Ghasem H Salekdeh

List of Publications by Year
in descending order

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244	13,930	31976 53	27406 106
papers	citations	h-index	g-index

259	259	259	22196
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
2	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. Nature Biotechnology, 2011, 29, 1132-1144.	17.5	509
3	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
4	Proteomic analysis of rice leaves during drought stress and recovery. Proteomics, 2002, 2, 1131-1145.	2.2	415
5	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
6	Proteome analysis of sugar beet leaves under drought stress. Proteomics, 2005, 5, 950-960.	2.2	256
7	A proteomic approach to analyzing drought- and salt-responsiveness in rice. Field Crops Research, 2002, 76, 199-219.	5.1	245
8	Advanced glycation end-products produced systemically and by macrophages: A common contributor to inflammation and degenerative diseases. , 2017, 177, 44-55.		232
9	Conceptual framework for drought phenotyping during molecular breeding. Trends in Plant Science, 2009, 14, 488-496.	8.8	213
10	Proteomics Uncovers a Role for Redox in Drought Tolerance in WheatÂ§. Journal of Proteome Research, 2007, 6, 1451-1460.	3.7	179
11	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	14.5	177
12	Effects of salinity levels on proteome ofSuaeda aegyptiaca leaves. Proteomics, 2006, 6, 2542-2554.	2.2	173
13	Crop proteomics: Aim at sustainable agriculture of tomorrow. Proteomics, 2007, 7, 2976-2996.	2.2	155
14	Generation of Liver Disease-Specific Induced Pluripotent Stem Cells Along with Efficient Differentiation to Functional Hepatocyte-Like Cells. Stem Cell Reviews and Reports, 2010, 6, 622-632.	5.6	152
15	Proteomics study reveals the molecular mechanisms underlying water stress tolerance induced by Piriformospora indica in barley. Journal of Proteomics, 2013, 94, 289-301.	2.4	150
16	Proteomic responses of rice young panicles to salinity. Proteomics, 2006, 6, 6498-6507.	2.2	144
17	Proteomics Reveals New Salt Responsive Proteins Associated with Rice Plasma Membrane. Bioscience, Biotechnology and Biochemistry, 2007, 71, 2144-2154.	1.3	141
18	Identification of genes differentially expressed during interaction of Mexican lime tree infected with "Candidatus Phytoplasma aurantifolia". BMC Microbiology, 2011, 11, 1.	3.3	135

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19	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	3.7	135
20	Identification of squamous cell carcinoma associated proteins by proteomics and loss of beta tropomyosin expression in esophageal cancer. World Journal of Gastroenterology, 2006, 12, 7104.	3.3	132
21	A proteomics view on the role of drought-induced senescence and oxidative stress defense in enhanced stem reserves remobilization in wheat. Journal of Proteomics, 2011, 74, 1959-1973.	2.4	111
22	Proteome response of Elymus elongatum to severe water stress and recovery. Journal of Experimental Botany, 2006, 58, 291-300.	4.8	106
23	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. Scientific Reports, 2017, 7, 12685.	3.3	105
24	Reference genome of wild goat (capra aegagrus) and sequencing of goat breeds provide insight into genic basis of goat domestication. BMC Genomics, 2015, 16, 431.	2.8	103
25	Comparative physiology and proteomic analysis of two wheat genotypes contrasting in drought tolerance. Journal of Proteomics, 2015, 114, 1-15.	2.4	99
26	Comparative proteomic analysis of canola leaves under salinity stress. Proteomics, 2011, 11, 1965-1975.	2.2	97
27	A metagenomic analysis of the camel rumenâ€™s microbiome identifies the major microbes responsible for lignocellulose degradation and fermentation. Biotechnology for Biofuels, 2018, 11, 216.	6.2	96
28	Feeder- and serum-free establishment and expansion of human induced pluripotent stem cells. International Journal of Developmental Biology, 2010, 54, 877-886.	0.6	93
29	Shotgun Proteomic Analysis of Long-distance Drought Signaling in Rice Roots. Journal of Proteome Research, 2012, 11, 348-358.	3.7	92
30	In-depth diversity analysis of the bacterial community resident in the camel rumen. Systematic and Applied Microbiology, 2015, 38, 67-76.	2.8	92
31	Proteomic signature of human embryonic stem cells. Proteomics, 2006, 6, 3544-3549.	2.2	91
32	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions to utilize high lignocellulosic forages in the cattle rumen. ISME Journal, 2021, 15, 1108-1120.	9.8	87
33	Concise Review: Trends in Stem Cell Proteomics. Stem Cells, 2007, 25, 1888-1903.	3.2	82
34	A comparative proteome approach to decipher the mechanism of rice adaptation to phosphorous deficiency. Proteomics, 2009, 9, 159-170.	2.2	80
35	Root endophytic fungus Piriformospora indica improves drought stress adaptation in barley by metabolic and proteomic reprogramming. Environmental and Experimental Botany, 2019, 157, 197-210.	4.2	80
36	Induced pluripotent stem cells: A new era for hepatology. Journal of Hepatology, 2010, 53, 738-751.	3.7	77

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37	The dynamics of the bacterial communities developed in maize silage. Microbial Biotechnology, 2017, 10, 1663-1676.	4.2	77
38	Metabolic and transcriptional response of central metabolism affected by root endophytic fungus Piriformospora indica under salinity in barley. Plant Molecular Biology, 2016, 90, 699-717.	3.9	73
39	Application of the immobilized enzyme on magnetic graphene oxide nano-carrier as a versatile bi-functional tool for efficient removal of dye from water. Bioresource Technology, 2021, 319, 124228.	9.6	73
40	Comprehensive Gene Expression Analysis of Human Embryonic Stem Cells during Differentiation into Neural Cells. PLoS ONE, 2011, 6, e22856.	2.5	72
41	Retinal changes in Alzheimer's diseaseâ€" integrated prospects of imaging, functional and molecular advances. Progress in Retinal and Eye Research, 2021, 82, 100899.	15.5	71
42	A proteomics approach to study the molecular basis of enhanced salt tolerance in barley (Hordeum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2013, 9, 1498.	2.9	67
43	Mining alfalfa (Medicago sativa L.) nodules for salinity tolerant non-rhizobial bacteria to improve growth of alfalfa under salinity stress. Ecotoxicology and Environmental Safety, 2018, 162, 129-138.	6.0	66
44	An efficient and easy-to-use cryopreservation protocol for human ES and iPS cells. Nature Protocols, 2010, 5, 588-594.	12.0	65
45	A New Efficient Protocol for Directed Differentiation of Retinal Pigmented Epithelial Cells from Normal and Retinal Disease Induced Pluripotent Stem Cells. Stem Cells and Development, 2012, 21, 2262-2272.	2.1	64
46	Physiology and proteome responses of two contrasting rice mutants and their wild type parent under salt stress conditions at the vegetative stage. Journal of Plant Physiology, 2014, 171, 31-44.	3.5	62
47	Progress and Promise Towards Safe Induced Pluripotent Stem Cells for Therapy. Stem Cell Reviews and Reports, 2010, 6, 297-306.	5.6	61
48	DDX3Y, a Male-Specific Region of Y Chromosome Gene, May Modulate Neuronal Differentiation. Journal of Proteome Research, 2015, 14, 3474-3483.	3.7	61
49	Phytoplasma-Responsive microRNAs Modulate Hormonal, Nutritional, and Stress Signalling Pathways in Mexican Lime Trees. PLoS ONE, 2013, 8, e66372.	2.5	61
50	Inhibition of TGFÎ² Signaling Promotes Ground State Pluripotency. Stem Cell Reviews and Reports, 2014, 10, 16-30.	5.6	60
51	Comparative proteome and transcriptome analyses of embryonic stem cells during embryoid bodyâ€based differentiation. Proteomics, 2009, 9, 4859-4870.	2.2	58
52	Proteomic analysis of rice anthers under salt stress. Plant Physiology and Biochemistry, 2012, 58, 280-287.	5.8	58
53	Cold Acclimation Proteome Analysis Reveals Close Link between the Up-Regulation of Low-Temperature Associated Proteins and Vernalization Fulfillment. Journal of Proteome Research, 2010, 9, 5658-5667.	3.7	56
54	MicroRNA Signatures of Drought Signaling in Rice Root. PLoS ONE, 2016, 11, e0156814.	2.5	56

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55	Stable cellulase immobilized on graphene oxide@CMC-g-poly(AMPS-co-AAm) hydrogel for enhanced enzymatic hydrolysis of lignocellulosic biomass. Carbohydrate Polymers, 2020, 230, 115661.	10.2	55
56	Shotgun Proteomic Analysis of the Mexican Lime Tree Infected with â€œCandidatusPhytoplasma aurantifoliaâ€• Journal of Proteome Research, 2013, 12, 785-795.	3.7	54
57	Highly efficient removal of dyes from wastewater using nanocellulose from quinoa husk as a carrier for immobilization of laccase. Bioresource Technology, 2022, 349, 126833.	9.6	54
58	Growth and Water Use Response of Doubled-Haploid Rice Linesto Drought and Rewatering during the Vegetative Stage. Plant Production Science, 2006, 9, 141-151.	2.0	53
59	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	3.7	53
60	Study of Sperm Protein Profile in Men With and Without Varicocele Using Two-Dimensional Gel Electrophoresis. Urology, 2013, 81, 293-300.	1.0	52
61	A Fresh Look at the Male-specific Region of the Human Y Chromosome. Journal of Proteome Research, 2013, 12, 6-22.	3.7	52
62	Manipulating Root Water Supply Elicits Major Shifts in the Shoot Proteome. Journal of Proteome Research, 2014, 13, 517-526.	3.7	52
63	Assessing wheat (Triticum aestivum L.) genetic diversity using quality traits, amplified fragment length polymorphisms, simple sequence repeats and proteome analysis. Annals of Applied Biology, 2008, 152, 81-91.	2.5	51
64	Identification and characterization of a novel thermostable xylanase from camel rumen metagenome. International Journal of Biological Macromolecules, 2019, 126, 1295-1302.	7.5	48
65	A novel thermostable cellulase cocktail enhances lignocellulosic bioconversion and biorefining in a broad range of pH. International Journal of Biological Macromolecules, 2020, 154, 349-360.	7.5	47
66	The contrasting microRNA content of a drought tolerant and a drought susceptible wheat cultivar. Journal of Plant Physiology, 2017, 216, 35-43.	3.5	45
67	Small RNA Sequencing Reveals Dlk1-Dio3 Locus-Embedded MicroRNAs as Major Drivers of Ground-State Pluripotency. Stem Cell Reports, 2017, 9, 2081-2096.	4.8	45
68	Identification of Mouse Embryonic Stem Cell-Associated Proteins. Journal of Proteome Research, 2008, 7, 412-423.	3.7	44
69	Application of carboxymethyl cellulose-g-poly(acrylic acid-co-acrylamide) hydrogel sponges for improvement of efficiency, reusability and thermal stability of a recombinant xylanase. Chemical Engineering Journal, 2019, 375, 122022.	12.7	44
70	Proteomic analysis of the Mexican lime tree response to â€œCandidatus Phytoplasma aurantifoliaâ€• infection. Molecular BioSystems, 2011, 7, 3028.	2.9	43
71	Salinity-associated microRNAs and their potential roles in mediating salt tolerance in rice colonized by the endophytic root fungus Piriformospora indica. Functional and Integrative Genomics, 2019, 19, 659-672.	3.5	42
72	Mining of camel rumen metagenome to identify novel alkali-thermostable xylanase capable of enhancing the recalcitrant lignocellulosic biomass conversion. Bioresource Technology, 2019, 281, 343-350.	9.6	42

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73	Concise Review: Alchemy of Biology: Generating Desired Cell Types from Abundant and Accessible Cells. Stem Cells, 2011, 29, 1933-1941.	3.2	41
74	Disease-Corrected Hepatocyte-Like Cells from Familial Hypercholesterolemia-Induced Pluripotent Stem Cells. Molecular Biotechnology, 2013, 54, 863-873.	2.4	41
75	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050.	3.7	41
76	Upregulation of Proteolytic Pathways and Altered Protein Biosynthesis Underlie Retinal Pathology in a Mouse Model of Alzheimerâ€™s Disease. Molecular Neurobiology, 2019, 56, 6017-6034.	4.0	41
77	Elucidation of salt stress defense and tolerance mechanisms of crop plants using proteomics-Current achievements and perspectives. Proteomics, 2013, 13, 1885-1900.	2.2	40
78	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. PLoS ONE, 2015, 10, e0130425.	2.5	39
79	Loss of Shp2 Rescues BDNF/TrkB Signaling and Contributes to Improved Retinal Ganglion Cell Neuroprotection. Molecular Therapy, 2019, 27, 424-441.	8.2	39
80	Root Growth and Water Extraction Response of Doubled-Haploid Rice Lines to Drought and Rewatering during the Vegetative Stage. Plant Production Science, 2005, 8, 497-508.	2.0	38
81	An efficient nano-biocatalyst for lignocellulosic biomass hydrolysis: Xylanase immobilization on organically modified biogenic mesoporous silica nanoparticles. International Journal of Biological Macromolecules, 2020, 164, 3462-3473.	7.5	38
82	A Novel High Glucose-Tolerant Î²-Glucosidase: Targeted Computational Approach for Metagenomic Screening. Frontiers in Bioengineering and Biotechnology, 2020, 8, 813.	4.1	38
83	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	3.8	37
84	PlantPReS: A database for plant proteome response to stress. Journal of Proteomics, 2016, 143, 69-72.	2.4	37
85	Drought responsive microRNAs in two barley cultivars differing in their level of sensitivity to drought stress. Plant Physiology and Biochemistry, 2017, 118, 121-129.	5.8	37
86	A novel high performance in-silico screened metagenome-derived alkali-thermostable endo-Î²-1,4-glucanase for lignocellulosic biomass hydrolysis in the harsh conditions. BMC Biotechnology, 2020, 20, 56.	3.3	37
87	Immobilization of enzyme cocktails on dopamine functionalized magnetic cellulose nanocrystals to enhance sugar bioconversion: A biomass reusing loop. Carbohydrate Polymers, 2021, 256, 117511.	10.2	37
88	Efficient removal of various textile dyes from wastewater by novel thermo-halotolerant laccase. Bioresource Technology, 2021, 337, 125468.	9.6	37
89	Complete nucleotide sequence of Iranian tomato yellow leaf curl virus isolate: further evidence for natural recombination amongst begomoviruses. Archives of Virology, 2004, 149, 1435-43.	2.1	36
90	Detection and Characterization of Phytoplasmas Infecting Ornamental and Weed Plants in Iran. Journal of Phytopathology, 2007, 155, 368-372.	1.0	36

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91	Y Chromosome Missing Protein, TBL1Y, May Play an Important Role in Cardiac Differentiation. Journal of Proteome Research, 2017, 16, 4391-4402.	3.7	36
92	Two Splice Variants of Y Chromosome-Located Lysine-Specific Demethylase 5D Have Distinct Function in Prostate Cancer Cell Line (DU-145). Journal of Proteome Research, 2015, 14, 3492-3502.	3.7	35
93	Isoform-Level Gene Expression Profiles of Human Y Chromosome Azoospermia Factor Genes and Their X Chromosome Paralogs in the Testicular Tissue of Non-Obstructive Azoospermia Patients. Journal of Proteome Research, 2015, 14, 3595-3605.	3.7	35
94	Comparative proteomic analysis of tobacco expressing cyanobacterial flavodoxin and its wild type under drought stress. Journal of Plant Physiology, 2015, 175, 48-58.	3.5	35
95	Comparative Analysis of Aducanumab, Zagotenemab and Pioglitazone as Targeted Treatment Strategies for Alzheimerâ€™s Disease. , 2021, 12, 1964.		35
96	Generation of human induced pluripotent stem cells from a Bombay individual: Moving towards â€œuniversal-donorâ€•red blood cells. Biochemical and Biophysical Research Communications, 2010, 391, 329-334.	2.1	34
97	ISL1 Protein Transduction Promotes Cardiomyocyte Differentiation from Human Embryonic Stem Cells. PLoS ONE, 2013, 8, e55577.	2.5	34
98	Machine Learning and Network Analysis of Molecular Dynamics Trajectories Reveal Two Chains of Red/Ox-specific Residue Interactions in HumanÂProtein Disulfide Isomerase. Scientific Reports, 2017, 7, 3666.	3.3	33
99	An integrated proteomic approach to decipher the effect of methyl jasmonate elicitation on the proteome of Silybum marianum L. hairy roots. Plant Physiology and Biochemistry, 2013, 70, 115-122.	5.8	32
100	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. FEMS Microbiology Ecology, 2020, 96, .	2.7	32
101	Proteome Analysis of Ground State Pluripotency. Scientific Reports, 2016, 5, 17985.	3.3	31
102	Effects of Synbiotic Supplementation on Breast Milk Levels of IgA, TGF-Î²1, and TGF-Î²2. Journal of Human Lactation, 2013, 29, 591-596.	1.6	30
103	Distinct changes in the proteome profile of endometrial tissues in polycystic ovary syndrome compared with healthy fertile women. Reproductive BioMedicine Online, 2018, 37, 184-200.	2.4	30
104	Transcriptomic analysis of Aegilops tauschii during long-term salinity stress. Functional and Integrative Genomics, 2019, 19, 13-28.	3.5	30
105	Amyloid Î² Induces Early Changes in the Ribosomal Machinery, Cytoskeletal Organization and Oxidative Phosphorylation in Retinal Photoreceptor Cells. Frontiers in Molecular Neuroscience, 2019, 12, 24.	2.9	28
106	Nesterenkonia sp. strain F, a halophilic bacterium producing acetone, butanol and ethanol under aerobic conditions. Scientific Reports, 2016, 6, 18408.	3.3	27
107	Mitochondrial dysfunction in Alzheimerâ€™s disease - a proteomics perspective. Expert Review of Proteomics, 2021, 18, 295-304.	3.0	27
108	The Asia Oceania Human Proteome Organisation Membrane Proteomics Initiative. Preparation and characterisation of the carbonateâ€•washed membrane standard. Proteomics, 2010, 10, 4142-4148.	2.2	26

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109	Defining pluripotent stem cells through quantitative proteomic analysis. Expert Review of Proteomics, 2011, 8, 29-42.	3.0	26
110	Comparative proteomic analysis of mouse embryonic stem cells and neonatal-derived cardiomyocytes. Biochemical and Biophysical Research Communications, 2006, 349, 1041-1049.	2.1	25
111	Quantitative proteomics analysis highlights the role of redox hemostasis and energy metabolism in human embryonic stem cell differentiation to neural cells. Journal of Proteomics, 2014, 101, 1-16.	2.4	25
112	The Art of Validating Quantitative Proteomics Data. Proteomics, 2018, 18, e1800222.	2.2	25
113	Induction of Neural Progenitor-Like Cells from Human Fibroblasts via a Genetic Material-Free Approach. PLoS ONE, 2015, 10, e0135479.	2.5	25
114	Quantitative proteomic analysis of human testis reveals system-wide molecular and cellular pathways associated with non-obstructive azoospermia. Journal of Proteomics, 2017, 162, 141-154.	2.4	24
115	A novel metagenome-derived thermostable and poultry feed compatible Î±-amylase with enhanced biodegradation properties. International Journal of Biological Macromolecules, 2020, 164, 2124-2133.	7.5	24
116	Upgrading the enzymatic hydrolysis of lignocellulosic biomass by immobilization of metagenome-derived novel halotolerant cellulase on the carboxymethyl cellulose-based hydrogel. Cellulose, 2021, 28, 3485-3503.	4.9	24
117	The effect of purmorphamine and sirolimus on osteogenic differentiation of human bone marrow-derived mesenchymal stem cells. Biomedicine and Pharmacotherapy, 2013, 67, 31-38.	5.6	23
118	Low Focal Adhesion Signaling Promotes Ground State Pluripotency of Mouse Embryonic Stem Cells. Journal of Proteome Research, 2017, 16, 3585-3595.	3.7	23
119	Prospective Isolation of ISL1+ Cardiac Progenitors from Human ESCs forÂMyocardial Infarction Therapy. Stem Cell Reports, 2018, 10, 848-859.	4.8	23
120	A computational method for prediction of xylanase enzymes activity in strains of Bacillus subtilis based on pseudo amino acid composition features. PLoS ONE, 2018, 13, e0205796.	2.5	23
121	Distribution and development of molecularly distinct perineuronal nets in visual thalamus. Journal of Neurochemistry, 2018, 147, 626-646.	3.9	23
122	Discovery of Novel Cell Surface Markers for Purification of Embryonic Dopamine Progenitors for Transplantation in Parkinson's Disease Animal Models. Molecular and Cellular Proteomics, 2018, 17, 1670-1684.	3.8	23
123	The Stabilizing Mechanism of Immobilized Metagenomic Xylanases on Bio-Based Hydrogels to Improve Utilization Performance: Computational and Functional Perspectives. Bioconjugate Chemistry, 2020, 31, 2158-2171.	3.6	23
124	Quantitative Proteomic Analysis of Human Embryonic Stem Cell Differentiation by 8-Plex iTRAQ Labelling. PLoS ONE, 2012, 7, e38532.	2.5	23
125	Direct conversion of human fibroblasts into dopaminergic neural progenitor-like cells using TAT-mediated protein transduction of recombinant factors. Biochemical and Biophysical Research Communications, 2015, 459, 655-661.	2.1	22
126	Plantâ€“Microbe Symbiosis: What Has Proteomics Taught Us?. Proteomics, 2019, 19, e1800105.	2.2	22

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127	Efficient saccharification of ionic liquid-pretreated rice straw in a one-pot system using novel metagenomics derived cellulases. Bioresource Technology, 2022, 345, 126536.	9.6	22
128	Effects of Selenite and Tellurite on Growth, Physiology, and Proteome of a Moderately Halophilic Bacterium. Journal of Proteome Research, 2009, 8, 3098-3108.	3.7	21
129	Efficient Differentiation of Human Embryonic Stem Cells Toward Dopaminergic Neurons Using Recombinant LMX1A Factor. Molecular Biotechnology, 2015, 57, 184-194.	2.4	21
130	Cold-induced physiological and biochemical responses of three grapevine cultivars differing in cold tolerance. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	21
131	Retinal proteomics of experimental glaucoma model reveal intraocular pressureâ€induced mediators of neurodegenerative changes. Journal of Cellular Biochemistry, 2020, 121, 4931-4944.	2.6	21
132	Human-Induced Pluripotent Stem Cells: Derivation, Propagation, and Freezing in Serum- and Feeder Layer-Free Culture Conditions. Methods in Molecular Biology, 2009, 584, 425-443.	0.9	21
133	Biological and Molecular Variability of Zucchini yellow mosaic virus in Iran*. Journal of Phytopathology, 2008, 156, 654-659.	1.0	20
134	Comparative proteomic and physiological characterisation of two closely related rice genotypes with contrasting responses to salt stress. Functional Plant Biology, 2015, 42, 527.	2.1	20
135	In-silico discovery of bifunctional enzymes with enhanced lignocellulose hydrolysis from microbiota big data. International Journal of Biological Macromolecules, 2021, 177, 211-220.	7.5	20
136	Proteomic Analysis of Monkey Embryonic Stem Cell during Differentiation. Journal of Proteome Research, 2009, 8, 1527-1539.	3.7	19
137	Epigenetic analysis of human embryonic carcinoma cells during retinoic acid-induced neural differentiation. Biochemistry and Cell Biology, 2010, 88, 527-538.	2.0	19
138	Subcellular Proteome Landscape of Human Embryonic Stem Cells Revealed Missing Membrane Proteins. Journal of Proteome Research, 2018, 17, 4138-4151.	3.7	19
139	A generalized machineâ€learning aided method for targeted identification of industrial enzymes from metagenome: A xylanase temperature dependence case study. Biotechnology and Bioengineering, 2021, 118, 759-769.	3.3	19
140	Molecular analysis of a stress-induced cDNA encoding the translation initiation factor, eIF1, from the salt-tolerant wild relative of rice, Porteresia coarctata. Functional Plant Biology, 2004, 31, 1035.	2.1	18
141	Proteome analysis of brain in murine experimental autoimmune encephalomyelitis. Proteomics, 2010, 10, 2822-2832.	2.2	18
142	Extensive genetic diversity in Iranian pomegranate (Punica granatum L.) germplasm revealed by microsatellite markers. Scientia Horticulturae, 2012, 146, 104-114.	3.6	18
143	Cellular and Molecular Characterization of Human Cardiac Stem Cells Reveals Key Features Essential for Their Function and Safety. Stem Cells and Development, 2015, 24, 1390-1404.	2.1	18
144	Chromosome-Centric Human Proteome Project Allies with Developmental Biology: A Case Study of the Role of Y Chromosome Genes in Organ Development. Journal of Proteome Research, 2017, 16, 4259-4272.	3.7	18

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145	MicroRNA-340 inhibits the proliferation and promotes the apoptosis of colon cancer cells by modulating REV3L. Oncotarget, 2018, 9, 5155-5168.	1.8	18
146	MCIC: Automated Identification of Cellulases From Metagenomic Data and Characterization Based on Temperature and pH Dependence. Frontiers in Microbiology, 2020, 11, 567863.	3.5	18
147	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. PeerJ, 2021, 9, e10463.	2.0	18
148	200+ Protein Concentrations in Healthy Human Blood Plasma: Targeted Quantitative SRM SIS Screening of Chromosomes 18, 13, Y, and the Mitochondrial Chromosome Encoded Proteome. Journal of Proteome Research, 2019, 18, 120-129.	3.7	17
149	Simultaneous hydrolysis of various protein-rich industrial wastes by a naturally evolved protease from tannery wastewater microbiota. Science of the Total Environment, 2022, 815, 152796.	8.0	17
150	Complete Genome Sequence of Oceanimonas sp. GK1, a Halotolerant Bacterium from Gavkhouni Wetland in Iran. Journal of Bacteriology, 2012, 194, 2123-2124.	2.2	16
151	Proteomics of Important Food Crops in the Asia Oceania Region: Current Status and Future Perspectives. Journal of Proteome Research, 2015, 14, 2723-2744.	3.7	16
152	A cold-adapted endoglucanase from camel rumen with high catalytic activity at moderate and low temperatures: an anomaly of truly cold-adapted evolution in a mesophilic environment. Extremophiles, 2018, 22, 315-326.	2.3	16
153	Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome. Scientific Reports, 2020, 10, 4995.	3.3	16
154	Key Genes and Biochemical Networks in Various Brain Regions Affected in Alzheimerâ€™s Disease. Cells, 2022, 11, 987.	4.1	16
155	Identification and validation of Asteraceae miRNAs by the expressed sequence tag analysis. Gene, 2012, 493, 253-259.	2.2	15
156	Down-Regulation of a Male-Specific H3K4 Demethylase, KDM5D, Impairs Cardiomyocyte Differentiation. Journal of Proteome Research, 2019, 18, 4277-4282.	3.7	15
157	Defining microRNA signatures of hair follicular stem and progenitor cells in healthy and androgenic alopecia patients. Journal of Dermatological Science, 2021, 101, 49-57.	1.9	15
158	Root endophytic fungus Serendipita indica modulates barley leaf blade proteome by increasing the abundance of photosynthetic proteins in response to salinity. Journal of Applied Microbiology, 2021, 131, 1870-1889.	3.1	15
159	Cloning, expression and functional characterization of in-house prepared human basic fibroblast growth factor. Cell Journal, 2013, 14, 282-91.	0.2	15
160	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	15
161	Preconditioning of sperm with sublethal nitrosative stress: a novel approach to improve frozenâ€“thawed sperm function. Reproductive BioMedicine Online, 2019, 38, 413-425.	2.4	14
162	Pinpointing genomic regions associated with root system architecture in rice through an integrative meta-analysis approach. Theoretical and Applied Genetics, 2022, 135, 81-106.	3.6	14

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163	Induced Neural Lineage Cells as Repair Kits: So Close, Yet So Far Away. Journal of Cellular Physiology, 2014, 229, 728-742.	4.1	13
164	Transient Activation of Reprogramming Transcription Factors Using Protein Transduction Facilitates Conversion of Human Fibroblasts Toward Cardiomyocyte-Like Cells. Molecular Biotechnology, 2017, 59, 207-220.	2.4	13
165	Proteomic and metabolomic analysis of desiccation tolerance in wheat young seedlings. Plant Physiology and Biochemistry, 2020, 146, 349-362.	5.8	13
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