

# Takeshi Itoh

## List of Publications by Citations

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**Version:** 2024-04-23

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38  
papers

3,548  
citations

21  
h-index

40  
g-index

40  
ext. papers

4,474  
ext. citations

6.3  
avg, IF

4.36  
L-index

#	Paper	IF	Citations
38	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , <b>2013</b> , 6, 4	5.8	1110
37	Rice Annotation Project Database (RAP-DB): an integrative and interactive database for rice genomics. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, e6	4.9	409
36	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D1028-330.1	20.1	262
35	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , <b>2004</b> , 2, e162	9.7	255
34	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , <b>2007</b> , 17, 175-83	9.7	200
33	The Rice Annotation Project Database (RAP-DB): hub for <i>Oryza sativa</i> ssp. japonica genome information. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D741-4	20.1	193
32	Simultaneous RNA-seq analysis of a mixed transcriptome of rice and blast fungus interaction. <i>PLoS ONE</i> , <b>2012</b> , 7, e49423	3.7	178
31	Comprehensive sequence analysis of 24,783 barley full-length cDNAs derived from 12 clone libraries. <i>Plant Physiology</i> , <b>2011</b> , 156, 20-8	6.6	165
30	Genome editing in plants by engineered CRISPR-Cas9 recognizing NG PAM. <i>Nature Plants</i> , <b>2019</b> , 5, 14-1711.5	11.5	112
29	Genome-wide transcriptome analysis reveals that cadmium stress signaling controls the expression of genes in drought stress signal pathways in rice. <i>PLoS ONE</i> , <b>2014</b> , 9, e96946	3.7	83
28	A novel rice cytochrome P450 gene, CYP72A31, confers tolerance to acetolactate synthase-inhibiting herbicides in rice and <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2014</b> , 166, 1232-40	6.6	73
27	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice ( <i>Oryza sativa</i> L.). <i>BMC Genomics</i> , <b>2010</b> , 11, 683	4.5	64
26	TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, e7	4.9	54
25	Construction of pseudomolecule sequences of the aus rice cultivar Kasalath for comparative genomics of Asian cultivated rice. <i>DNA Research</i> , <b>2014</b> , 21, 397-405	4.5	53
24	The power of single molecule real-time sequencing technology in the de novo assembly of a eukaryotic genome. <i>Scientific Reports</i> , <b>2015</b> , 5, 16780	4.9	51
23	Independent domestication of Asian rice followed by gene flow from japonica to indica. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1471-9	8.3	51
22	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , <b>2011</b> , 4, 50-65	5.8	36

21	Massive gene losses in Asian cultivated rice unveiled by comparative genome analysis. <i>BMC Genomics</i> , <b>2010</b> , 11, 121	4.5	32
20	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D787-92	20.1	31
19	TASUKE: a web-based visualization program for large-scale resequencing data. <i>Bioinformatics</i> , <b>2013</b> , 29, 1806-8	7.2	27
18	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. <i>Plant Journal</i> , <b>2011</b> , 66, 796-805	6.9	24
17	The Nipponbare genome and the next-generation of rice genomics research in Japan. <i>Rice</i> , <b>2016</b> , 9, 33	5.8	18
16	MEGANTE: a web-based system for integrated plant genome annotation. <i>Plant and Cell Physiology</i> , <b>2014</b> , 55, e2	4.9	17
15	TASUKE+: a web-based platform for exploring genome-wide association studies results and large-scale resequencing data. <i>DNA Research</i> , <b>2019</b> , 26, 445-452	4.5	9
14	Transcriptome analysis of barley identifies heat shock and HD-Zip I transcription factors up-regulated in response to multiple abiotic stresses. <i>Molecular Breeding</i> , <b>2014</b> , 34, 761-768	3.4	8
13	Mikan Genome Database (MiGD): integrated database of genome annotation, genomic diversity, and CAPS marker information for mandarin molecular breeding. <i>Breeding Science</i> , <b>2020</b> , 70, 200-211	2	7
12	Foreign DNA detection by high-throughput sequencing to regulate genome-edited agricultural products. <i>Scientific Reports</i> , <b>2020</b> , 10, 4914	4.9	6
11	Simultaneous induction of mutant alleles of two allergenic genes in soybean by using site-directed mutagenesis. <i>BMC Plant Biology</i> , <b>2020</b> , 20, 513	5.3	6
10	Gene tree discordance of wild and cultivated Asian rice deciphered by genome-wide sequence comparison. <i>Gene</i> , <b>2011</b> , 477, 53-60	3.8	5
9	Genome-wide validation of <i>Magnaporthe grisea</i> gene structures based on transcription evidence. <i>FEBS Letters</i> , <b>2009</b> , 583, 797-800	3.8	3
8	Rice Genome Annotation: Beginnings of Functional Genomics <b>2007</b> , 21-30		3
7	Genome Sequences of <i>Oryza</i> Species <b>2018</b> , 1-20		1
6	Databases for Rice Omics Studies <b>2018</b> , 541-554		1
5	Development of an SSR marker-based genetic linkage map and identification of a QTL associated with flowering time in. <i>Breeding Science</i> , <b>2021</b> , 71, 344-353	2	0
4	Omics databases for plant breeding. <i>Ikushugaku Kenkyu</i> , <b>2017</b> , 19, 41-47	0.1	

- 3 The First Monocot Genome Sequence. *Advances in Botanical Research*, **2014**, 119-135 2.2
- 2 Bioinformatics and Database of the Rice Genome. *Biotechnology in Agriculture and Forestry*, **2008**, 13-21
- 1 Sequencing of Wheat Chromosome 6B: Toward Functional Genomics **2015**, 111-116