

# Takeshi Itoh

## List of Publications by Year in descending order

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Version: 2024-02-01

38  
papers

4,934  
citations

279487

23  
h-index

395343

33  
g-index

40  
all docs

40  
docs citations

40  
times ranked

6528  
citing authors

#	ARTICLE	IF	CITATIONS
1	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , 2013, 6, 4.	1.7	1,777
2	Rice Annotation Project Database (RAP-DB): An Integrative and Interactive Database for Rice Genomics. <i>Plant and Cell Physiology</i> , 2013, 54, e6-e6.	1.5	614
3	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
4	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
5	Simultaneous RNA-Seq Analysis of a Mixed Transcriptome of Rice and Blast Fungus Interaction. <i>PLoS ONE</i> , 2012, 7, e49423.	1.1	242
6	The Rice Annotation Project Database (RAP-DB): hub for <i>Oryza sativa</i> ssp. japonica genome information. <i>Nucleic Acids Research</i> , 2006, 34, D741-D744.	6.5	219
7	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
8	Comprehensive Sequence Analysis of 24,783 Barley Full-Length cDNAs Derived from 12 Clone Libraries. <i>Plant Physiology</i> , 2011, 156, 20-28.	2.3	201
9	Genome editing in plants by engineered CRISPR-Cas9 recognizing NG PAM. <i>Nature Plants</i> , 2019, 5, 14-17.	4.7	154
10	A Novel Rice Cytochrome P450 Gene, <i>CYP72A31</i> , Confers Tolerance to Acetolactate Synthase-Inhibiting Herbicides in Rice and <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2014, 166, 1232-1240.	2.3	115
11	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> , 2014, 9, e96946.	1.1	102
12	TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. <i>Plant and Cell Physiology</i> , 2016, 57, e7-e7.	1.5	84
13	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice ( <i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2010, 11, 683.	1.2	76
14	Construction of Pseudomolecule Sequences of the aus Rice Cultivar Kasalath for Comparative Genomics of Asian Cultivated Rice. <i>DNA Research</i> , 2014, 21, 397-405.	1.5	74
15	The power of single molecule real-time sequencing technology in the de novo assembly of a eukaryotic genome. <i>Scientific Reports</i> , 2015, 5, 16780.	1.6	73
16	Independent Domestication of Asian Rice Followed by Gene Flow from japonica to indica. <i>Molecular Biology and Evolution</i> , 2012, 29, 1471-1479.	3.5	70
17	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65.	1.7	45
18	Massive gene losses in Asian cultivated rice unveiled by comparative genome analysis. <i>BMC Genomics</i> , 2010, 11, 121.	1.2	36

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19	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	6.5	33
20	<scp>Tasuke</scp>: a web-based visualization program for large-scale resequencing data. <i>Bioinformatics</i> , 2013, 29, 1806-1808.	1.8	30
21	Simultaneous induction of mutant alleles of two allergenic genes in soybean by using site-directed mutagenesis. <i>BMC Plant Biology</i> , 2020, 20, 513.	1.6	30
22	The Nipponbare genome and the next-generation of rice genomics research in Japan. <i>Rice</i> , 2016, 9, 33.	1.7	29
23	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. <i>Plant Journal</i> , 2011, 66, 796-805.	2.8	28
24	MEGANTE: A Web-Based System for Integrated Plant Genome Annotation. <i>Plant and Cell Physiology</i> , 2014, 55, e2-e2.	1.5	27
25	TASUKE+: a web-based platform for exploring GWAS results and large-scale resequencing data. <i>DNA Research</i> , 2019, 26, 445-452.	1.5	20
26	Foreign DNA detection by high-throughput sequencing to regulate genome-edited agricultural products. <i>Scientific Reports</i> , 2020, 10, 4914.	1.6	12
27	Mikan Genome Database (MiGD): integrated database of genome annotation, genomic diversity, and CAPS marker information for mandarin molecular breeding. <i>Breeding Science</i> , 2020, 70, 200-211.	0.9	11
28	Gene tree discordance of wild and cultivated Asian rice deciphered by genome-wide sequence comparison. <i>Gene</i> , 2011, 477, 53-60.	1.0	8
29	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> , 2014, 34, 761-768.	1.0	8
30	Rice Genome Annotation: Beginnings of Functional Genomics. , 2007, , 21-30.		3
31	Genome-wide validation of <i>Magnaporthe grisea</i> gene structures based on transcription evidence. <i>FEBS Letters</i> , 2009, 583, 797-800.	1.3	3
32	Genome Sequences of Oryza Species. , 2018, , 1-20.		2
33	Development of an SSR marker-based genetic linkage map and identification of a QTL associated with flowering time in <i>Eustoma</i> . <i>Breeding Science</i> , 2021, 71, 344-353.	0.9	2
34	The First Monocot Genome Sequence. <i>Advances in Botanical Research</i> , 2014, , 119-135.	0.5	1
35	Databases for Rice Omics Studies. , 2018, , 541-554.		1
36	Bioinformatics and Database of the Rice Genome. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 13-21.	0.2	0

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37	Omics databases for plant breeding. <i>Ikushugaku Kenkyu</i> , 2017, 19, 41-47.	0.1	0
38	Sequencing of Wheat Chromosome 6B: Toward Functional Genomics. , 2015, , 111-116.		0