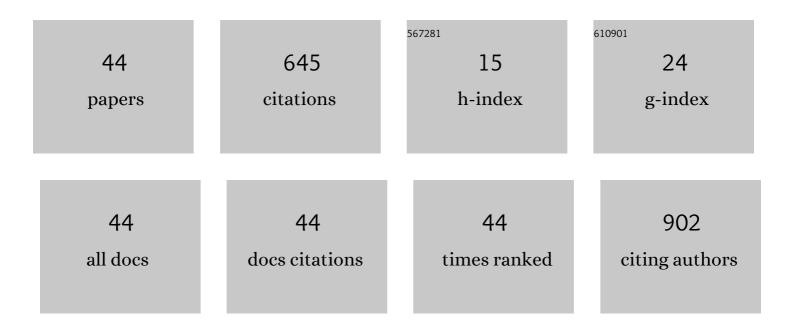
Babak Rabiei

List of Publications by Year in descending order

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RARAK PARIEL

#	Article	IF	CITATIONS
1	Mapping QTLs for Traits Related to Salinity Tolerance at Seedling Stage of Rice (<i>Oryza sativa</i> L.): An Agrigenomics Study of an Iranian Rice Population. OMICS A Journal of Integrative Biology, 2013, 17, 242-251.	2.0	67
2	Improvement of nitrogen management in rice paddy fields using chlorophyll meter (SPAD). Paddy and Water Environment, 2008, 6, 181-188.	1.8	61
3	Identification of QTLs for rice grain size and shape of Iranian cultivars using SSR markers. Euphytica, 2004, 137, 325-332.	1.2	53
4	Biochemical, physiological and molecular evaluation of rice cultivars differing in salt tolerance at the seedling stage. Physiology and Molecular Biology of Plants, 2017, 23, 529-544.	3.1	43
5	Evaluation of selection indices for improving rice grain shape. Field Crops Research, 2004, 89, 359-367.	5.1	36
6	Biotechnological Production of Flavonoids: An Update on Plant Metabolic Engineering, Microbial Host Selection, and Genetically Encoded Biosensors. Biotechnology Journal, 2020, 15, e1900432.	3.5	35
7	Association analysis, genetic diversity and haplotyping of rice plants under salt stress using SSR markers linked to SalTol and morpho-physiological characteristics. Plant Systematics and Evolution, 2016, 302, 871-890.	0.9	30
8	Identification of molecular markers linked to saltâ€ŧolerant genes at germination stage of rice. Plant Breeding, 2014, 133, 196-202.	1.9	26
9	Effect of land use and topography on soil properties and agronomic productivity on calcareous soils of a semiarid region, Iran. Land Degradation and Development, 2012, 23, 496-504.	3.9	24
10	Use of Selection Indices Based on Multivariate Analysis for Improving Grain Yield in Rice. Rice Science, 2008, 15, 303-310.	3.9	23
11	Identification of key genes involved in the biosynthesis of triterpenic acids in the mint family. Scientific Reports, 2019, 9, 15826.	3.3	22
12	Different physiobiochemical and transcriptomic reactions of rice (Oryza sativa L.) cultivars differing in terms of salt sensitivity under salinity stress. Environmental Science and Pollution Research, 2017, 24, 7184-7196.	5.3	21
13	Griffing's Methods Comparison for General and Specific Combining Ability in Cucumber. Scientific World Journal, The, 2012, 2012, 1-4.	2.1	19
14	Genetic Variation and Association Analysis of the SSR Markers Linked to the Major Drought-Yield QTLs of Rice. Biochemical Genetics, 2018, 56, 356-374.	1.7	19
15	Impacts of flushing and fermentation times on the quality of black tea. Genetika, 2011, 43, 537-548.	0.4	17
16	Biochemical systematic, population structure and genetic variability studies among Iranian Cucurbita (Cucurbita pepo L.) accessions, using genomic SSRs and implications for their breeding potential. Biochemical Systematics and Ecology, 2013, 50, 187-198.	1.3	15
17	Mapping of QTLs for Germination Characteristics under Non-stress and Drought Stress in Rice. Rice Science, 2013, 20, 391-399.	3.9	13
18	Selection and validation of reference genes for quantitative real-time PCR in Rosmarinus officinalis L. in various tissues and under elicitation. Biocatalysis and Agricultural Biotechnology, 2019, 20, 101246.	3.1	10

Βαβακ Παβιει

#	Article	IF	CITATIONS
19	Salinity Stress Tolerance in Plants: Physiological, Molecular, and Biotechnological Approaches. , 2019, , 101-127.		10
20	Amplified Fragment Length Polymorphism Mapping of Quantitative Trait Loci for Economically Important Traits in the Silkworm, <i>Bombyx mori</i> . Journal of Insect Science, 2010, 10, 1-21.	1.5	9
21	Four genetic loci control compact plant size with yellow pearâ€shaped fruit in ornamental tomato (Solanum lycopersicumL.). Plant Genome, 2020, 13, e20017.	2.8	9
22	Molecular characterization and genetic diversity analysis of different rice cultivars by microsatellite markers. Genetika, 2014, 46, 187-198.	0.4	9
23	Identification and mapping of QTLs for agronomic traits in <i>indica — indica</i> cross of rice (<i>Oryza sativa</i> L.). Cereal Research Communications, 2010, 38, 317-326.	1.6	8
24	Association Analysis of Charcoal Rot Disease Resistance in Soybean. Plant Pathology Journal, 2019, 35, 189-199.	1.7	8
25	Optimizing Seed Germination and Seedling Growth in Different Kiwifruit Genotypes. Horticulturae, 2021, 7, 314.	2.8	8
26	Phylogenetic relationships and genetic diversity of landrace populations of thyme (Thymus spp.) of Iran using AFLP markers and GC–MS. Revista Brasileira De Botanica, 2019, 42, 613-621.	1.3	7
27	Association analysis, genetic diversity and population structure of barley (Hordeum vulgare L.) under heat stress conditions using SSR and ISSR markers linked to primary and secondary metabolites. Molecular Biology Reports, 2021, 48, 6673-6694.	2.3	6
28	The expression of monoterpene synthase genes and their respective end products are affected by gibberellic acid in Thymus vulgaris. Journal of Plant Physiology, 2018, 230, 101-108.	3.5	5
29	Statistical analysis of phenotypic traits of rice (Oryza sativa L.) related to grain yield under neck blast disease. Journal of Plant Diseases and Protection, 2019, 126, 293-306.	2.9	5
30	Effect of silver nano particles and 8-hydroxyquinoline citrate on the longer life of cut Gerbera (Gerbera jamesonii) 'Sunway' flowers. Scientia Horticulturae, 2021, 289, 110474.	3.6	4
31	Dominant variance has an important role in downy mildew resistance in cucumber. Horticulture Environment and Biotechnology, 2011, 52, 422-426.	2.1	3
32	Characterising the genetic diversity of Pseudomonas syringae pv. syringae isolated from rice and wheat in Iran. Plant Protection Science, 2012, 48, 162-169.	1.4	3
33	Evaluation of pre-harvest foliar calcium applications on â€~Fuji' apple fruit quality during cold storage. Australian Journal of Crop Science, 2017, 11, 228-233.	0.3	3
34	Combining ability and heritability of selected rice varieties for grain yield, its components and grain quality characters. Genetika, 2015, 47, 559-570.	0.4	3
35	Identification of Fusarium wilt resistance sources in melon (Cucumis melo L.) landraces of Iran using marker-assisted selection technique. Australasian Plant Pathology, 2020, 49, 413-423.	1.0	2
36	Genetic diversity of Aegilops tauschii accessions and its relationship with tetraploid and hexaploid wheat using retrotransposon-based molecular markers. Cereal Research Communications, 2022, 50, 219-226.	1.6	2

Βαβακ Καβιει

#	Article	IF	CITATIONS
37	Genetic diversity of Iranian rice recombinant inbred lines at the reproductive stage in normal conditions and salinity. Plant Genetic Researches, 2019, 6, 69-86.	0.1	2
38	Identification of AFLP markers linked with cocoon weight genes in silkworm (Bombyx mori L.). African Journal of Biotechnology, 2010, 9, 1427-1433.	0.6	1
39	Association mapping of traits related to leaf blast disease in rice (Oryza sativa L.). Australasian Plant Pathology, 2020, 49, 31-43.	1.0	1
40	Investigation of gene effects on fruit shape index and seed size in generations resulting from the crossing of Zucchini and hull-less seed Pumpkin. Euphytica, 2021, 217, 1.	1.2	1
41	QTLs detection for mohair traits in Iranian Angora goats (Markhoz goats). Small Ruminant Research, 2021, 202, 106460.	1.2	1
42	Analysis and comparison of fragrant gene sequence in some rice cultivars. Genetika, 2016, 48, 597-607.	0.4	1
43	Differentiation by Simplified AFLP of Pseudomonas Syringe Pv. Syringae Isolates from Fields, Panicles and Nurseries of the Guilan Province - Iran. Journal of Plant Protection Research, 2012, 52, .	1.0	0
44	PCR optimization and allele distribution of SNAC1 gene coding region in rice (Oryza sativa L.). Agri Gene, 2017, 4, 30-36.	1.9	0