene interaction network to unravel the role of gut bacterial species in cardiovascular diseases: <i>E. coli</i> O157:H7 host-bacterial interaction study. 2021 , 133, 104417	6
676	Alternative splicing associated with cancer stemness in kidney renal clear cell carcinoma. 2021 , 21, 703	4
675	PhosIDN: an integrated deep neural network for improving protein phosphorylation site prediction by combining sequence and protein-protein interaction information. 2021 ,	6
674	Identification of N-linked Glycoproteins in Silkworm Serum Using Con A Lectin Affinity Chromatography and Mass Spectrometry. 2021 , 21,	
673	Quantitative Proteomics Reveals a Novel Role of the E3 Ubiquitin-Protein Ligase FANCL in the Activation of the Innate Immune Response through Regulation of TBK1 Phosphorylation during Peste des Petits Ruminants Virus Infection. 2021 , 20, 4113-4130	1
672	Transcriptome Profile Analysis of Triple-Negative Breast Cancer Cells in Response to a Novel Cytostatic Tetrahydroisoquinoline Compared to Paclitaxel. 2021 , 22,	2
671	Analysis of Hub Genes and the Mechanism of Immune Infiltration in Stanford Type a Aortic Dissection. 2021 , 8, 680065	6
670	Exogenous cysteine alleviates chromium stress via reducing its uptake and regulating proteome in roots of <i>Brassica napus</i> L. seedlings. 2021 , 139, 114-121	4
669	A Novel Expression Signature from the Perspective of Mesenchymal-Epithelial Transition for Hepatocellular Carcinoma with Regard to Prognosis, Clinicopathological Features, Immune Cell Infiltration, Chemotherapeutic Efficacy, and Immunosuppressive Molecules. 2021 , 2021, 5033416	1
668	Ferroptosis-Related Gene Signature and Patterns of Immune Infiltration Predict the Overall Survival in Patients With Lung Adenocarcinoma. 2021 , 8, 692530	5
667	Application of Modular Response Analysis to Medium- to Large-Size Biological Systems.	0
666	Transcriptome analysis of the spleen provides insight into the immunoregulation of <i>Cyprinus carpio</i> koi under <i>Aeromonas veronii</i> infection. 2021 , 540, 736650	3

665	Bioinformatics analysis of the role of CXC ligands in the microenvironment of head and neck tumor. 2021 , 13, 17789-17817	2
664	Autophagy-Related Genes in Atherosclerosis. 2021 , 2021, 6402206	1
663	Interaction between early in ovo stimulation of the gut microbiota and chicken host - splenic changes in gene expression and methylation. 2021 , 12, 73	1
662	Rhamnolipid Enhances the Nitrogen Fixation Activity of by Influencing Lysine Succinylation. 2021 , 12, 697963	0
661	Identification of Potential Genomic Alterations and the circRNA-miRNA-mRNA Regulatory Network in Primary and Recurrent Synovial Sarcomas. 2021 , 8, 707151	2
660	Identification and Functional Validation of Differentially Expressed microRNAs in Ascites-Derived Ovarian Cancer Cells Compared with Primary Tumour Tissue. 2021 , 13, 6585-6597	3
659	Glycation modulates glutamatergic signalling and exacerbates Parkinson's disease-like phenotypes.	
658	Cisplatin's potential for type 2 diabetes repositioning by inhibiting CDKN1A, FAS, and SESN1. 2021 , 135, 104640	0
657	What's in the BAGs? Intrinsic disorder angle of the multifunctionality of the members of a family of chaperone regulators. 2021 ,	1
656	Regulation of follistatin-like 3 expression by miR-486-5p modulates gastric cancer cell proliferation, migration and tumor progression. 2021 , 13, 20302-20318	2
655	A novel survival model based on a Ferroptosis-related gene signature for predicting overall survival in bladder cancer. 2021 , 21, 943	5
654	Quest for Novel Preventive and Therapeutic Options Against Multidrug-Resistant. 2021 , 1-19	
653	Identification of novel biomarkers for arthrofibrosis after total knee arthroplasty in animal models and clinical patients. 2021 , 70, 103486	1
652	Prognostic targets recognition of rectal adenocarcinoma based on transcriptomics. 2021 , 100, e25909	1
651	The first human induced pluripotent stem cell line of Kashin-Beck disease reveals involvement of heparan sulfate proteoglycan biosynthesis and PPAR pathway. 2021 ,	0
650	Aquaculture industry prospective from gut microbiome of fish and shellfish: An overview. 2021 ,	3
649	The Salivary Secretome.	
648	Maturation State-Specific Alternative Splicing in -ITD and NPM1 Mutated AML. 2021 , 13,	1

647	Key Gene and Functional Pathways Identified in Unexplained Recurrent Spontaneous Abortion Using Targeted RNA Sequencing and Clinical Analysis. 2021 , 12, 717832	1
646	The CCAAT/Enhancer Binding Protein Beta (cebpb) is essential for the development of enveloping layer (EVL) in zebrafish. 2021 ,	
645	Global analysis of lysine acetylation in soybean leaves. 2021 , 11, 17858	1
644	Integrative Analysis of the Roles of lncRNAs and mRNAs in Itaconate-Mediated Protection Against Liver Ischemia-Reperfusion Injury in Mice. 2021 , 14, 4519-4536	2
643	Transcriptome-Guided Insights Into Plastic Degradation by the Marine Bacterium. 2021 , 12, 751571	2
642	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. 2021 , 93, 104921	9
641	ProteinPrompt: a webserver for predicting protein-protein interactions.	
640	Integrative analysis of miRNA-mRNA network in idiopathic membranous nephropathy by bioinformatics analysis. 2021 , 9, e12271	0
639	MAGI-MS: Multiple seed-centric module discovery.	
638	Proximity Interactome Map of the Vac14-Fig4 Complex Using BioID. 2021 , 20, 4959-4973	1
637	Identification and validation of hub genes of synovial tissue for patients with osteoarthritis and rheumatoid arthritis. 2021 , 158, 37	3
636	Circulating MicroRNAs Highly Correlate to Expression of Cartilage Genes Potentially Reflecting OA Susceptibility-Towards Identification of Applicable Early OA Biomarkers. 2021 , 11,	2
635	L-Methionine Protects against Oxidative Stress and Mitochondrial Dysfunction in an In Vitro Model of Parkinson's Disease. 2021 , 10,	2
634	Stem cells from human exfoliated deciduous teeth affect mitochondria and reverse cognitive decline in a senescence-accelerated mouse prone 8 model. 2021 ,	1
633	Redox-Mediated Regulation of Mitochondrial Biogenesis, Dynamics, and Respiratory Chain Assembly in Yeast and Human Cells. 2021 , 9, 720656	4
632	Computational analysis of missense variants in MMP2 gene linked with Winchester syndrome and Nodulosis-Arthropathy-Osteolysis reveals structural shift in protein-protein and protein-ligand complexes. 2021 , 29, 100931	0
631	Transcriptomic analysis of ovarian signaling at the emergence of the embryo from obligate diapause in the American mink (<i>Neovison vison</i>). 2021 , 232, 106823	1
630	Bioinformatics analysis reveals the roles of cytoskeleton protein transgelin in occurrence and development of proteinuria. 2021 , 10, 2250-2268	0

629	Co-expression analysis identifies networks of miRNAs implicated in biological ageing and modulated by short-term interval training. 2021 , 199, 111552	2
628	Isoforskolin, an adenylyl cyclase activator, attenuates cigarette smoke-induced COPD in rats. 2021 , 91, 153701	1
627	Galectin-9 and PSMB8 overexpression predict unfavorable prognosis in patients with AML. 2021 , 12, 4257-4263	2
626	Profiles of alternative splicing landscape in breast cancer and their clinical significance: an integrative analysis based on large-sequencing data. 2021 , 9, 58	1
625	Identification of hub genes and biological pathways in hepatocellular carcinoma by integrated bioinformatics analysis. 2021 , 9, e10594	2
624	Research on Drug Response Prediction Model Based on Big Data. 2021 , 524-537	
623	A systematic study on the chemical diversity and efficacy of the inflorescence and succulent stem of <i>Cynomorium songaricum</i> . 2021 , 12, 7501-7513	2
622	Impact of Missense Variants on Protein-Protein Interactions.	1
621	Quantitative proteome profiles help reveal efficient xylose utilization mechanisms in solventogenic <i>Clostridium</i> sp. strain BOH3. 2017 , 114, 1959-1969	5
620	Encyclopedia of Systems Biology. 2013 , 1609-1611	1
619	The Complexity Hypothesis and Other Connectivity Barriers to Lateral Gene Transfer. 2013 , 137-145	1
618	High-throughput translational medicine: challenges and solutions. 2014 , 799, 39-67	7
617	Computational approaches for human disease gene prediction and ranking. 2014 , 799, 69-84	13
616	Biological information extraction and co-occurrence analysis. 2014 , 1159, 77-92	13
615	Candidate gene discovery and prioritization in rare diseases. 2014 , 1168, 295-312	2
614	Protein-protein interaction databases. 2015 , 1278, 39-56	27
613	Proteomic Characterization of Exosomes from HIV-1-Infected Cells. 2016 , 1354, 311-26	7
612	Systems Analysis for Interpretation of Phosphoproteomics Data. 2016 , 1355, 341-60	12

611	Computational analysis of virus-host interactomes. 2013 , 1064, 115-30	2
610	Integrative data-mining tools to link gene and function. 2014 , 1101, 43-66	4
609	A Review on Protein-Protein Interaction Network Databases. 2014 , 511-519	1
608	Management and Analysis of Protein-to-Protein Interaction Data. 2011 , 1-12	1
607	Lagrangian Relaxation Applied to Sparse Global Network Alignment. 2011 , 225-236	21
606	Conditional Random Fields for Protein Function Prediction. 2013 , 184-195	3
605	proSQLite: Prolog File Based Databases via an SQLite Interface. 2013 , 222-227	2
604	Network Pharmacology to Aid the Drug Discovery Process. 2012 , 161-172	1
603	Proteomics Defines Protein Interaction Network of Signaling Pathways. 2013 , 17-38	1
602	A Survey of Current Integrative Network Algorithms for Systems Biology. 2013 , 479-495	3
601	Properties of Biological Networks. 2013 , 129-178	1
600	Putative serum protein biomarkers for epsilon toxin exposure in mouse model using LC-MS/MS analysis. 2020 , 63, 102209	1
599	Quantitative SUMO proteomics identifies PIAS1 substrates involved in cell migration and motility. 2020 , 11, 834	26
598	KRT8 and KRT19, associated with EMT, are hypomethylated and overexpressed in lung adenocarcinoma and link to unfavorable prognosis. 2020 , 40,	11
597	Identification of cell division cycle 20 as a candidate biomarker and potential therapeutic target in bladder cancer using bioinformatics analysis. 2020 , 40,	1
596	Lamin A/C in renal tubular cells is important for tissue repair, cell proliferation, and calcium oxalate crystal adhesion, and is associated with potential crystal receptors. 2016 , 30, 3368-3377	21
595	uS10, a novel Npro-interacting protein, inhibits classical swine fever virus replication. 2017 , 98, 1679-1692	13
594	DprA from <i>Neisseria meningitidis</i> : properties and role in natural competence for transformation. 2017 , 163, 1016-1029	13

593	The functional impact of alternative splicing in cancer.	2
592	ALPK1 and TIFA dependent innate immune response triggered by the Helicobacter pylori type IV secretion system.	2
591	Evolution leads to emergence: An analysis of protein interactomes across the tree of life.	0
590	High Throughput RNA Sequencing of Germ-Free Mouse Retina Reveals Metabolic Pathways Involved in the Gut-Retina Axis.	2
589	Drug repurposing through joint learning on knowledge graphs and literature.	6
588	Stronger selective constraint on downstream genes in the oxidative phosphorylation pathway of cetaceans. 2018 , 31, 217-228	5
587	OrpheusDB. 2017 ,	10
586	Computational Prediction of Protein Complexes from Protein Interaction Networks. 2017 ,	11
585	Constructing Reliable Protein-Protein Interaction (PPI) Networks. 2017 , 15	1
584	A misplaced lncRNA causes brachydactyly in humans. 2012 , 122, 3990-4002	95
583	HPV-related methylation signature predicts survival in oropharyngeal squamous cell carcinomas. 2013 , 123, 2488-501	87
582	Both Peripheral Blood and Urinary miR-195-5p, miR-192-3p, miR-328-5p and Their Target Genes PPM1A, RAB1A and BRSK1 May Be Potential Biomarkers for Membranous Nephropathy. 2019 , 25, 1903-1916	8
581	Identification and Integrated Analysis of Key Biomarkers for Diagnosis and Prognosis of Non-Small Cell Lung Cancer. 2019 , 25, 9280-9289	12
580	Identification of Hub Genes and Pathways in a Rat Model of Renal Ischemia-Reperfusion Injury Using Bioinformatics Analysis of the Gene Expression Omnibus (GEO) Dataset and Integration of Gene Expression Profiles. 2019 , 25, 8403-8411	9
579	On the intrinsic disorder status of the major players in programmed cell death pathways. 2013 , 2, 190	18
578	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. 2014 , 3, 140	7
577	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. 2014 , 3, 140	8
576	NetMatchStar: an enhanced Cytoscape network querying app. 2015 , 4, 479	13

575	NetMatchStar: an enhanced Cytoscape network querying app. 2015 , 4, 479	8
574	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. 2015 , 4, 259	22
573	A network-based approach for predicting missing pathway interactions. 2012 , 8, e1002640	25
572	A Novel Feedback Loop That Controls Bimodal Expression of Genetic Competence. 2015 , 11, e1005047	24
571	Functional correlations of pathogenesis-driven gene expression signatures in tuberculosis. 2011 , 6, e26938	124
570	SPPS: a sequence-based method for predicting probability of protein-protein interaction partners. 2012 , 7, e30938	18
569	HIPPIE: Integrating protein interaction networks with experiment based quality scores. 2012 , 7, e31826	235
568	A role for nonsense-mediated mRNA decay in plants: pathogen responses are induced in <i>Arabidopsis thaliana</i> NMD mutants. 2012 , 7, e31917	94
567	Evolution of <i>Burkholderia pseudomallei</i> in recurrent melioidosis. 2012 , 7, e36507	83
566	Proteomic identification of calumenin as a G551D-CFTR associated protein. 2012 , 7, e40173	15
565	Comparative transcriptional analysis of clinically relevant heat stress response in <i>Clostridium difficile</i> strain 630. 2012 , 7, e42410	25
564	Fetal mesenchymal stromal cells differentiating towards chondrocytes acquire a gene expression profile resembling human growth plate cartilage. 2012 , 7, e44561	13
563	Bioinformatic analysis of epigenetic and microRNA mediated regulation of drought responsive genes in rice. 2012 , 7, e49331	35
562	Global effect of inauhzin on human p53-responsive transcriptome. 2012 , 7, e52172	16
561	canEvolve: a web portal for integrative oncogenomics. 2013 , 8, e56228	30
560	Integrative bioinformatics analysis of genomic and proteomic approaches to understand the transcriptional regulatory program in coronary artery disease pathways. 2013 , 8, e57193	9
559	Structural insights into putative molybdenum cofactor biosynthesis protein C (MoaC2) from <i>Mycobacterium tuberculosis</i> H37Rv. 2013 , 8, e58333	2
558	Landscape of transcriptional deregulations in the preeclamptic placenta. 2013 , 8, e65498	58

557	Characterization of a Novel Putative S-Adenosylmethionine Decarboxylase-Like Protein from <i>Leishmania donovani</i> . 2013 , 8, e65912	3
556	Complementing the Eukaryotic Protein Interactome. 2013 , 8, e66635	6
555	Differentially expressed genes in the pre-eclamptic placenta: a systematic review and meta-analysis. 2013 , 8, e68991	61
554	Evaluating the pharmacological mechanism of Chinese medicine Si-Wu-Tang through multi-level data integration. 2013 , 8, e72334	36
553	PhenoTimer: software for the visual mapping of time-resolved phenotypic landscapes. 2013 , 8, e72361	1
552	Beta cell 5'-shifted isomiRs are candidate regulatory hubs in type 2 diabetes. 2013 , 8, e73240	58
551	Inference of gene-phenotype associations via protein-protein interaction and orthology. 2013 , 8, e77478	8
550	Perturbation centrality and turbine: a novel centrality measure obtained using a versatile network dynamics tool. 2013 , 8, e78059	16
549	Differential stress transcriptome landscape of historic and recently emerged hypervirulent strains of <i>Clostridium difficile</i> strains determined using RNA-seq. 2013 , 8, e78489	18
548	Activity of <i>Bdellovibrio</i> hit locus proteins, Bd0108 and Bd0109, links Type IVa pilus extrusion/retraction status to prey-independent growth signalling. 2013 , 8, e79759	32
547	Functional annotation of conserved hypothetical proteins from <i>Haemophilus influenzae</i> Rd KW20. 2013 , 8, e84263	59
546	Identification of salivary gland proteins depleted after blood feeding in the malaria vector <i>Anopheles campestris</i> -like mosquitoes (Diptera: Culicidae). 2014 , 9, e90809	8
545	Prediction of multi-type membrane proteins in human by an integrated approach. 2014 , 9, e93553	14
544	GASOLINE: a Greedy And Stochastic algorithm for optimal Local multiple alignment of Interaction NEtworks. 2014 , 9, e98750	21
543	Decellularized allogeneic heart valves demonstrate self-regeneration potential after a long-term preclinical evaluation. 2014 , 9, e99593	61
542	Salt-induced changes in cardiac phosphoproteome in a rat model of chronic renal failure. 2014 , 9, e100331	11
541	Proteomic analysis of <i>Apis cerana</i> and <i>Apis mellifera</i> larvae fed with heterospecific royal jelly and by CSBV challenge. 2014 , 9, e102663	13
540	An siRNA screen of membrane trafficking genes highlights pathways common to HIV-1 and M-PMV virus assembly and release. 2014 , 9, e106151	8

539	High-throughput screening of dipeptide utilization mediated by the ABC transporter DppBCDF and its substrate-binding proteins DppA1-A5 in <i>Pseudomonas aeruginosa</i> . 2014 , 9, e111311	28
538	An integrative computational approach for prioritization of genomic variants. 2014 , 9, e114903	6
537	De novo transcriptomic analysis of peripheral blood lymphocytes from the Chinese goose: gene discovery and immune system pathway description. 2015 , 10, e0121015	13
536	A multi-omics approach identifies key hubs associated with cell type-specific responses of airway epithelial cells to staphylococcal alpha-toxin. 2015 , 10, e0122089	14
535	Genomic heterogeneity of osteosarcoma - shift from single candidates to functional modules. 2015 , 10, e0123082	18
534	Evolutionarily conserved network properties of intrinsically disordered proteins. 2015 , 10, e0126729	12
533	Micro-RNAs Let7e and 126 in Plasma as Markers of Metabolic Dysfunction in 10 to 12 Years Old Children. 2015 , 10, e0128140	23
532	In Silico Analysis of Tumor Necrosis Factor Induced Protein 8-Like-1 (TIPE1) Protein. 2015 , 10, e0134114	8
531	Molecular Architecture of Spinal Cord Injury Protein Interaction Network. 2015 , 10, e0135024	6
530	Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. 2015 , 10, e0138524	18
529	Transcriptomic Changes in Coral Holobionts Provide Insights into Physiological Challenges of Future Climate and Ocean Change. 2015 , 10, e0139223	47
528	Bioinformatics Analyses of the Role of Vascular Endothelial Growth Factor in Patients with Non-Small Cell Lung Cancer. 2015 , 10, e0139285	10
527	Codon Bias Patterns of <i>E. coli</i> 's Interacting Proteins. 2015 , 10, e0142127	16
526	The FgNot3 Subunit of the Ccr4-Not Complex Regulates Vegetative Growth, Sporulation, and Virulence in <i>Fusarium graminearum</i> . 2016 , 11, e0147481	3
525	Quantitative Proteome Analysis of <i>Leishmania donovani</i> under Spermidine Starvation. 2016 , 11, e0154262	9
524	Whole Transcriptome Profiling Identifies CD93 and Other Plasma Cell Survival Factor Genes Associated with Measles-Specific Antibody Response after Vaccination. 2016 , 11, e0160970	15
523	Lumican and versican protein expression are associated with colorectal adenoma-to-carcinoma progression. 2017 , 12, e0174768	19
522	Network based stratification of major cancers by integrating somatic mutation and gene expression data. 2017 , 12, e0177662	8

521	Identification of key microRNAs and genes in preeclampsia by bioinformatics analysis. 2017 , 12, e0178549	32
520	Riboproteomics: A versatile approach for the identification of host protein interaction network in plant pathogenic noncoding RNAs. 2017 , 12, e0186703	1
519	Integrative analysis of super enhancer SNPs for type 2 diabetes. 2018 , 13, e0192105	8
518	Speeding up the drug discovery process: structural similarity searches using molecular surfaces. 2012 , 18, 6-9	3
517	The TP53 fertility network. 2012 , 35, 939-46	12
516	A decline in PABPN1 induces progressive muscle weakness in oculopharyngeal muscle dystrophy and in muscle aging. 2013 , 5, 412-26	33
515	Frailty in middle age is associated with frailty status and race-specific changes to the transcriptome. 2019 , 11, 5518-5534	10
514	Overexpressed pseudogenes, DUXAP8 and DUXAP9, promote growth of renal cell carcinoma and serve as unfavorable prognostic biomarkers. 2019 , 11, 5666-5688	23
513	Prognostic risk signature based on the expression of three m6A RNA methylation regulatory genes in kidney renal papillary cell carcinoma. 2020 , 12, 22078-22094	9
512	RWCFusion: identifying phenotype-specific cancer driver gene fusions based on fusion pair random walk scoring method. 2016 , 7, 61054-61068	4
511	In-depth phenotyping of lymphoblastoid cells suggests selective cellular vulnerability in Marinesco-Sjögren syndrome. 2017 , 8, 68493-68516	14
510	Overexpression of AGT promotes bronchopulmonary dysplasia via the JAK/STAT signal pathway. 2017 , 8, 96079-96088	7
509	Construction of key signal regulatory network in metastatic colorectal cancer. 2018 , 9, 6086-6094	11
508	Network analysis of microRNAs, genes and their regulation in diffuse and follicular B-cell lymphomas. 2018 , 9, 7928-7941	9
507	Identification of prefrontal cortex protein alterations in Alzheimer's disease. 2018 , 9, 10847-10867	19
506	New insights into the genetics of glioblastoma multiforme by familial exome sequencing. 2015 , 6, 5918-31	19
505	Control of glioma cell migration and invasiveness by GDF-15. 2016 , 7, 7732-46	31
504	Systematic drug perturbations on cancer cells reveal diverse exit paths from proliferative state. 2016 , 7, 7415-25	11

503	Dissecting dysfunctional crosstalk pathways regulated by miRNAs during glioma progression. 2016 , 7, 25769-82	6
502	KCNN4 and S100A14 act as predictors of recurrence in optimally debulked patients with serous ovarian cancer. 2016 , 7, 43924-43938	24
501	Serum Proteomic Profiling of Obsessive-Compulsive Disorder, Washing Subtype: A Preliminary Study. 2017 , 8, 307-316	5
500	Mapping of Protein-Protein Interactions: Web-Based Resources for Revealing Interactomes. 2019 , 26, 3890-3910	8
499	In-Silico Identification of Drug Lead Molecule Against Pesticide Exposed-neurodevelopmental Disorders Through Network-Based Computational Model Approach. 2019 , 14, 460-467	13
498	Identification of Potential Molecular Mechanisms and Candidate Genes Involved in The Acute Phase of Myocardial Infarction. 2018 , 20, 435-442	5
497	ETS2 and microRNA-155 regulate the pathogenesis of heart failure through targeting and regulating GPR18 expression. 2020 , 19, 3469-3478	3
496	Prediction of crucial epigenetically-associated, differentially expressed genes by integrated bioinformatics analysis and the identification of S100A9 as a novel biomarker in psoriasis. 2020 , 45, 93-102	11
495	Identification of biomarkers and construction of a microRNA-mRNA regulatory network for ependymoma using integrated bioinformatics analysis. 2019 , 18, 6079-6089	4
494	Reduced expression of microRNA-139-5p in hepatocellular carcinoma results in a poor outcome: An exploration the roles of microRNA-139-5p in tumorigenesis, advancement and prognosis at the molecular biological level using an integrated meta-analysis and bioinformatic investigation. 2019 , 18, 6704-6724	2
493	Multiple functions of TBCK protein in neurodevelopment disorders and tumors. 2021 , 21, 17	5
492	Integrative analysis of mRNA and miRNA expression profiles reveals seven potential diagnostic biomarkers for non-small cell lung cancer. 2020 , 43, 99-112	15
491	Proteomic analysis of the anticancer effect of various extracts of endemic <i>Thermopsis turcica</i> in human cervical cancer cells. 2020 , 50, 1993-2004	1
490	Biosynthesis of Autoinducer-2 as the Possible Mechanism to Enhance Decolourisation of Azo Dye by <i>Citrobacter freundii</i> A1. 2012 , 12, 91-97	1
489	Identification and analysis of biomarkers for mismatch repair proteins: A bioinformatic approach. 2012 , 3, 139-46	6
488	Unfoldomics of prostate cancer: on the abundance and roles of intrinsically disordered proteins in prostate cancer. 2016 , 18, 662-72	5
487	Novel network biomarkers profile based coronary artery disease risk stratification in Asian Indians. 2013 , 2, 59	6
486	Identification of biomarkers and mechanisms of diabetic cardiomyopathy using microarray data. 2020 , 27, 807-816	3

485	In Silico Structural and Functional Annotation of Hypothetical Proteins of <i>Vibrio cholerae</i> O139. 2015 , 13, 53-9	25
484	Drug Target Identification and Elucidation of Natural Inhibitors for : An Study. 2016 , 14, 241-254	6
483	Functional Prediction of Hypothetical Proteins from <i>Shigella flexneri</i> and Validation of the Predicted Models by Using ROC Curve Analysis. 2018 , 16, e26	5
482	Identification of Dysregulated Pathways Associated with Ankylosing Spondylitis Using Pathway Interaction Network. 2017 , 19,	1
481	Computational analysis of Concanavalin A binding glycoproteins of human seminal plasma. 2011 , 7, 69-75	4
480	Homology modeling, docking studies and functional analysis of various azoreductase accessory interacting proteins of <i>Nostoc</i> sp.PCC7120. 2012 , 8, 296-300	6
479	Qualitative and Quantitative analysis of 3D predicted arachidonate 15-lipoxygenase-B (15-LOX-2) from <i>Homo sapiens</i> . 2012 , 8, 555-61	5
478	Computational structural and functional analysis of hypothetical proteins of <i>Staphylococcus aureus</i> . 2012 , 8, 722-8	22
477	Novel genes underlying beta cell survival in metabolic stress. 2013 , 9, 37-41	13
476	A two-step drug repositioning method based on a protein-protein interaction network of genes shared by two diseases and the similarity of drugs. 2013 , 9, 89-93	23
475	Microarray Integrated Analysis of a Gene Network for the CD36 Myocardial Phenotype. 2016 , 12, 332-339	1
474	Net2Align: An Algorithm For Pairwise Global Alignment of Biological Networks. 2016 , 12, 408-411	3
473	MicroRNA expression profile analysis reveals diagnostic biomarker for human prostate cancer. 2012 , 13, 3313-7	18
472	Screening of differentially expressed genes related to bladder cancer and functional analysis with DNA microarray. 2013 , 14, 4553-7	8
471	Binding Pattern Elucidation of NNK and NNAL Cigarette Smoke Carcinogens with NER Pathway Enzymes: an Onco- Informatics Study. 2015 , 16, 5311-7	8
470	The deca-GX3 proteins Yae1-Lto1 function as adaptors recruiting the ABC protein Rli1 for iron-sulfur cluster insertion. 2015 , 4, e08231	42
469	Human Nup98 regulates the localization and activity of DEXH/D-box helicase DHX9. 2017 , 6,	21
468	DGPathinter: a novel model for identifying driver genes via knowledge-driven matrix factorization with prior knowledge from interactome and pathways. 3, e133	3

467	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. 2015 , 3, e1265	7
466	Malleable ribonucleoprotein machine: protein intrinsic disorder in the <i>Saccharomyces cerevisiae</i> spliceosome. 2013 , 1, e2	30
465	Biblio-MetReS for user-friendly mining of genes and biological processes in scientific documents. 2014 , 2, e276	3
464	Identifying genes and regulatory pathways associated with the scleractinian coral calcification process. 2017 , 5, e3590	10
463	ksrMKL: a novel method for identification of kinase-substrate relationships using multiple kernel learning. 2017 , 5, e4182	3
462	Increased chemical acetylation of peptides and proteins in rats after daily ingestion of diacetyl analyzed by Nano-LC-MS/MS. 2018 , 6, e4688	2
461	Identification of primary genes in glomeruli compartment of immunoglobulin A nephropathy by bioinformatic analysis. 2019 , 7, e7067	2
460	A reproducible approach to high-throughput biological data acquisition and integration. 2015 , 3, e791	11
459	Effects of Wild Yam Root () Extract on the Gene Expression Profile of Triple-negative Breast Cancer Cells. 2021 , 18, 735-755	0
458	Exploring the mechanism of Jianpi Qushi Huayu Formula in the treatment of chronic glomerulonephritis based on network pharmacology. 2021 , 394, 2451-2470	2
457	Screening Hub Genes of Hepatocellular Carcinoma Based on Public Databases. 2021 , 2021, 7029130	1
456	Identification of a Novel Pyroptosis-Related Gene Signature for Predicting Prognosis in Bladder Cancer. 2021 , 1-17	2
455	Genome-Wide Analysis of Major Facilitator Superfamily and Its Expression in Response of Poplar to. 2021 , 12, 769888	0
454	Ferroptosis-Related Genes in Bronchoalveolar Lavage Fluid Serves as Prognostic Biomarkers for Idiopathic Pulmonary Fibrosis. 2021 , 8, 693959	2
453	S-Carboxymethyl Cysteine Protects against Oxidative Stress and Mitochondrial Impairment in a Parkinson's Disease In Vitro Model. 2021 , 9,	2
452	Study of Clinical Predictive Value and Immune Characterization of SLFN11 in Clear Cell Renal Cell Carcinoma. 2021 , 14, 6741-6754	0
451	Development and validation of a ferroptosis-related prognostic model for the prediction of progression-free survival and immune microenvironment in patients with papillary thyroid carcinoma. 2021 , 101, 108156	1
450	Protein-Protein Interaction Network Inference. 2004 ,	

- 449 SNPboost: Interaction Analysis and Risk Prediction on GWA Data. **2011**, 111-118
- 448 Genome-wide Association Study Identification of a New Genetic Locus with Susceptibility to Osteoporotic Fracture in the Korean Population. **2011**, 9, 52-58 2
- 447 Genome-wide Association Study Identified TIMP2 Genetic Variant with Susceptibility to Osteoarthritis. **2011**, 9, 121-126 1
- 446 References. 157-176
- 445 Web-Based Computational System for Protein-Protein Interaction Inference. **2012**, 8, 459-470 2
- 444 Protein Family Databases.
- 443 Systems Biology Study of Yeast Mitogen Activated Protein Kinase (MAPK) Cascade for Novel Drug Target Identification against Fungal Pathogens. **2013**, 149-153
- 442 Semi-Global Inference in Phenotype-Protein Network. **2013**, 05, 181-188
- 441 On Different Aspects of Network Analysis in Systems Biology. **2013**, 181-207 3
- 440 Active Learning for Protein Function Prediction in Protein-Protein Interaction Networks. **2013**, 172-183
- 439 Bioinformation editorial erratum. **2013**, 9, 168
- 438 Helicases. **2013**, 1-13
- 437 Quantitative Characterization of Protein Networks of the Oral Cavity. **2013**, 61-68
- 436 Lateral Gene Transfer and the Synthesis of Thymidine. **2013**, 3-14 0
- 435 Text Mining in Medicine. **2013**, 105-134
- 434 Biologia de Sistemas de Pectinases do Fungo *Moniliophthora perniciosa*. **2013**, 11, 27-30
- 433 TRPP2 in Polycystic Kidney Disease. **2014**, 491-522
- 432 Bioinformatics for proteomics: opportunities at the interface between the scientists, their experiments, and the community. **2014**, 1156, 239-48

431 Analysis of Chaperone Network Throughput. **2014**, 3-23

430 Molecular Networks [Representation and Analysis. **2014**, 399-418

429 OMICS for Tumor Biomarker Research. **2014**, 1-22

428 Identification of Synchronized Role of Transcription Factors, Genes, and Enzymes in Arabidopsis thaliana under Four Abiotic Stress Responsive Pathways. **2014**, 2014, 1-13

1

427 Porosome in Cystic Fibrosis. **2014**, 2,

0

426 Network based meta-analysis prediction of microenvironmental relays involved in stemness of human embryonic stem cells. **2014**, 2, e618

1

425 Systems Approaches to Study Infectious Diseases. **2015**, 151-172

424 HOODS: finding context-specific neighborhoods of proteins, chemicals and diseases. **2015**, 3, e1057

1

423 Genetics of Peptidoglycan Biosynthesis. 511-533

422 Genetic heterogeneity in autism: from single gene to a pathway perspective.

421 Structural and Functional View of Polypharmacology.

2

420 Structure, interaction and post-translational modification study of arsenic reduction system in Bifidobacterium longum.

419 Network Modules Driving Plant Stress Response, Tolerance and Adaptation: A case study using Abscisic acid Induced Protein-protein Interactome of Arabidopsis thaliana.

418 Mechanism-based disease similarity. **2016**, 1, 1-4

2

417 Integrating Multidimensional Data Sources to Identify Genes Regulating Complex Phenotypes. **2017**, 1488, 239-250

416 Structure Modeling and Molecular Docking Studies of Schizophrenia Candidate Genes, Synapsins 2 (SYN2) and Trace Amino Acid Receptor (TAAR6). **2017**, 291-301

1

415 Background. **2017**, 9-21

414 Cancer Specific Non-Synonymous Single Nucleotide Polymorphism Prediction in the Context of Haplotype and Protein Interacting Sites. **2017**, 10, 28-44

- 413 Chromone scaffold-mediated reprogramming of the epithelial-mesenchymal transition prevents fibrosis.
- 412 Cellular responses to proteostasis perturbations reveal non-optimal feedback in chaperone networks. 1
- 411 A Novel Method to Identify Differential Pathways in Hippocampus Alzheimer's Disease. **2017**, 23, 2179-2188
- 410 Evaluating Protein Complex Prediction Methods. **2017**, 91
- 409 Identifying Evolutionarily Conserved Protein Complexes. **2017**, 165
- 408 Identifying Dynamic Protein Complexes. **2017**, 145
- 407 Introduction to Protein Complex Prediction. **2017**, 1
- 406 Open Challenges in Protein Complex Prediction. **2017**, 107
- 405 Preface. **2017**, xi
- 404 References. **2017**, 233
- 403 Computational Methods for Protein Complex Prediction from PPI Networks. **2017**, 59
- 402 Protein Complex Prediction in the Era of Systems Biology. **2017**, 185
- 401 Conclusion. **2017**, 225
- 400 Post-transcriptional remodelling is temporally deregulated during motor neurogenesis in human ALS models.
- 399 Sporulation-specific cell division defects in ylmE mutants of *Streptomyces coelicolor* are rescued by additional deletion of ylmD.
- 398 ALPK1 and TIFA Dependent Innate Immune Response Triggered by the *Helicobacter pylori* Type IV Secretion System.
- 397 Spatio-Temporal Gene Discovery For Autism Spectrum Disorder.
- 396 A prize-collecting Steiner tree application for signature selection to stratify diffuse large B-cell lymphoma subtypes. 1

- 395 Exploring the Molecular Mechanism of Thoracic Aortic Aneurysm via Bioinformatics Analysis. **2018**, 24, 1533-1539 1
- 394 Interaction paths promote module integration and network-level robustness of spliceosome to cascading effects.
- 393 Semantic Disease Gene Embeddings (SmuDGE): phenotype-based disease gene prioritization without phenotypes.
- 392 Proteomics reveals ablation of placental growth factor inhibits the insulin resistance pathways in diabetic mouse retina.
- 391 Proteomics study of the antifibrotic effects of ß-mangostin in a rat model of renal fibrosis. **2019**, 12, 149-160
- 390 Biomarker identification of thyroid associated ophthalmopathy using microarray data. **2018**, 11, 1482-1488 2
- 389 Protein Network Analysis to Prioritize Key Genes and Pathway for Stress-Mediated Neurodegeneration. **2018**, 11, 240-251 3
- 388 Next-Generation Genome-Scale Models Incorporating Multilevel 'Omics Data: From Yeast to Human. **2019**, 2049, 347-363 0
- 387 Allele-specific silencing ameliorates restrictive cardiomyopathy due to a human myosin regulatory light chain mutation. 0
- 386 Effect of Intestinal Flora Clearance on Liver Proteomics in Mice. **2019**, 16, 199-209
- 385 Quantitative proteomics identifies novel PIAS1 substrates involved in cell migration and motility.
- 384 Microarray-based differential expression profiling of long noncoding RNAs and messenger RNAs in formalin-fixed paraffin-embedded human papillary thyroid carcinoma samples.. **2019**, 8, 439-451
- 383 The Ras family members follow the blood progesterone level during formation and regression in bovine corpus luteum.
- 382 Verify Hub Genes of expression profile in aortic dissection.
- 381 Fishing for vaccines against using pan-proteomic reverse vaccinology approach. **2019**, 7, e6223 4
- 380 Bioinformatics analysis of hepatic gene expression profiles in type 2 diabetes mellitus. **2019**, 18, 4303-4312 1
- 379 RUN-ONCO. **2019**,
- 378 SingleCellSignalR: Inference of intercellular networks from single-cell transcriptomics. 1

- 377 Identification for Exploring Underlying Pathogenesis and Therapy Strategy of Oral Squamous Cell Carcinoma by Bioinformatics Analysis. **2019**, 25, 9216-9226 1
- 376 Porosome: Cells Secretory Nanomachine. **2020**, 1-39
- 375 Integrative analysis of outer membrane vesicles proteomics and whole-cell transcriptome analysis of eravacycline induced *Acinetobacter baumannii* strains.
- 374 Comprehensive analysis of long non-coding RNAs and mRNAs in skeletal muscle of diabetic Goto-Kakizaki rats during the early stage of type 2 diabetes. **2020**, 8, e8548 0
- 373 Extensive In Silico Analysis of the Functional and Structural Consequences of SNPs in Human ARX Gene.
- 372 UBTD1 regulates ceramide balance and endolysosomal positioning to coordinate EGFR signaling.
- 371 Identification of SPRR3 as a novel diagnostic/prognostic biomarker for oral squamous cell carcinoma via RNA sequencing and bioinformatic analyses. **2020**, 8, e9393 4
- 370 Overexpression of novel long intergenic non-coding RNA LINC02454 is associated with a poor prognosis in papillary thyroid cancer. **2020**, 44, 1489-1501 6
- 369 Identification of prognostic biomarkers associated with tumor microenvironment in ceRNA network for esophageal squamous cell carcinoma: a bioinformatics study based on TCGA database.. **2021**, 12, 46 0
- 368 Characterization of genome-wide association study data reveals spatiotemporal heterogeneity of mental disorders. **2020**, 13, 192 0
- 367 iDMer: an integrative and mechanism-driven response system for identifying compound interventions for sudden virus outbreak. **2021**, 22, 976-987 1
- 366 Drug compound prediction-based analysis of cigarette smoking to Pancreatic Cancer patients: A Bioinformatics study. **2020**,
- 365 Muscle Recovery Is Highlighted by IR Laser Therapy. **2019**, 10, S49-S53 3
- 364 Integrative analysis of outer membrane vesicles proteomics and whole-cell transcriptome analysis of eravacycline induced *Acinetobacter baumannii* strains.
- 363 Integrative analysis of outer membrane vesicles proteomics and whole-cell transcriptome analysis of eravacycline induced *Acinetobacter baumannii* strains.
- 362 Unraveling the genetic causes in large pedigrees with gout by whole-exome sequencing. **2020**, 45, 1047-1058
- 361 Atg5 Regulates Selective Autophagy of the Parental Macronucleus during Sexual Reproduction. **2021**, 10, 0
- 360 Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. **2021**, 12, 783128 1

- 359 Prognostic Model and Nomogram Construction Based on a Novel Ferroptosis-Related Gene Signature in Lower-Grade Glioma. **2021**, 12, 753680 3
- 358 Identification of differentially expressed genes associated with precocious puberty by suppression subtractive hybridization in goat pituitary tissues. **2021**, 1-14
- 357 Creatine utilization as a sole nitrogen source in *Pseudomonas putida* KT2440 is transcriptionally regulated by CahR.
- 356 TRIAGE: A web-based iterative analysis platform integrating pathway and network approaches optimizes hit selection from high-throughput assays.
- 355 BioKG. **2020**, 2
- 354 StrongestPath: a Cytoscape application for protein-protein interaction analysis.
- 353 Methods, challenges, and promise of next-generation sequencing in cancer biology. **2011**, 84, 439-46 13
- 352 *Gastrodia elata* Blume (tianma) mobilizes neuro-protective capacities. **2012**, 3, 219-41 19
- 351 Functional Analysis and Molecular Docking studies of Medicinal Compounds for AChE and BChE in Alzheimer's Disease and Type 2 Diabetes Mellitus. **2013**, 4, 186-200 1
- 350 Sharing information to reconstruct patient-specific pathways in heterogeneous diseases. **2014**, 39-50 4
- 349 Probing the unknowns in cytokinin-mediated immune defense in *Arabidopsis* with systems biology approaches. **2014**, 8, 35-44 5
- 348 Analysis of the placental tissue transcriptome of normal and preeclampsia complicated pregnancies. **2014**, 6, 71-83 11
- 347 Screening feature genes of osteosarcoma with DNA microarray: a bioinformatic analysis. **2015**, 8, 7134-42 2
- 346 Gene function analysis in osteosarcoma based on microarray gene expression profiling. **2015**, 8, 10401-10 9
- 345 Mutation near the binding interfaces at hemoglobin stabilizing protein is highly pathogenic. **2016**, 8, 4224-4232 12
- 344 Interactome analysis of gene expression profiles of cervical cancer reveals dysregulated mitotic gene clusters. **2017**, 9, 3048-3059 13
- 343 Computational Analysis of High Risk Missense Variant in Human UTY Gene: A Candidate Gene of AZFa Sub-region. **2017**, 18, 298-306 6
- 342 A systems biology analysis protein-protein interaction of NASH and IBD based on comprehensive gene information. **2017**, 10, 194-201 23

341	Protein-protein interaction analysis of Alzheimer's disease and NAFLD based on systems biology methods unhide common ancestor pathways. 2018 , 11, 27-33	20
340	MicroRNAs and regulated interaction networks reveal differences between adult and pediatric acute myeloid leukemia. 2017 , 10, 10576-10583	
339	Development of RNA binding proteins expression signature for prognosis prediction in gastric cancer patients. 2020 , 12, 6775-6792	1
338	Laryngeal squamous cell carcinoma cell lines show high tolerance for siRNA-mediated CDK1 knockdown. 2021 , 11, 2081-2094	1
337	Prediction of Key Proteins Via Topological Analysis of Protein-Protein Interaction Network. 2018 , 7, e1129	1
336	Construction of Risk Prediction Model for Pyroptosis Related Genes in Pancreatic Adenocarcinoma. 2021 , 11, 5304-5312	
335	Computational detection, analysis and interpretations of genomic variants in human diseases associated GENEMDM 2. 2021 , 7, 141-154	
334	Protein-protein interactions: Methods, databases, and applications in virus-host study.. 2021 , 10, 288-300	0
333	Effect of APOB polymorphism rs562338 (G/A) on serum proteome of coronary artery disease patients: a "proteogenomic" approach. 2021 , 11, 22766	
332	In Silico Prediction of Potential Drug Combinations for Type 2 Diabetes Mellitus by an Integrated Network and Transcriptome Analysis. 2021 ,	
331	Bulk Gene Expression Deconvolution Reveals Infiltration of M2 Macrophages in Retinal Neovascularization. 2021 , 62, 22	0
330	Intraocular Viral Communities Associated With Post-fever Retinitis. 2021 , 8, 724195	3
329	analysis of variants demonstrates main contribution to congenital heart disease.. 2021 , 13, 336-354	0
328	Network based analysis identifies TP53m-BRCA1/2wt-homologous recombination proficient (HRP) population with enhanced susceptibility to Vigil immunotherapy. 2021 ,	1
327	Identification and Integrate Analysis of Key Biomarkers for Diagnosis and Prognosis of Non-Small Cell Lung Cancer Based on Bioinformatics Analysis. 2021 , 20, 15330338211060202	3
326	The Increased Neuromedin B Is Associated with Poor Prognosis in Glioblastoma Multiforme.	
325	Uncovering the mechanism of quercetin for treating spermatogenesis impairment by a network pharmacology approach. 2021 , 14, 699-708	
324	Waves of sumoylation support transcription dynamics during adipocyte differentiation.. <i>Nucleic Acids Research</i> , 2022 ,	20.1 1

323	Impaired generation of mature neurons due to extended expression of Tlx by repressing Sox2 transcriptional activity. 2021 , 39, 1520-1531	1
322	Amphotericin B resistance in <i>Leishmania mexicana</i> : Alterations to sterol metabolism, lipid transport and oxidative stress response.	0
321	Identification of Potential Prognostic Biomarkers Associated With Macrophage M2 Infiltration in Gastric Cancer.. 2021 , 12, 827444	2
320	The effects of sequencing depth on the assembly of coding and noncoding transcripts in the human genome.	
319	Erythropoietin Interacts with Specific S100 Proteins.. 2022 , 12,	0
318	Path to Clonal Theranostics in Luminal Breast Cancers.. 2021 , 11, 802177	1
317	Identification of mRNA-miRNA-lncRNA regulatory network associated with the immune response to <i>Aeromonas salmonicida</i> infection in the black rockfish (<i>Sebastes schlegelii</i>).. 2022 , 104357	0
316	Analysis of Microarray Data from Medulloblastoma Tissue Samples.. 2022 , 2423, 59-64	
315	Kinome Analysis of Cattle Peripheral Lymph Nodes to Elucidate Differential Response to spp.. 2022 , 10,	1
314	An 8-ferroptosis-related genes signature from Bronchoalveolar Lavage Fluid for prognosis in patients with idiopathic pulmonary fibrosis.. 2022 , 22, 15	0
313	Cation/Proton Antiporter Genes in Tomato: Genomic Characterization, Expression Profiling, and Co-Localization with Salt Stress-Related QTLs. 2022 , 12, 245	0
312	The genes for sensory perception of sound should be considered in gene diagnosis of congenital sensorineural hearing loss and microtia.. 2022 , 63, 327	
311	Identification of immunophenotypes in esophageal squamous cell carcinoma based on immune gene sets.. 2022 , 1	
310	Genome survey sequence of black carp provides insights into development-related gene duplications.	
309	NetSeekR: a network analysis pipeline for RNA-Seq time series data.. 2022 , 23, 54	1
308	qPCR Analysis Reveals Association of Differential Expression of , , and Genes With Type 2 Diabetes Mellitus.. 2021 , 12, 774696	
307	Trh positive strain of <i>Vibrio parahaemolyticus</i> induce immunity by modulating MAPK pathway: A molecular pathogenic insight in immune-related gene regulation.. 2022 , 164, 105436	1
306	The aqueous humor proteome is intrinsically disordered.. 2022 , 29, 101202	

305	HIF-1 β inhibition promotes the efficacy of immune checkpoint blockade in the treatment of non-small cell lung cancer.. 2022 ,	4
304	Identification of miRNA and their target genes in L. and L. in stress responses.. 2022 , 28, 31-49	0
303	A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis.	2
302	A Novel Prognostic Signature Based on Ferroptosis-Related Genes Predicts the Prognosis of Patients With Advanced Bladder Urothelial Carcinoma.. 2021 , 11, 726486	0
301	Evolution and emergence: higher order information structure in protein interactomes across the tree of life.. 2021 ,	2
300	Identification of Potential Immune Checkpoint Inhibitor Targets in Gliomas via Bioinformatic Analyses.. 2022 , 2022, 1734847	0
299	Reactive astrocytes transduce blood-brain barrier dysfunction through a TNF β STAT3 signaling axis and secretion of alpha 1-antichymotrypsin.	1
298	Interferon- γ Activity Is Affected by S100B Protein.. 2022 , 23,	0
297	Clinical Prognostic Value of the Gene Family in Lung Adenocarcinoma.. 2021 , 8, 770729	1
296	Combination of ferroptosis and pyroptosis to construct a prognostic classifier and predict immune landscape, chemotherapeutic efficacy and immunosuppressive molecules in hepatocellular carcinoma.. 2022 , 22, 229	2
295	PCBP2 maintains antiviral signaling homeostasis by regulating cGAS enzymatic activity via antagonizing its condensation.. 2022 , 13, 1564	3
294	Comprehensive analysis of ferroptosis-related genes and prognosis of cutaneous melanoma.. 2022 , 15, 39	0
293	In silico analysis and experimental validation to exhibit anti-nasopharyngeal carcinoma effects of plumbagin, an anti-cancer compound.. 2022 ,	
292	RAGE is a potential biomarker implicated in immune infiltrates and cellular senescence in lung adenocarcinoma.. 2022 , e24382	0
291	CCDC134 as a Prognostic-Related Biomarker in Breast Cancer Correlating With Immune Infiltrates.. 2022 , 12, 858487	0
290	Identification of Key microRNAs and Genes in Infantile Hemangiomas.. 2022 , 13, 766561	0
289	Otto Aufranc Award: Identification of Key Molecular Players in the Progression of Hip Osteoarthritis through Transcriptomes and Epigenetics.. 2022 ,	0
288	The Key Genes Underlying Pathophysiology Correlation Between the Acute Myocardial Infarction and COVID-19.. 2022 , 15, 2479-2490	2

287	Protein interaction networks provide insight into fetal origins of chronic obstructive pulmonary disease.. 2022 , 23, 69	0
286	Multiple types of noncoding RNA are involved in potential modulation of PTTG1's expression and function in breast cancer.. 2022 , 110352	
285	RAB2A promotes cervical cancer progression as revealed by comprehensive analysis of HPV integration and proteome in longitudinal cervical samples.. 2022 , 12, e767	
284	Whole-genome sequencing reveals novel ethnicity-specific rare variants associated with Alzheimer's disease.. 2022 ,	3
283	Computational Identification of Guillain-Barré Syndrome-Related Genes by an mRNA Gene Expression Profile and a Protein-Protein Interaction Network.. 2022 , 15, 850209	
282	An Integrative Multi-Omics Analysis Reveals MicroRNA-143 as Potential Therapeutics to Attenuate Retinal Angiogenesis.. 2022 ,	0
281	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications.. 2022 , 10, e13061	0
280	Bioinformatics Screening of Potential Biomarkers from mRNA Expression Profiles to Discover Drug Targets and Agents for Cervical Cancer.. 2022 , 23,	4
279	Gene and protein interaction network analysis in the epithelial-mesenchymal transition of Hertwig's Epithelial Root Sheath reveals periodontal regenerative drug targets [An in silico study. 2022 , 29, 3822-3829	0
278	A Proximal Alternating-direction-method-of-multipliers-based Nonnegative Latent Factor Model. 2021 ,	2
277	Integrated transcriptomic and metabolomic analysis of rat serum to investigate potential target of puerarin in the treatment post-traumatic stress disorder.. 2021 , 9, 1771	0
276	Interaction of host factors in response to yeast K2 toxin stress [attractiveness for plant protection. 2021 , 108, 313-320	
275	PI4-kinase and PfCDPK7 signaling regulate phospholipid biosynthesis in Plasmodium falciparum. 2021 , e54022	2
274	Therapeutic potential of methylxanthine drug on alpha synuclein protein in Parkinson's disease.	
273	Circulating extracellular vesicles and rheumatoid arthritis: a proteomic analysis.. 2021 , 79, 1	2
272	QTL and candidate gene identification of the node of the first fruiting branch (NFFB) by QTL-seq in upland cotton (<i>Gossypium hirsutum</i> L.). 2021 , 22, 882	0
271	Mechanism of Elian granules in the treatment of precancerous lesions of gastric cancer in rats through the MAPK signalling pathway based on network pharmacology.. 2022 , 60, 87-95	5
270	Protein Function Prediction Based on PPI Networks: Network Reconstruction vs Edge Enrichment.. 2021 , 12, 758131	0

269 prediction and interaction of resveratrol on methyl-CpG binding proteins by molecular docking and MD simulations study.. **2022**, 12, 11493-11504

268 Comparative transcriptomic analysis and antioxidant defense mechanisms in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.) genotypes with contrasting drought tolerance.. **2022**, ○

267 Application of modular response analysis to medium- to large-size biological systems.. **2022**, 18, e1009312

266 MAGI-MS: Multiple seed-centric module discovery.

265 Data_Sheet_1.pdf. **2019**,

264 Table_1.DOC. **2019**,

263 Table_2.DOC. **2019**,

262 Table_3.DOC. **2019**,

261 Table_4.DOC. **2019**,

260 Table_5.DOC. **2019**,

259 Image_1.PDF. **2018**,

258 Table_1.docx. **2018**,

257 Table_2.docx. **2018**,

256 Table_3.docx. **2018**,

255 Table_4.docx. **2018**,

254 Table_5.docx. **2018**,

253 Image1.TIF. **2018**,

252 Image2.TIF. **2018**,

251 Image_1.tif. **2020**,

250 Table_1.xls. **2020**,

249 Table_2.xls. **2020**,

248 Table_3.xls. **2020**,

247 Table_4.xls. **2020**,

246 Image1.JPEG. **2018**,

245 Image2.JPEG. **2018**,

244 Table1.xlsx. **2018**,

243 Data_Sheet_1.zip. **2020**,

242 Image_1.PNG. **2020**,

241 Image_2.pdf. **2020**,

240 Table_1.XLSX. **2020**,

239 Table_2.XLSX. **2020**,

238 Table_3.XLSX. **2020**,

237 Table_4.XLSX. **2020**,

236 DataSheet_1.pdf. **2019**,

235 Image_1.JPEG. **2019**,

234 Image_2.JPEG. **2019**,

233 Table_1.DOCX. 2019,

232 Table_2.DOCX. 2019,

231 Table_3.DOCX. 2019,

230 Table_4.DOCX. 2019,

229 Table_5.DOCX. 2019,

228 Table_6.DOCX. 2019,

227 Table_7.DOCX. 2019,

226 Data_Sheet_1.pdf. 2018,

225 Image_1.tif. 2020,

224 Table_1.xlsx. 2020,

223 Table_2.xlsx. 2020,

222 Table_3.xlsx. 2020,

221 Table_4.xlsx. 2020,

220 Table_1.XLSX. 2020,

219 Table_2.XLSX. 2020,

218 Table_1.xlsx. 2019,

217 Table_1.XLSX. 2020,

216 Table_2.XLSX. 2020,

215 Table_3.XLSX. 2020,

214 Table_4.XLSX. 2020,

213 Table_5.XLSX. 2020,

212 Image_1.TIF. 2020,

211 Image_2.TIF. 2020,

210 Table_1.DOC. 2020,

209 Table_2.DOC. 2020,

208 Table_3.DOC. 2020,

207 Table_4.DOC. 2020,

206 Table_5.DOC. 2020,

205 Table1.XLS. 2018,

204 Table10.XLS. 2018,

203 Table11.XLSX. 2018,

202 Table2.XLS. 2018,

201 Table3.XLS. 2018,

200 Table4.XLSX. 2018,

199 Table5.XLS. 2018,

198 Table6.XLSX. 2018,

197 Table7.XLSX. 2018,

196 Table8.XLSX. 2018,

195 Table9.XLS. 2018,

194 Table_1.xls. 2018,

193 Table_2.xls. 2018,

192 Table_3.xls. 2018,

191 Table_4.xls. 2018,

190 Table_5.xls. 2018,

189 Table_6.xls. 2018,

188 Table_1.xlsx. 2018,

187 Table_10.xlsx. 2018,

186 Table_11.xlsx. 2018,

185 Table_2.xlsx. 2018,

184 Table_3.xlsx. 2018,

183 Table_4.xlsx. 2018,

182 Table_5.xlsx. 2018,

181 Table_6.xlsx. 2018,

180 Table_7.xlsx. 2018,

179 Table_8.xlsx. **2018**,

178 Table_9.xlsx. **2018**,

177 Glycation modulates glutamatergic signaling and exacerbates Parkinson's disease-like phenotypes.. **2022**, 8, 51 0

176 What Is Parvalbumin for?. **2022**, 12, 656 2

175 Identification of the Pyroptosis-Related Prognosis Gene Signature and Immune Infiltration in Hepatocellular Carcinoma.. **2022**, 2022, 9124216 1

174 Cell type-specific response of colon cancer tumor cell lines to oncolytic HSV-1 virotherapy in hypoxia.. **2022**, 22, 164 0

173 Identification of Immunological Characteristics and Immune Subtypes Based on Single-Sample Gene Set Enrichment Analysis Algorithm in Lower-Grade Glioma. **2022**, 13, 1

172 Identification of a new five-gene risk score for risk stratification and prognosis prediction in HCC.. **2022**, 1-19 0

171 Distribution of Common and Rare Genetic Markers of Second-Line-Injectable-Drug Resistance in Mycobacterium tuberculosis Revealed by a Genome-Wide Association Study.. **2022**, e0207521

170 Efficient Simultaneous Introduction of Premature Stop Codons in Three Tumor Suppressor Genes in PFFs via a Cytosine Base Editor. **2022**, 13, 835 1

169 Genome-Wide Association Study of Phenylalanine Derived Glucosinolates in .. **2022**, 11, 0

168 Bioinformatics-Based Approaches to Study Virus-Host Interactions During SARS-CoV-2 Infection.. **2022**, 2452, 197-212 0

167 PRKCB is relevant to prognosis of lung adenocarcinoma through methylation and immune infiltration.. **2022**,

166 Visual barcodes for clonal-multiplexing of live microscopy-based assays.. **2022**, 13, 2725 0

165 Transcriptional ITPR3 as potential targets and biomarkers for human pancreatic cancer.. **2022**, 14,

164 FBXW7 isoform drives transcriptional activation of a proinflammatory TNF cluster in normal and malignant pro-B cells.

163 An Myh11 single lysine deletion causes aortic dissection by reducing aortic structural integrity and contractility. **2022**, 12, 0

162 Putative Biomarkers in Tears for Diabetic Retinopathy Diagnosis. **2022**, 9, 1

161	MLBioIGE: Integration and Interplay of Machine Learning and Bioinformatics Approach to Identify the Genetic Effect of SARS-COV-2 on Idiopathic Pulmonary Fibrosis Patients.	3
160	Multi-omics analysis reveals the mechanism of seed coat color formation in <i>Brassica rapa</i> L..	0
159	Elemeene regulates M1-M2 macrophage balance through the ERK/JNK/P38 MAPK signaling pathway. 2022 , 5,	2
158	Target and drug predictions for SARS-CoV-2 infection in hepatocellular carcinoma patients. 2022 , 17, e0269249	0
157	Analysis of microarray-identified genes and MicroRNAs associated with Trifluridine resistance in colorectal cancer. 2022 , 15, 636-648	
156	Microphysiological system for studying contractile differences in young, active, and old, sedentary adult derived skeletal muscle cells.	1
155	Exploring Drought-Responsive Crucial Genes in <i>Sorghum</i> .	
154	Comprehensive analysis reveals an arachidonic acid metabolism-related gene signature in patients with pancreatic ductal adenocarcinoma. 2022 , 46, 2241-2256	
153	Weighted Gene Co-Expression Network Analysis (WGCNA) Reveals the Functions of Syndecan-1 to Regulate Immune Infiltration by Influenced T Cells in Glioma. 13,	1
152	Presence of rare potential pathogenic variants in subjects under 65 years old with very severe or fatal COVID-19. 2022 , 12,	2
151	Genome-wide Meta-analysis Reveals New Gene Signatures and Potential Drug Targets of Hypertension.	
150	Quantitative Succinyl-Proteome Profiling of Turnip (<i>Brassica rapa</i> var. <i>rapa</i>) in Response to Cadmium Stress. 2022 , 11, 1947	0
149	Identification of hub genes and pathways in colitis-associated colon cancer by integrated bioinformatic analysis. 2022 , 23,	1
148	Comparative transcriptome analysis of differentially expressed genes and pathways in <i>Procambarus clarkii</i> (Louisiana crawfish) at different acute temperature stress. 2022 , 114, 110415	1
147	Genome-wide identification, expression analyses of Wuschel-related homeobox (WOX) genes in <i>Brachypodium distachyon</i> and functional characterization of BdWOX12. 2022 , 836, 146691	
146	Expression profile of radiotherapy sensitive genes and tumor-associated immune cell infiltration and prognosis in multiple human cancers. 2022 , 15, 5-11	
145	An integrated study of Shenling Baizhu San against hyperuricemia: Efficacy evaluation, core target identification and active component discovery. 2022 , 295, 115450	0
144	Functional Characterization of p53 in NPC C666-1 Cells by CRISPR-Based Gene Knockout and Transcriptome Sequencing.	

- 143 A Novel Cuproptosis-Related Gene Signature for Overall Survival Prediction in Patients with Hepatocellular Carcinoma.
- 142 Differential proteomics of placentas reveals metabolic disturbance and oxidative damage participate yak spontaneous miscarriage during late pregnancy. **2022**, 18,
- 141 Network Pharmacology and In Vivo Experimental Validation to Uncover the Renoprotective Mechanisms of Fangji Huangqi Decoction on Nephrotic Syndrome. **2022**, 2022, 1-17 ○
- 140 New Insights into Cypermethrin Insecticide Resistance Mechanisms of *Culex pipiens pallens* by Proteome Analysis. 1
- 139 A convolutional neural network model for survival prediction based on prognosis-related cascaded Wx feature selection. 1
- 138 Application of proteomics in shrimp and shrimp aquaculture. **2022**, 101015 ○
- 137 Development and Validation of an ADME-Related Gene Signature for Survival, Treatment Outcome and Immune Cell Infiltration in Head and Neck Squamous Cell Carcinoma. 13,
- 136 Prognostic value and potential biological functions of ferroptosis-related gene signature in bladder cancer. **2022**, 24, ○
- 135 BTC as a Novel Biomarker Contributing to EMT via the PI3K-AKT Pathway in OSCC. 13, ○
- 134 Mass Spectrometry-Based Peptide Profiling of Haemolymph from *Pterostichus melas* Exposed to Pendimethalin Herbicide. **2022**, 27, 4645 ○
- 133 Anlotinib Combined with Toripalimab as Second-Line Therapy for Advanced, Relapsed Gastric or Gastroesophageal Junction Carcinoma. 1
- 132 Proteomic Biomarkers of Kleine-Levin Syndrome. ○
- 131 Hepatitis C Virus Infection and Intrinsic Disorder in the Signaling Pathways Induced by Toll-Like Receptors. **2022**, 11, 1091 ○
- 130 Web-Based Protein Interactions Calculator Identifies Likely Proteome Coevolution with Alzheimer's Disease-Associated Proteins. **2022**, 13, 1346
- 129 Genome-wide identification of the pectin methylesterase inhibitor genes in *Brassica napus* and expression analysis of selected members. 13, ○
- 128 A Novel Cuproptosis-Related Gene Signature Predicts Survival Outcomes in Patients with Clear-Cell Renal Cell Carcinoma. **2022**, 260-269
- 127 Proteomic and physiological analyses to elucidate nitric oxide-mediated adaptive responses of barley under cadmium stress. ○
- 126 The RIPK family: expression profile and prognostic value in lung adenocarcinoma. **2022**, 14, 5946-5958

- 125 An Updated Genome Assembly Improves Understanding of the Transcriptional Regulation of Coloration in Midas Cichlid. 9, 0
- 124 Metadata analysis to explore hub of the hub-genes highlighting their functions, pathways and regulators for cervical cancer diagnosis and therapies. **2022**, 13, 1
- 123 A structural database of chain-chain and domain-domain interfaces of proteins. **2022**, 31, 0
- 122 Identification of novel salt tolerance-associated proteins from the secretome of *Enterococcus faecalis*. **2022**, 38, 0
- 121 Proteomics and bioinformatics analysis of follicular fluid from patients with polycystic ovary syndrome. 9, 0
- 120 Elevated expression of ISY1, APOA-1, SYNE1, MTG1, and MMP10 at HCC initiation: HCC specific protein network involving interactions of key regulators of lipid metabolism, EGFR signaling, MAPK, and splicing pathways. 0
- 119 Exploration of *Streptococcus* core genome to reveal druggable targets and novel therapeutics against *S. pneumoniae*. **2022**, 17, e0272945 0
- 118 Integrative analyses identify HIF-1 α as a potential protective role with immune cell infiltration in adamantinomatous craniopharyngioma. 13, 1
- 117 Bioinformatics analysis of mRNA profiles and identification of microRNA-mRNA network in CD4+ cells in seasonal allergic rhinitis. **2022**, 50, 030006052211139 0
- 116 ProteinPrompt: a webserver for predicting protein-protein interactions. 0
- 115 Intrinsically disordered BMP4 morphogen and the beak of the finch: Co-option of an ancient axial patterning system. **2022**, 219, 366-373 0
- 114 LncRNA C9orf139 can regulate the progression of esophageal squamous carcinoma by mediating the miR-661/HDAC11 axis. **2022**, 24, 101487 0
- 113 LONP1 downregulation with ageing contributes to osteoarthritis via mitochondrial dysfunction. **2022**, 191, 176-190 1
- 112 Polypharmacology in Old Drug Rediscovery: Drug Repurposing. **2022**, 535-592 0
- 111 Novel ferroptosis-related gene signature as a potential prognostic tool for gastric cancer. **2022**, 20, 1721727X2211227 0
- 110 Classification of pyroptosis patterns and construction of a novel prognostic model for prostate cancer based on bulk and single-cell RNA sequencing. 13, 0
- 109 RPNs Levels Are Prognostic and Diagnostic Markers for Hepatocellular Carcinoma. **2022**, 2022, 1-17 0
- 108 Identification of key genes with prognostic value in gastric cancer by bioinformatics analysis. 13, 0

107	Construction and validation model of necroptosis-related gene signature associates with immunity for osteosarcoma patients. 2022 , 12,	0
106	miR-21-5p/PRKCE axis implicated in immune infiltration and poor prognosis of kidney renal clear cell carcinoma. 13,	0
105	Subcellular Localization Prediction of Human Proteins Using Multifeature Selection Methods. 2022 , 2022, 1-12	0
104	Deep Sc-RNA sequencing decoding the molecular dynamic architecture of the human retina.	0
103	Amphotericin B resistance in <i>Leishmania mexicana</i> : Alterations to sterol metabolism and oxidative stress response. 2022 , 16, e0010779	1
102	Functional and Structural Impact of Deleterious Missense Single Nucleotide Polymorphisms in the NR3C1, CYP3A5, and TNF- α Genes: An In Silico Analysis. 2022 , 12, 1307	1
101	Determining the optimal stage for cryopreservation of human embryonic stem cell-derived retinal pigment epithelial cells. 2022 , 13,	1
100	Identification and verification of hub genes associated with the progression of non-small cell lung cancer by integrated analysis. 13,	0
99	G protein-coupled Receptor Contributions to Wing Growth and Morphogenesis in <i>Drosophila melanogaster</i> .	0
98	A 9-gene prognostic signature for kidney renal clear cell carcinoma overall survival based on co-expression and regression analyses.	0
97	The Ni(II)-Binding Activity of the Intrinsically Disordered Region of Human NDRG1, a Protein Involved in Cancer Development. 2022 , 12, 1272	0
96	Poor prognosis, hypomethylation, and immune infiltrates are associated with downregulation of INMT in head and neck squamous cell carcinoma. 13,	0
95	Genome-wide analysis suggests the potential role of lncRNAs during seed development and seed size/weight determination in chickpea. 2022 , 256,	0
94	A novel T-cell proliferation-associated regulator signature pre-operatively predicted the prognostic of bladder cancer. 13,	0
93	Transcriptomic analysis of uterine receptivity in Guinea pigs. 2022 ,	0
92	Analysis of protein-protein interaction and weighted co-expression networks revealed key modules and genes in multiple tissues of <i>Agave sisalana</i> .	0
91	Identification of an 11 immune-related gene signature as the novel biomarker for acute myocardial infarction diagnosis.	0
90	Analysis of TRIM27 prognosis value and immune infiltrates in hepatocellular carcinoma. 2022 , 36, 039463202211329	1

- 89 MAGEA11 as a STAD Prognostic Biomarker Associated with Immune Infiltration. **2022**, 12, 2506 ○
- 88 Identification of a novel ferroptosis-related gene signature associated with prognosis, the immune landscape, and biomarkers for immunotherapy in ovarian cancer. 13, ○
- 87 Computational quantification and characterization of independently evolving cellular subpopulations within tumors is critical to inhibit anti-cancer therapy resistance. **2022**, 14, ○
- 86 Yiqi Huayu decoction alleviates bleomycin-induced pulmonary fibrosis in rats by inhibiting senescence. 13, ○
- 85 A comprehensive analysis of the prognostic value and immune infiltration of low expression DBT in clear cell renal cell carcinoma. 13, ○
- 84 Identifying Key Lysosome-Related Genes Associated with Drug-Resistant Breast Cancer Using Computational and Systems Biology Approach. **2022**, 21, ○
- 83 Ferritin self-assembly, structure, function, and biotechnological applications. **2022**, ○
- 82 Decoding Diabetes Biomarkers and Related Molecular Mechanisms by Using Machine Learning, Text Mining, and Gene Expression Analysis. **2022**, 19, 13890 1
- 81 Integrative analyses of immune-related biomarkers and associated mechanisms in coronary heart disease. **2022**, 15, ○
- 80 Cuproptosis-related gene signature stratifies lower-grade glioma patients and predicts immune characteristics. 13, ○
- 79 Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics. **2022**, 12, 1436 ○
- 78 Methylation-Mediated Silencing of RBP7 Promotes Breast Cancer Progression through PPAR and PI3K/AKT Pathway. **2022**, 2022, 1-18 ○
- 77 Inhibition of FOXP3 by stapled alpha-helical peptides dampens regulatory T cell function. **2022**, 119, 1
- 76 A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis. **2022**, 2, 100190 ○
- 75 Reactive astrocytes transduce inflammation in a blood-brain barrier model through a TNF-STAT3 signaling axis and secretion of alpha 1-antichymotrypsin. **2022**, 13, ○
- 74 Characterization based on genotypeBiochemical phenotype association in fructose-1,6-bisphosphatase deficiency. ○
- 73 eccDNA Atlas: a comprehensive resource of eccDNA catalog. ○
- 72 Identification of GLS as a cuproptosis-related diagnosis gene in acute myocardial infarction. 9, 1

71	Regulatory mechanisms of miRNA-21 in the progression of ischemia/reperfusion induced acute kidney injury to chronic kidney disease.	o
70	Network approaches for identification of human genetic disease genes. 2022 , 60, 700-712	o
69	Transcriptome Sequencing Reveals Tgf- β Mediated Noncoding RNA Regulatory Mechanisms Involved in DNA Damage in the 661W Photoreceptor Cell Line. 2022 , 13, 2140	o
68	Identification of key genes in platelets associated with COVID-19 using a weighted gene co-expression network analysis.	o
67	The various facets of protein promiscuity: not just broad specificity of proteins. 2023 , 241-277	o
66	Construction of a prognostic classifier and prediction of the immune landscape and immunosuppressive molecules in gliomas based on combination of inflammatory response-related genes and angiogenesis-associated genes. 2022 , 20, 1721727X2211337	o
65	Robust identification of common genomic biomarkers from multiple gene expression profiles for the prognosis, diagnosis, and therapies of pancreatic cancer. 2023 , 152, 106411	1
64	In vitro digestibility of proteins, peptidomic analysis and antioxidant ability of sodium-reduced pork sausage with partial substitution of NaCl by KCl. 2023 , 197, 109049	o
63	Intrinsic Disorder as a Natural Preservative: High Levels of Intrinsic Disorder in Proteins Found in the 2600-Year-Old Human Brain. 2022 , 11, 1704	o
62	Bioinformatics insights on the physicochemical properties of SCN5A mutant proteins associated with the Brugada Syndrome. 2022 , 30,	o
61	Exploration of the Mechanism of Linoleic Acid Metabolism Dysregulation in Metabolic Syndrome. 2022 , 2022, 1-7	o
60	A novel defined cuproptosis-related gene signature for predicting the prognosis of colon adenocarcinoma. 12,	o
59	A novel cuproptosis-related gene signature for overall survival prediction in patients with hepatocellular carcinoma. 2022 , 8, e11768	o
58	Differentiation of action mechanisms between natural and synthetic repellents through neuronal electroantennogram and proteomic in <i>Aedes aegypti</i> (Diptera: Culicidae). 2022 , 12,	o
57	Identification of key genes in late-onset major depressive disorder through a co-expression network module. 13,	o
56	Common Assays in Mammalian Golgi Studies. 2023 , 303-332	o
55	Identification of key genes and miRNAs related to polycystic ovary syndrome by comprehensive analysis of microarray. 2022 , 15,	o
54	Transcriptome and proteome profiling of activated cardiac fibroblasts supports target prioritization in cardiac fibrosis. 9,	o

- 53 Comparative RNA-Sequencing Analysis Reveals High Complexity and Heterogeneity of Transcriptomic and Immune Profiles in Hepatocellular Carcinoma Tumors of Viral (HBV, HCV) and Non-Viral Etiology. **2022**, 58, 1803 ○
- 52 Identification of hub genes associated with prognosis of lung cancer via integrated bioinformatics and in vitro approach. 1-15 ○
- 51 Identification of deleterious nsSNPs in human HGF gene: in silico approach. 1-15 ○
- 50 The m6A Reader YTHDF2 Modulates Antiviral and Antibacterial Activity by Suppressing METTL3 Methylation-Modified STING in Fish. ○
- 49 Microbiota-dependent proteolysis of gluten subverts diet-mediated protection against type 1 diabetes. **2023**, ○
- 48 Regulatory mechanisms of miRNA-21 in the progression of ischemia/reperfusion induced acute kidney injury to chronic kidney disease. ○
- 47 Identification and validation of a novel ferroptosis-related gene signature for prognosis and potential therapeutic target prediction in cholangiocarcinoma. 13, ○
- 46 Neuroprotection by Preconditioning in Mice is Dependent on MyD88-Mediated CXCL10 Expression in Endothelial Cells. **2023**, 15, 175909142211463 ○
- 45 Histone Deacetylase 1 Expression and Regulatory Network in Lung Adenocarcinoma Based on Data Mining and Implications for Targeted Treatment. **2023**, 2023, 1-16 ○
- 44 NADPH oxidase 4 is dispensable for skin myofibroblast differentiation and wound healing. **2023**, 102609 ○
- 43 A signature of immune-related genes correlating with clinical prognosis and immune microenvironment in sepsis. **2023**, 24, ○
- 42 Development and validation of a cuproptosis-associated prognostic model for diffuse large B-cell lymphoma. 12, ○
- 41 Cox-ResNet: A Survival Analysis Model Based on Residual Neural Networks for Gene Expression Data. **2022**, ○
- 40 S100A8 and S100A12 Proteins as Biomarkers of High Disease Activity in Patients with Rheumatoid Arthritis That Can Be Regulated by Epigenetic Drugs. **2023**, 24, 710 ○
- 39 Liaisons dangereuses: Intrinsic Disorder in Cellular Proteins Recruited to Viral Infection-Related Biocondensates. **2023**, 24, 2151 ○
- 38 FHL1 as a novel prognostic biomarker and correlation with immune infiltration levels in lung adenocarcinoma. ○
- 37 Proteomic analysis of canine vaccines. **2023**, 1-7 ○
- 36 Identification of epigenetically regulated genes distinguishing intracranial from extracranial melanoma metastases. **2023**, ○

- 35 Bioinformatics pipeline to unveil the heterogeneity of Glioblastoma Multiforme. **2022**, ○
- 34 Protein-protein networks analysis of differentially expressed genes unveils the key phenomenon of biological process with respect to reproduction in endangered catfish, *C. Magur*. **2023**, 860, 147235 ○
- 33 Identifying Natural Bioactive Peptides from the Common Octopus (*Octopus vulgaris* Cuvier, 1797) Skin Mucus By-Products Using Proteogenomic Analysis. **2023**, 24, 7145 ○
- 32 Gene network analyses of larvae under different egg-protecting behaviors provide novel insights into immune response mechanisms of *Amphioctopus fangsiao*. **2023**, 136, 108733 ○
- 31 Systems biology approach to understand the interplay between *Bacillus anthracis* and human host genes that leads to CVDs. **2023**, 176, 106019 ○
- 30 Systematic Identification of Novel Ferroptosis-Associated Multigene Models for Predicting Patient Prognosis Based on Endometrial Cancer. **2023**, 2023, 1-16 ○
- 29 Shu-Xie decoction alleviates oxidative stress and colon injury in acute sleep-deprived mice by suppressing p62/KEAP1/NRF2/HO1/NQO1 signaling. 14, ○
- 28 Integrative transcriptomic profiling reveals the key pathways in the regulation mechanism of fish intestine-spleen immunity during the bacterial challenges. **2023**, 568, 739320 ○
- 27 eccDNA Atlas: a comprehensive resource of eccDNA catalog. **2023**, 24, ○
- 26 Reverse predictive analysis of *Rhizoma Pinelliae* and *Rhizoma Coptidis* on differential miRNA target genes in lung adenocarcinoma. **2023**, 102, e32999 ○
- 25 NUF2 Promotes Breast Cancer Development as a New Tumor Stem Cell Indicator. **2023**, 24, 4226 ○
- 24 Exploring Core Genes by Comparative Transcriptomics Analysis for Early Diagnosis, Prognosis, and Therapies of Colorectal Cancer. **2023**, 15, 1369 ○
- 23 Bioinformatic analysis of underlying mechanisms of Kawasaki disease via Weighted Gene Correlation Network Analysis (WGCNA) and the Least Absolute Shrinkage and Selection Operator method (LASSO) regression model. **2023**, 23, ○
- 22 Network pharmacology and bioinformatics study on the treatment of renal fibrosis with *persicae semen-carthami flos* drug pair. **2023**, 102, e32946 ○
- 21 Integrated proteome and acetylome analyses provide novel insights into early somatic embryogenesis of *Dimocarpus longan*. **2023**, 196, 903-916 ○
- 20 Exploration of the Shared Molecular Mechanisms between COVID-19 and Neurodegenerative Diseases through Bioinformatic Analysis. **2023**, 24, 4839 ○
- 19 Different immunological mechanisms between AQP4 antibody-positive and MOG antibody-positive optic neuritis based on RNA sequencing analysis of whole blood. 14, ○
- 18 Leveraging quantum computing for dynamic analyses of logical networks in systems biology. **2023**, 4, 100705 ○

- 17 Predictive Value of Gene Databases in Discovering New Biomarkers and New Therapeutic Targets in Lung Cancer. **2023**, 59, 547 ○
- 16 Comprehensive Analysis of Universal Stress Protein Family Genes and Their Expression in *Fusarium oxysporum* Response of *Populus davidiana* [P. alba var. *pyramidalis* Louche Based on the Transcriptome. **2023**, 24, 5405 ○
- 15 Pan-cancer analysis identifies PD-L2 as a tumor promotor in the tumor microenvironment. 14, ○
- 14 Genetic/Protein Association of Atopic Dermatitis and Tooth Agenesis. **2023**, 24, 5754 ○
- 13 Bioinformatics-based investigation on the genetic influence between SARS-CoV-2 infections and idiopathic pulmonary fibrosis (IPF) diseases, and drug repurposing. **2023**, 13, ○
- 12 Insights into Common Octopus (*Octopus vulgaris*) Ink Proteome and Bioactive Peptides Using Proteomic Approaches. **2023**, 21, 206 ○
- 11 RNA-Seq Profiling between Commercial and Indigenous Iranian Chickens Highlights Differences in Innate Immune Gene Expression. **2023**, 14, 793 ○
- 10 Downregulated annexin A1 expression correlates with poor prognosis, metastasis, and immunosuppressive microenvironment in Ewing's sarcoma. **2023**, 15, 2321-2346 ○
- 9 Searching for the Resistance Interactome of *Pseudomonas aeruginosa*. ○
- 8 An automated proximity proteomics pipeline for subcellular proteome and protein interaction mapping. ○
- 7 The NF- κ B p50 subunit generated by KPC1-mediated ubiquitination and limited proteasomal processing, suppresses tumor growth. **2023**, 23, ○
- 6 Towards a Protein-Protein Interactions Framework using Graph Analytics on Apache Spark. **2023**, ○
- 5 Identification and validation of a novel cuproptosis-related gene signature in multiple myeloma. 11, ○
- 4 Exploring the mechanism of Jingshen Xiaoke decoction in treating T2DM mice based on network pharmacology and molecular docking. **2023**, 1-17 ○
- 3 Integrating Network Pharmacology and Experimental Validation to Explore the Pharmacological Mechanism of Astragaloside IV in Treating Bleomycin-Induced Pulmonary Fibrosis. Volume 17, 1289-1302 ○
- 2 DBLiPro: A Database for Lipids and Proteins in Human Lipid Metabolism. ○
- 1 Integrative analysis of cancer dependency data and comprehensive phosphoproteomics data revealed the EPHA2-PARD3 axis as a cancer vulnerability in KRAS-mutant colorectal cancer. ○