

Mohammad Pourkheirandish

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9258184/publications.pdf>

Version: 2024-02-01

39
papers

2,973
citations

361413

20
h-index

302126

39
g-index

41
all docs

41
docs citations

41
times ranked

3622
citing authors

#	ARTICLE	IF	CITATIONS
1	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	12.6	781
2	Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1424-1429.	7.1	563
3	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	28.9	265
4	Cleistogamous flowering in barley arises from the suppression of microRNA-guided <i>HvAP2</i> mRNA cleavage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 490-495.	7.1	201
5	<i>Six-rowed spike4</i> (<i>Vrs4</i>) controls spikelet determinacy and row-type in barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13198-13203.	7.1	140
6	An ATP-binding cassette subfamily G full transporter is essential for the retention of leaf water in both wild barley and rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12354-12359.	7.1	134
7	The Importance of Barley Genetics and Domestication in a Global Perspective. <i>Annals of Botany</i> , 2007, 100, 999-1008.	2.9	125
8	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. <i>Current Biology</i> , 2016, 26, 775-781.	3.9	85
9	Divergence of expression pattern contributed to neofunctionalization of duplicated <i>HD-ZIP</i> transcription factor in barley. <i>New Phytologist</i> , 2013, 197, 939-948.	7.3	67
10	On the Origin of the Non-brittle Rachis Trait of Domesticated Einkorn Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2031.	3.6	58
11	Duplication of a well-conserved homeodomain-leucine zipper transcription factor gene in barley generates a copy with more specific functions. <i>Functional and Integrative Genomics</i> , 2010, 10, 123-133.	3.5	49
12	Molecular genetics of leaf rust resistance in wheat and barley. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2035-2050.	3.6	46
13	Global Role of Crop Genomics in the Face of Climate Change. <i>Frontiers in Plant Science</i> , 2020, 11, 922.	3.6	45
14	A <i>GDSL</i> motif esterase/acyltransferase/lipase is responsible for leaf water retention in barley. <i>Plant Direct</i> , 2017, 1, e00025.	1.9	39
15	Analysis of Intraspecies Diversity in Wheat and Barley Genomes Identifies Breakpoints of Ancient Haplotypes and Provides Insight into the Structure of Diploid and Hexaploid Triticeae Gene Pools. <i>Plant Physiology</i> , 2009, 149, 258-270.	4.8	38
16	Molecular evolution and phylogeny of the <i>RPB2</i> gene in the genus <i>Hordeum</i> . <i>Annals of Botany</i> , 2009, 103, 975-983.	2.9	33
17	Allelic variation of row type gene <i>Vrs1</i> in barley and implication of the functional divergence. <i>Breeding Science</i> , 2009, 59, 621-628.	1.9	30
18	Structure, transcription and post-transcriptional regulation of the bread wheat orthologs of the barley cleistogamy gene <i>Cly1</i> . <i>Theoretical and Applied Genetics</i> , 2013, 126, 1273-1283.	3.6	27

#	ARTICLE	IF	CITATIONS
19	miR172 downregulates the translation of cleistogamy 1 in barley. <i>Annals of Botany</i> , 2018, 122, 251-265.	2.9	25
20	Wheat domestication in light of haplotype analyses of the Brittle rachis 1 genes (BTR1-A and BTR1-B). <i>Plant Science</i> , 2019, 285, 193-199.	3.6	23
21	High-resolution genetic mapping and physical map construction for the fertility restorer Rfm1 locus in barley. <i>Theoretical and Applied Genetics</i> , 2015, 128, 283-290.	3.6	20
22	Elucidation of the origin of <i>agriocrithon</i> based on domestication genes questions the hypothesis that Tibet is one of the centers of barley domestication. <i>Plant Journal</i> , 2018, 94, 525-534.	5.7	17
23	Quantitative Trait Loci and Maternal Effects Affecting the Strong Grain Dormancy of Wild Barley (<i>Hordeum vulgare</i> ssp. <i>spontaneum</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1840.	3.6	16
24	Mapping of the eibi1 gene responsible for the drought hypersensitive cuticle in wild barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.9	15
25	Variation in the wheat <i>AP2</i> homoeologs, the genes underlying lodicule development. <i>Breeding Science</i> , 2013, 63, 255-266.	1.9	15
26	An eceriferum locus, cer-zv, is associated with a defect in cutin responsible for water retention in barley (<i>Hordeum vulgare</i>) leaves. <i>Theoretical and Applied Genetics</i> , 2013, 126, 637-646.	3.6	14
27	Wheat yellow mosaic virus resistance in wheat cultivar Madsen acts in roots but not in leaves. <i>Journal of General Plant Pathology</i> , 2016, 82, 261-267.	1.0	13
28	An alternative mechanism for cleistogamy in barley. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2753-2762.	3.6	12
29	The barley leaf rust resistance gene Rph3 encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of <i>Puccinia hordei</i> . <i>Nature Communications</i> , 2022, 13, 2386.	12.8	12
30	Detection of photoperiod responsive and non-responsive flowering time QTL in barley. <i>Breeding Science</i> , 2011, 61, 183-188.	1.9	11
31	Population-genetic analysis of HvABCG31 promoter sequence in wild barley (<i>Hordeum vulgare</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overlock 11 Tf 50 22	3.2	11
32	Genetic targeting of candidate genes for drought sensitive gene eibi1 of wild barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.9	9
33	Diversification of the promoter sequences of wheat Mother of FT and TFL1 on chromosome 3A. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	7
34	Mapping of QTL for intermedium spike on barley chromosome 4H using EST-based markers. <i>Breeding Science</i> , 2009, 59, 383-390.	1.9	7
35	Genetic Diversity of Cultivated Barley Landraces in Iran Measured Using Microsatellites. <i>International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB)</i> , 2012, , 287-290.	0.2	7
36	Molecular variability and population structure of a core collection of date palm (<i>Phoenix dactylifera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.3	4

#	ARTICLE	IF	CITATIONS
37	Grain Disarticulation in Wild Wheat and Barley. <i>Plant and Cell Physiology</i> , 2022, 63, 1584-1591.	3.1	4
38	Allele mining of wheat ABA receptor at TaPYL4 suggests neo-functionalization among the wheat homoeologs. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2183-2196.	3.5	3
39	Grain dispersal mechanism in cereals arose from a genome duplication followed by changes in spatial expression of genes involved in pollen development. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1263-1277.	3.6	1