Ghasem H Salekdeh

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4849042/publications.pdf

Version: 2024-02-01

244 papers

13,930 citations

53 h-index 27406 106 g-index

259 all docs

259 docs citations

times ranked

259

22196 citing authors

#	Article	IF	CITATIONS
1	Synergistic Effect of Metagenomeâ€Derived Starchâ€Degrading Enzymes on Quality of Functional Bread with Antioxidant Activity. Starch/Staerke, 2022, 74, 2100098.	2.1	8
2	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
3	Proteomics study reveals the molecular mechanisms underlying cryotolerance induced by mild sublethal stress in human sperm. Cell and Tissue Research, 2022, 387, 143-157.	2.9	9
4	In vitro bioprocessing of corn as poultry feed additive by the influence of carbohydrate hydrolyzing metagenome derived enzyme cocktail. Scientific Reports, 2022, 12, 405.	3.3	6
5	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
6	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
7	Y chromosome is moving out of sex determination shadow. Cell and Bioscience, 2022, 12, 4.	4.8	5
8	A computational learning paradigm to targeted discovery of biocatalysts from metagenomic data: A case study of lipase identification. Biotechnology and Bioengineering, 2022, 119, 1115-1128.	3.3	13
9	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
10	Genome-Wide Expression Analysis of Root Tips in Contrasting Rice Genotypes Revealed Novel Candidate Genes for Water Stress Adaptation. Frontiers in Plant Science, 2022, 13, 792079.	3.6	10
11	Changes in root microbiome during wheat evolution. BMC Microbiology, 2022, 22, 64.	3.3	12
12	Key Genes and Biochemical Networks in Various Brain Regions Affected in Alzheimer's Disease. Cells, 2022, 11, 987.	4.1	16
13	The novel homologue of the human αâ€glucosidase inhibited by the nonâ€germinated and germinated quinoa protein hydrolysates after in vitro gastrointestinal digestion. Journal of Food Biochemistry, 2022, 46, e14030.	2.9	7
14	Enzymatically triggered delignification through a novel stable laccase: A mixed in-silico /in-vitro exploration of a complex environmental microbiota. International Journal of Biological Macromolecules, 2022, 211, 328-341.	7.5	9
15	BMP4 signaling plays critical roles in self-renewal of R2i mouse embryonic stem cells. Biochemical and Biophysical Research Communications, 2022, 617, 8-15.	2.1	1
16	Y Chromosome Genes May Play Roles in the Development of Neural Rosettes from Human Embryonic Stem Cells. Stem Cell Reviews and Reports, 2022, 18, 3008-3020.	3.8	2
17	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	15
18	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

#	Article	IF	CITATIONS
19	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
20	The quest of cell surface markers for stem cell therapy. Cellular and Molecular Life Sciences, 2021, 78, 469-495.	5.4	12
21	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
22	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
23	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
24	Whole-Genome Resequencing Reveals Adaptation Prior to the Divergence of Buffalo Subspecies. Genome Biology and Evolution, 2021, 13 , .	2.5	4
25	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
26	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
27	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. PeerJ, 2021, 9, e10463.	2.0	18
28	Inner retinal injury in experimental glaucoma is prevented upon AAV mediated Shp2 silencing in a caveolin dependent manner. Theranostics, 2021, 11, 6154-6172.	10.0	12
29	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
30	Bi-functionalized aminoguanidine-PEGylated periodic mesoporous organosilica nanoparticles: a promising nanocarrier for delivery of Cas9-sgRNA ribonucleoproteine. Journal of Nanobiotechnology, 2021, 19, 95.	9.1	9
31	Mouse model of Alzheimer's disease demonstrates differential effects of early disease pathology on various brain regions. Proteomics, 2021, 21, e2000213.	2.2	5
32	Biophysical, Rheological, and Functional Properties of Complex of Sodium Caseinate and Olive Leaf Aqueous Polyphenolic Extract Obtained Using Ultrasound-Assisted Extraction. Food Biophysics, 2021, 16, 325-336.	3.0	13
33	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
34	Root endophytic fungus <i>Serendipita indica</i> 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
35	Mitochondrial dysfunction in Alzheimer's disease - a proteomics perspective. Expert Review of Proteomics, 2021, 18, 295-304.	3.0	27
36	Highly Efficient Computationally Derived Novel Metagenome α-Amylase With Robust Stability Under Extreme Denaturing Conditions. Frontiers in Microbiology, 2021, 12, 713125.	3.5	7

#	Article	IF	CITATIONS
37	A Proteomic View of Cellular and Molecular Effects of Cannabis. Biomolecules, 2021, 11, 1411.	4.0	11
38	Efficient removal of various textile dyes from wastewater by novel thermo-halotolerant laccase. Bioresource Technology, 2021, 337, 125468.	9.6	37
39	Application of free and immobilized novel bifunctional biocatalyst in biotransformation of recalcitrant lignocellulosic biomass. Chemosphere, 2021, 285, 131412.	8.2	12
40	Zeolite-based nanocomposite as a smart pH-sensitive nanovehicle for release of xylanase as poultry feed supplement. Scientific Reports, 2021, 11, 21386.	3.3	5
41	The Contribution of Y Chromosome Genes to Spontaneous Differentiation of Human Embryonic Stem Cells into Embryoid Bodies. Cell Journal, 2021, 23, 40-50.	0.2	1
42	Comparative Analysis of Aducanumab, Zagotenemab and Pioglitazone as Targeted Treatment Strategies for Alzheimer's Disease. , 2021, 12, 1964.		35
43	Transcriptomic and Metabolomic Analyses Reveal Inhibition of Hepatic Adipogenesis and Fat Catabolism in Yak for Adaptation to Forage Shortage During Cold Season. Frontiers in Cell and Developmental Biology, 2021, 9, 759521.	3.7	5
44	Proteomic and metabolomic analysis of desiccation tolerance in wheat young seedlings. Plant Physiology and Biochemistry, 2020, 146, 349-362.	5.8	13
45	Differential adaptation strategies to different levels of soil water deficit in two upland and lowland genotypes of rice: a physiological and metabolic approach. Journal of the Science of Food and Agriculture, 2020, 100, 1458-1469.	3.5	5
46	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
47	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
48	A novel high performance in-silico screened metagenome-derived alkali-thermostable endo- \hat{l}^2 -1,4-glucanase for lignocellulosic biomass hydrolysis in the harsh conditions. BMC Biotechnology, 2020, 20, 56.	3.3	37
49	A novel metagenome-derived thermostable and poultry feed compatible \hat{l} ±-amylase with enhanced biodegradation properties. International Journal of Biological Macromolecules, 2020, 164, 2124-2133.	7. 5	24
50	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
51	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
52	Recent Advances of Functional Proteomics in Gastrointestinal Cancers- a Path towards the Identification of Candidate Diagnostic, Prognostic, and Therapeutic Molecular Biomarkers. International Journal of Molecular Sciences, 2020, 21, 8532.	4.1	13
53	A Novel High Glucose-Tolerant \hat{l}^2 -Glucosidase: Targeted Computational Approach for Metagenomic Screening. Frontiers in Bioengineering and Biotechnology, 2020, 8, 813.	4.1	38
54	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

#	Article	IF	Citations
55	The Dynamic Proteome of Oligodendrocyte Lineage Differentiation Features Planar Cell Polarity and Macroautophagy Pathways. GigaScience, 2020, 9, .	6.4	10
56	Proteome analysis of endometrial tissue from patients with PCOS reveals proteins predicted to impact the disease. Molecular Biology Reports, 2020, 47, 8763-8774.	2.3	8
57	Human Proteome Project and Human Pluripotent Stem Cells: Odd Bedfellows or a Perfect Match?. Journal of Proteome Research, 2020, 19, 4747-4753.	3.7	2
58	Plant isomiRs: origins, biogenesis, and biological functions. Genomics, 2020, 112, 3382-3395.	2.9	12
59	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
60	Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome. Scientific Reports, 2020, 10, 4995.	3.3	16
61	Proteomic analysis of wheat contrasting genotypes reveals the interplay between primary metabolic and regulatory pathways in anthers under drought stress. Journal of Proteomics, 2020, 226, 103895.	2.4	7
62	SOX2 protein transduction directly converts human fibroblasts into oligodendrocyte-like cells. Biochemical and Biophysical Research Communications, 2020, 525, 1-7.	2.1	5
63	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. FEMS Microbiology Ecology, 2020, 96, .	2.7	32
64	Proteomics Analysis of Trastuzumab Toxicity in the H9c2 Cardiomyoblast Cell Line and its Inhibition by Carvedilol. Current Pharmaceutical Biotechnology, 2020, 21, 1377-1385.	1.6	1
65	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
66	Transcriptomic analysis of Aegilops tauschii during long-term salinity stress. Functional and Integrative Genomics, 2019, 19, 13-28.	3.5	30
67	Down-Regulation of a Male-Specific H3K4 Demethylase, <i>KDM5D</i> , Impairs Cardiomyocyte Differentiation. Journal of Proteome Research, 2019, 18, 4277-4282.	3.7	15
68	Inhibition of Human Y Chromosome Gene, <i>SRY</i> , Promotes NaÃ-ve State of Human Pluripotent Stem Cells. Journal of Proteome Research, 2019, 18, 4254-4261.	3.7	5
69	Upregulation of Proteolytic Pathways and Altered Protein Biosynthesis Underlie Retinal Pathology in a Mouse Model of Alzheimer's Disease. Molecular Neurobiology, 2019, 56, 6017-6034.	4.0	41
70	Plant–Microbe Symbiosis: What Has Proteomics Taught Us?. Proteomics, 2019, 19, e1800105.	2.2	22
71	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
72	Abiotic stress responsive microRNome and proteome: How correlated are they?. Environmental and Experimental Botany, 2019, 165, 150-160.	4.2	4

#	Article	lF	Citations
73	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
74	Amyloid \hat{l}^2 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
75	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
76	The Quest for Missing Proteins in Rice. Molecular Plant, 2019, 12, 4-6.	8.3	8
77	Preconditioning of sperm with sublethal nitrosative stress: a novel approach to improve frozen–thawed sperm function. Reproductive BioMedicine Online, 2019, 38, 413-425.	2.4	14
78	Loss of Shp2 Rescues BDNF/TrkB Signaling and Contributes to Improved Retinal Ganglion Cell Neuroprotection. Molecular Therapy, 2019, 27, 424-441.	8.2	39
79	Identification and characterization of a novel thermostable xylanase from camel rumen metagenome. International Journal of Biological Macromolecules, 2019, 126, 1295-1302.	7.5	48
80	The comparative analysis of phenotypic and whole transcriptome gene expression data of ascites susceptible versus ascites resistant chickens. Molecular Biology Reports, 2019, 46, 793-804.	2.3	2
81	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
82	The impact of slaughtering methods on physicochemical characterization of sheep myoglobin. Journal of the Iranian Chemical Society, 2019, 16, 315-324.	2.2	4
83	Upstream Regulatory Elements, Potential Targets and Expression Patterns of Three Drought Responsive miRNAs in Two Grapevine Cultivars. Plant Genetic Researches, 2019, 6, 115-126.	0.1	0
84	Prospective Isolation of ISL1+ Cardiac Progenitors from Human ESCs forÂMyocardial Infarction Therapy. Stem Cell Reports, 2018, 10, 848-859.	4.8	23
85	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
86	MicroRNA-340 inhibits the proliferation and promotes the apoptosis of colon cancer cells by modulating REV3L. Oncotarget, 2018, 9, 5155-5168.	1.8	18
87	MicroRNA network analysis and target genes associated with human sperm cryopreservation. Cryobiology, 2018, 85, 122-123.	0.7	0
88	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
89	Surface markers of human embryonic stem cells: a meta analysis of membrane proteomics reports. Expert Review of Proteomics, 2018, 15, 911-922.	3.0	8
90	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

#	Article	IF	CITATIONS
91	The Art of Validating Quantitative Proteomics Data. Proteomics, 2018, 18, e1800222.	2.2	25
92	Distribution and development of molecularly distinct perineuronal nets in visual thalamus. Journal of Neurochemistry, 2018, 147, 626-646.	3.9	23
93	Subcellular Proteome Landscape of Human Embryonic Stem Cells Revealed Missing Membrane Proteins. Journal of Proteome Research, 2018, 17, 4138-4151.	3.7	19
94	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
95	A metagenomic analysis of the camel rumen's microbiome identifies the major microbes responsible for lignocellulose degradation and fermentation. Biotechnology for Biofuels, 2018, 11, 216.	6.2	96
96	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
97	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
98	Metabolic Signature of Pluripotent Stem Cells. Cell Journal, 2018, 20, 388-395.	0.2	6
99	Advanced glycation end-products produced systemically and by macrophages: A common contributor to inflammation and degenerative diseases., 2017, 177, 44-55.		232
100	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
101	Proteome analysis of human embryonic stem cells organelles. Journal of Proteomics, 2017, 162, 108-118.	2.4	12
102	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
103	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
104	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
105	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
106	Data for whole and mitochondrial proteome of human embryonic stem cells. Data in Brief, 2017, 13, 371-376.	1.0	2
107	Red/ox states of human protein disulfide isomerase regulate binding affinity of 17 beta-estradiol. Archives of Biochemistry and Biophysics, 2017, 619, 35-44.	3.0	4
108	Drought tolerance in four-day-old seedlings of a drought-sensitive cultivar of wheat. Journal of Plant Nutrition, 2017, 40, 574-583.	1.9	9

7

#	Article	IF	CITATIONS
109	Cold-induced physiological and biochemical responses of three grapevine cultivars differing in cold tolerance. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	21
110	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. Scientific Reports, 2017, 7, 12685.	3.3	105
111	Low Focal Adhesion Signaling Promotes Ground State Pluripotency of Mouse Embryonic Stem Cells. Journal of Proteome Research, 2017, 16, 3585-3595.	3.7	23
112	Y Chromosome Missing Protein, TBL1Y, May Play an Important Role in Cardiac Differentiation. Journal of Proteome Research, 2017, 16, 4391-4402.	3.7	36
113	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
114	The dynamics of the bacterial communities developed in maize silage. Microbial Biotechnology, 2017, 10, 1663-1676.	4.2	77
115	MicroRNAs regulate the main events in rice drought stress response by manipulating the water supply to shoots. Molecular BioSystems, 2017, 13, 2289-2302.	2.9	11
116	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
117	A Proteomics Approach to Discover Drought Tolerance Proteins in Wheat Pollen Grain at Meiosis Stage. Protein and Peptide Letters, 2016, 24, 26-36.	0.9	11
118	The suitability of some blood gas and biochemical parameters as diagnostic tools or early indicators of ascites syndrome in broiler sire lines. Journal of Animal Physiology and Animal Nutrition, 2016, 100, 456-463.	2.2	4
119	Proteome Analysis of Ground State Pluripotency. Scientific Reports, 2016, 5, 17985.	3.3	31
120	Proteomics in Detection of Contaminations and Adulterations in Agricultural Foodstuffs. , 2016, , 67-85.		0
121	Holistic Sequencing: Moving Forward from Plant Microbial Proteomics to Metaproteomics. , 2016, , 87-103.		2
122	Insight into Physiological, Molecular, and Proteomic Changes Associated with Phytoplasma Infection in Crop Plants., 2016,, 251-265.		2
123	Insect Pest Proteomics and Its Potential Application in Pest Control Management. , 2016, , 267-287.		3
124	Proteomic Analysis of Crop Plants Under Low Temperature: A Review of Cold Responsive Proteins. , 2016, , 97-127.		5
125	Applications of Quantitative Proteomics in Plant Research. , 2016, , 1-29.		5
126	Nesterenkonia sp. strain F, a halophilic bacterium producing acetone, butanol and ethanol under aerobic conditions. Scientific Reports, 2016, 6, 18408.	3.3	27

#	Article	IF	Citations
127	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	14.5	177
128	Two-dimensional blue native/SDS-PAGE analysis of whole cell lysate protein complexes of rice in response to salt stress. Journal of Plant Physiology, 2016, 200, 90-101.	3.5	8
129	PlantPReS: A database for plant proteome response to stress. Journal of Proteomics, 2016, 143, 69-72.	2.4	37
130	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
131	Comparative genome analysis of Oceanimonas sp. GK1, a halotolerant bacterium with considerable xenobiotics degradation potentials. Annals of Microbiology, 2016, 66, 703-716.	2.6	5
132	MicroRNA Signatures of Drought Signaling in Rice Root. PLoS ONE, 2016, 11, e0156814.	2.5	56
133	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. PLoS ONE, 2015, 10, e0130425.	2.5	39
134	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
135	Investigation of a Hot-Spring Extremophilic Ureibacillus thermosphaericus Strain Thermo-BF for Extracellular Biosynthesis of Functionalized Gold Nanoparticles. BioNanoScience, 2015, 5, 233-241.	3.5	11
136	Influence of Ascites Syndrome on Growth Pattern of Chickens Reared at Normal or Cold Ambient Temperature. Annals of Animal Science, 2015, 15, 373-385.	1.6	5
137	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
138	$\langle i \rangle$ DDX3Y $\langle i \rangle$, a Male-Specific Region of Y Chromosome Gene, May Modulate Neuronal Differentiation. Journal of Proteome Research, 2015, 14, 3474-3483.	3.7	61
139	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
140	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	3.7	53
141	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
142	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
143	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
144	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

#	Article	IF	CITATIONS
145	Data in support of comparative physiology and proteomic analysis of two wheat genotypes contrasting in drought tolerance. Data in Brief, 2015, 2, 26-28.	1.0	5
146	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
147	In-depth diversity analysis of the bacterial community resident in the camel rumen. Systematic and Applied Microbiology, 2015, 38, 67-76.	2.8	92
148	Comparative physiology and proteomic analysis of two wheat genotypes contrasting in drought tolerance. Journal of Proteomics, 2015, 114, 1-15.	2.4	99
149	Efficient Differentiation of Human Embryonic Stem Cells Toward Dopaminergic Neurons Using Recombinant LMX1A Factor. Molecular Biotechnology, 2015, 57, 184-194.	2.4	21
150	Induction of Neural Progenitor-Like Cells from Human Fibroblasts via a Genetic Material-Free Approach. PLoS ONE, 2015, 10, e0135479.	2.5	25
151	Genome-Wide Analysis of Oceanimonas sp. GK1 Isolated from Gavkhouni Wetland (Iran) Demonstrates Presence of Genes for Virulence and Pathogenicity. Cell Journal, 2015, 17, 451-60.	0.2	2
152	Comparative Proteomic Profiling of Leishmania tropica: Investigation of a Case Infected with Simultaneous Cutaneous and Viscerotropic Leishmaniasis by 2-Dimentional Electrophoresis and Mass Spectrometry. Iranian Journal of Parasitology, 2015, 10, 366-80.	0.6	9
153	Comparison of the Proteome Profiling of Iranian isolates of Leishmania tropica, L. major and L. infantum by Two-Dimensional Electrophoresis (2-DE) and Mass-spectrometry. Iranian Journal of Parasitology, 2015, 10, 530-40.	0.6	9
154	Induced Neural Lineage Cells as Repair Kits: So Close, Yet So Far Away. Journal of Cellular Physiology, 2014, 229, 728-742.	4.1	13
155	The effect of Rho-associated kinase inhibition on the proteome pattern of dissociated human embryonic stem cells. Molecular BioSystems, 2014, 10, 640.	2.9	10
156	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
157	Inhibition of TGFÎ ² Signaling Promotes Ground State Pluripotency. Stem Cell Reviews and Reports, 2014, 10, 16-30.	5.6	60
158	Manipulating Root Water Supply Elicits Major Shifts in the Shoot Proteome. Journal of Proteome Research, 2014, 13, 517-526.	3.7	52
159	Organellar Proteomics of Embryonic Stem Cells. Advances in Protein Chemistry and Structural Biology, 2014, 95, 215-230.	2.3	10
160	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
161	Characterization of Three Key MicroRNAs in Rice Root Architecture under Drought Stress using In silico Analysis and Quantitative Real-time PCR. Biosciences, Biotechnology Research Asia, 2014, 11, 555-565.	0.5	7
162	Stem Cell Research and Therapy in the Islamic Republic of Iran: Pioneering in the Islamic World. Stem Cells and Development, 2013, 22, 51-57.	2.1	12

#	Article	IF	Citations
163	Comparative SRY incorporation on the regulatory regions of pluripotency/differentiation genes in human embryonic carcinoma cells after retinoic acid induction. Molecular and Cellular Biochemistry, 2013, 376, 145-150.	3.1	7
164	Proteome analysis of post-transplantation recovery mechanisms of an EAE model of multiple sclerosis treated with embryonic stem cell-derived neural precursors. Journal of Proteomics, 2013, 94, 437-450.	2.4	12
165	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
166	Disease-Corrected Hepatocyte-Like Cells from Familial Hypercholesterolemia-Induced Pluripotent Stem Cells. Molecular Biotechnology, 2013, 54, 863-873.	2.4	41
167	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
168	Study of Sperm Protein Profile in Men With and Without Varicocele Using Two-Dimensional Gel Electrophoresis. Urology, 2013, 81, 293-300.	1.0	52
169	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
170	A Fresh Look at the Male-specific Region of the Human Y Chromosome. Journal of Proteome Research, 2013, 12, 6-22.	3.7	52
171	A proteomics approach to study the molecular basis of enhanced salt tolerance in barley (Hordeum) Tj ETQq1 1 (2013, 9, 1498.	0.784314 2.9	rgBT /Overlo 67
172	Shotgun Proteomic Analysis of the Mexican Lime Tree Infected with "⟨i⟩Candidatus⟨ i⟩⟨i⟩Phytoplasma aurantifolia⟨ i⟩― Journal of Proteome Research, 2013, 12, 785-795.	3.7	54
173	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
174	Effects of Synbiotic Supplementation on Breast Milk Levels of IgA, TGF-Î ² 1, and TGF-Î ² 2. Journal of Human Lactation, 2013, 29, 591-596.	1.6	30
175	ISL1 Protein Transduction Promotes Cardiomyocyte Differentiation from Human Embryonic Stem Cells. PLoS ONE, 2013, 8, e55577.	2.5	34
176	Phytoplasma-Responsive microRNAs Modulate Hormonal, Nutritional, and Stress Signalling Pathways in Mexican Lime Trees. PLoS ONE, 2013, 8, e66372.	2.5	61
177	Cloning, expression and functional characterization of in-house prepared human basic fibroblast growth factor. Cell Journal, 2013, 14, 282-91.	0.2	15
178	Cloning, expression, and functional characterization of in-house prepared human leukemia inhibitory factor. Cell Journal, 2013, 15, 190-7.	0.2	7
179	Draft Genome Sequence of Ureibacillus thermosphaericus Strain Thermo-BF, Isolated from Ramsar Hot Springs in Iran. Journal of Bacteriology, 2012, 194, 4431-4431.	2.2	7
180	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

#	Article	IF	Citations
181	Promoting Agriculture Proteome Research Activities in the Asia and Oceania Region. Journal of Proteome Research, 2012, 11, 1461-1461.	3.7	1
182	Identification and validation of Asteraceae miRNAs by the expressed sequence tag analysis. Gene, 2012, 493, 253-259.	2.2	15
183	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	3.7	135
184	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
185	Shotgun Proteomic Analysis of Long-distance Drought Signaling in Rice Roots. Journal of Proteome Research, 2012, 11, 348-358.	3.7	92
186	Proteomic analysis of rice anthers under salt stress. Plant Physiology and Biochemistry, 2012, 58, 280-287.	5.8	58
187	Extensive genetic diversity in Iranian pomegranate (Punica granatum L.) germplasm revealed by microsatellite markers. Scientia Horticulturae, 2012, 146, 104-114.	3.6	18
188	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
189	Embryonic Stem Cell Interactomics: The Beginning of a Long Road to Biological Function. Stem Cell Reviews and Reports, 2012, 8, 1138-1154.	5.6	8
190	An orthogonal comparison of the proteome of human embryonic stem cells with that of human induced pluripotent stem cells of different genetic background. Molecular BioSystems, 2012, 8, 1833.	2.9	9
191	Quantitative Proteomic Analysis of Human Embryonic Stem Cell Differentiation by 8-Plex iTRAQ Labelling. PLoS ONE, 2012, 7, e38532.	2.5	23
192	Identification of cytoplasmic and membrane-associated complexes in human embryonic stem cells using blue native PAGE. Molecular BioSystems, 2011, 7, 2688.	2.9	7
193	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
194	Proteomic analysis of the Mexican lime tree response to "Candidatus Phytoplasma aurantifolia― infection. Molecular BioSystems, 2011, 7, 3028.	2.9	43
195	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
196	Comprehensive Gene Expression Analysis of Human Embryonic Stem Cells during Differentiation into Neural Cells. PLoS ONE, 2011, 6, e22856.	2.5	72
197	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
198	Identification of genes differentially expressed during interaction of Mexican lime tree infected with "Candidatus Phytoplasma aurantifolia". BMC Microbiology, 2011, 11, 1.	3.3	135

#	Article	IF	Citations
199	Comparative proteomic analysis of canola leaves under salinity stress. Proteomics, 2011, 11, 1965-1975.	2.2	97
200	Concise Review: Alchemy of Biology: Generating Desired Cell Types from Abundant and Accessible Cells. Stem Cells, 2011, 29, 1933-1941.	3.2	41
201	Defining pluripotent stem cells through quantitative proteomic analysis. Expert Review of Proteomics, 2011, 8, 29-42.	3.0	26
202	Draft Genome Sequence of Nesterenkonia sp. Strain F, Isolated From Aran-Bidgol Salt Lake in Iran. Journal of Bacteriology, 2011, 193, 5580-5580.	2.2	12
203	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	3.8	37
204	Nuclear Proteome Analysis of Monkey Embryonic Stem Cells During Differentiation. Stem Cell Reviews and Reports, 2010, 6, 50-61.	5.6	8
205	Progress and Promise Towards Safe Induced Pluripotent Stem Cells for Therapy. Stem Cell Reviews and Reports, 2010, 6, 297-306.	5.6	61
206	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
207	Proteome analysis of brain in murine experimental autoimmune encephalomyelitis. Proteomics, 2010, 10, 2822-2832.	2.2	18
208	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
209	An efficient and easy-to-use cryopreservation protocol for human ES and iPS cells. Nature Protocols, 2010, 5, 588-594.	12.0	65
210	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
211	Induced pluripotent stem cells: A new era for hepatology. Journal of Hepatology, 2010, 53, 738-751.	3.7	77
212	Generation of human induced pluripotent stem cells from a Bombay individual: Moving towards "universal-donor―red blood cells. Biochemical and Biophysical Research Communications, 2010, 391, 329-334.	2.1	34
213	Epigenetic analysis of human embryonic carcinoma cells during retinoic acid-induced neural differentiation. Biochemistry and Cell Biology, 2010, 88, 527-538.	2.0	19
214	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
215	A comparative proteome approach to decipher the mechanism of rice adaptation to phosphorous deficiency. Proteomics, 2009, 9, 159-170.	2.2	80
216	Comparative proteome and transcriptome analyses of embryonic stem cells during embryoid bodyâ€based differentiation. Proteomics, 2009, 9, 4859-4870.	2.2	58

#	Article	IF	Citations
217	Begomoviruses Associated with Yellow Leaf Curl Disease of Tomato in Iran*. Journal of Phytopathology, 2009, 157, 243-247.	1.0	10
218	Conceptual framework for drought phenotyping during molecular breeding. Trends in Plant Science, 2009, 14, 488-496.	8.8	213
219	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
220	Proteomic Analysis of Monkey Embryonic Stem Cell during Differentiation. Journal of Proteome Research, 2009, 8, 1527-1539.	3.7	19
221	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
222	Assessing wheat (<i>Triticum aestivum</i> 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
223	Biological and Molecular Variability of <i>Zucchini yellow mosaic virus</i> in Iran*. Journal of Phytopathology, 2008, 156, 654-659.	1.0	20
224	Identification of Mouse Embryonic Stem Cell-Associated Proteins. Journal of Proteome Research, 2008, 7, 412-423.	3.7	44
225	Proteomics Reveals New Salt Responsive Proteins Associated with Rice Plasma Membrane. Bioscience, Biotechnology and Biochemistry, 2007, 71, 2144-2154.	1.3	141
226	Proteomics Uncovers a Role for Redox in Drought Tolerance in Wheat§. Journal of Proteome Research, 2007, 6, 1451-1460.	3.7	179
227	Concise Review: Trends in Stem Cell Proteomics. Stem Cells, 2007, 25, 1888-1903.	3.2	82
228	Crop proteomics: Aim at sustainable agriculture of tomorrow. Proteomics, 2007, 7, 2976-2996.	2.2	155
229	Detection and Characterization of Phytoplasmas Infecting Ornamental and Weed Plants in Iran. Journal of Phytopathology, 2007, 155, 368-372.	1.0	36
230	Comparative proteomic analysis of mouse embryonic stem cells and neonatal-derived cardiomyocytes. Biochemical and Biophysical Research Communications, 2006, 349, 1041-1049.	2.1	25
231	Effects of salinity levels on proteome of Suaeda aegyptiaca leaves. Proteomics, 2006, 6, 2542-2554.	2.2	173
232	Proteomic signature of human embryonic stem cells. Proteomics, 2006, 6, 3544-3549.	2.2	91
233	Proteomic responses of rice young panicles to salinity. Proteomics, 2006, 6, 6498-6507.	2.2	144
234	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

#	Article	IF	CITATIONS
235	Proteome response of Elymus elongatum to severe water stress and recovery. Journal of Experimental Botany, 2006, 58, 291-300.	4.8	106
236	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
237	Comparison of biologically distinct isolates of Citrus tristeza virus from Iran using major coat protein sequences. Australasian Plant Pathology, 2005, 34, 577.	1.0	3
238	Proteome analysis of sugar beet leaves under drought stress. Proteomics, 2005, 5, 950-960.	2.2	256
239	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
240	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
241	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
242	A proteomic approach to analyzing drought- and salt-responsiveness in rice. Field Crops Research, 2002, 76, 199-219.	5.1	245
243	Proteomic analysis of rice leaves during drought stress and recovery. Proteomics, 2002, 2, 1131-1145.	2.2	415
244	Association between early growth-related traits and ascites induced in broiler sire lines by saline drinking water or cool temperatures. , 0, , .		2