

# Takehiko Itoh

## List of Publications by Year in descending order

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106  
papers

36,261  
citations

43973

48  
h-index

26548

107  
g-index

117  
all docs

117  
docs citations

117  
times ranked

40053  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mining RNA-seq data reveals the massive regulon of GcvB small RNA and its physiological significance in maintaining amino acid homeostasis in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2022, 117, 160-178.	1.2	15
2	Integrated Population Genomic Analysis and Numerical Simulation to Estimate Larval Dispersal of <i>Acanthaster cf. solaris</i> Between Ogasawara and Other Japanese Regions. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	7
3	Global population structure of the <i>Serratia marcescens</i> complex and identification of hospital-adapted lineages in the complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
4	Targeted base editing in the mitochondrial genome of <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121177119.	3.3	31
5	Whole-genome sequencing analysis and protocol for RNA interference of the endoparasitoid wasp <i>Asobara japonica</i> . <i>DNA Research</i> , 2022, 29, .	1.5	1
6	Genomic architecture and functional unit of mimicry supergene in female limited Batesian mimic <i>Papilio</i> butterflies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	8
7	Evolutionary History of Sexual Differentiation Mechanism in Insects. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
8	Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. <i>Nucleic Acids Research</i> , 2021, 49, 2700-2720.	6.5	26
9	Genomic Signatures for Species-Specific Adaptation in Lake Victoria Cichlids Derived from Large-Scale Standing Genetic Variation. <i>Molecular Biology and Evolution</i> , 2021, 38, 3111-3125.	3.5	9
10	Genomics and transcriptomics of the green mussel explain the durability of its byssus. <i>Scientific Reports</i> , 2021, 11, 5992.	1.6	14
11	Comparative genomics of <i>Glandirana rugosa</i> using unsupervised AI reveals a high CG frequency. <i>Life Science Alliance</i> , 2021, 4, e202000905.	1.3	8
12	The full mitochondrial genome sequence of the greater argonaut <i>Argonauta argo</i> (Cephalopoda). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 Resources</i> , 2021, 6, 1451-1453.	0.2	5
13	Suv4-20h2 protects against influenza virus infection by suppression of chromatin loop formation. <i>IScience</i> , 2021, 24, 102660.	1.9	3
14	Insights into the genomic evolution of insects from cricket genomes. <i>Communications Biology</i> , 2021, 4, 733.	2.0	41
15	Targeted base editing in the plastid genome of <i>Arabidopsis thaliana</i> . <i>Nature Plants</i> , 2021, 7, 906-913.	4.7	62
16	Homology length dictates the requirement for Rad51 and Rad52 in gene targeting in the Basidiomycota yeast <i>Naganishia liquefaciens</i> . <i>Current Genetics</i> , 2021, 67, 919-936.	0.8	3
17	Elucidation of the speciation history of three sister species of crown-of-thorns starfish ( <i>Acanthaster</i> spp.) based on genomic analysis. <i>DNA Research</i> , 2021, 28, .	1.5	6
18	MetaPlatanus: a metagenome assembler that combines long-range sequence links and species-specific features. <i>Nucleic Acids Research</i> , 2021, 49, e130-e130.	6.5	6

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19	A chromosome-level genome sequence of <i>Chrysanthemum seticuspe</i> , a model species for hexaploid cultivated chrysanthemum. <i>Communications Biology</i> , 2021, 4, 1167.	2.0	32
20	Analysis of Sex Chromosome Evolution in the Clade Palaeognathae from Phased Genome Assembly. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
21	The global population structure and evolutionary history of the acquisition of major virulence factor-encoding genetic elements in Shiga toxin-producing <i>Escherichia coli</i> O121:H19. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
22	Platanus_B: an accurate <i>de novo</i> assembler for bacterial genomes using an iterative error-removal process. <i>DNA Research</i> , 2020, 27, .	1.5	26
23	A genome database for a Japanese population of the larvacean <i>Oikopleura dioica</i> . <i>Development Growth and Differentiation</i> , 2020, 62, 450-461.	0.6	13
24	Targeted gene disruption of <i>ATP synthases 6â€1</i> and <i>6â€2</i> in the mitochondrial genome of <i>Arabidopsis thaliana</i> by mitoTALENs. <i>Plant Journal</i> , 2020, 104, 1459-1471.	2.8	57
25	A ubiquitous subcuticular bacterial symbiont of a coral predator, the crown-of-thorns starfish, in the Indo-Pacific. <i>Microbiome</i> , 2020, 8, 123.	4.9	10
26	Expression profiling of sexually dimorphic genes in the Japanese quail, <i>Coturnix japonica</i> . <i>Scientific Reports</i> , 2020, 10, 20073.	1.6	4
27	Parallel reductive genome evolution in <i>Desulfovibrio</i> ectosymbionts independently acquired by <i>Trichonympha</i> protists in the termite gut. <i>ISME Journal</i> , 2020, 14, 2288-2301.	4.4	10
28	Differential dynamics and impacts of prophages and plasmids on the pangenome and virulence factor repertoires of Shiga toxin-producing <i>Escherichia coli</i> O145:H28. <i>Microbial Genomics</i> , 2020, 6, .	1.0	28
29	Draft Genome Sequence of <i>Naganishia liquefaciens</i> Strain N6, Isolated from the Japan Trench. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
30	Curing cytoplasmic male sterility via TALEN-mediated mitochondrial genome editing. <i>Nature Plants</i> , 2019, 5, 722-730.	4.7	126
31	<i>Bcl11b</i> controls odorant receptor class choice in mice. <i>Communications Biology</i> , 2019, 2, 296.	2.0	19
32	Genome Sequencing Verifies Relapsed Infection of <i>Helicobacter cinaedi</i> . <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz200.	0.4	5
33	Platanus-allee is a <i>de novo</i> haplotype assembler enabling a comprehensive access to divergent heterozygous regions. <i>Nature Communications</i> , 2019, 10, 1702.	5.8	92
34	3D genomic architecture reveals that neocentromeres associate with heterochromatin regions. <i>Journal of Cell Biology</i> , 2019, 218, 134-149.	2.3	31
35	Multi-step genomic dissection of a suspected intra-hospital <i>Helicobacter cinaedi</i> outbreak. <i>Microbial Genomics</i> , 2019, 5, .	1.0	8
36	Evaluation of SNP calling methods for closely related bacterial isolates and a novel high-accuracy pipeline: BactSNP. <i>Microbial Genomics</i> , 2019, 5, .	1.0	38

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37	Parallel evolution of Batesian mimicry supergene in two <i>Papilio</i> butterflies, <i>P. polytes</i> and <i>P. memnon</i> . <i>Science Advances</i> , 2018, 4, eaao5416.	4.7	48
38	Quantitative analyses of the metaphase-to-anaphase transition reveal differential kinetic regulation for securin and cyclin B1. <i>Biomedical Research</i> , 2018, 39, 75-85.	0.3	5
39	Genomic Characterization of $\beta$ -Glucuronidase-Positive <i>Escherichia coli</i> O157:H7 Producing Stx2a. <i>Emerging Infectious Diseases</i> , 2018, 24, 2219-2227.	2.0	29
40	Somatic copy number alterations have prognostic impact in patients with ovarian clear cell carcinoma. <i>Oncology Reports</i> , 2018, 40, 309-318.	1.2	16
41	Repeated inversions within a panner intron drive diversification of intraspecific colour patterns of ladybird beetles. <i>Nature Communications</i> , 2018, 9, 3843.	5.8	61
42	An acid-tolerant ammonia-oxidizing $\beta$ -proteobacterium from soil. <i>ISME Journal</i> , 2017, 11, 1130-1141.	4.4	123
43	Complete genome sequence and expression profile of the commercial lytic enzyme producer <i>Lysobacter enzymogenes</i> M497-1. <i>DNA Research</i> , 2017, 24, dsw055.	1.5	12
44	Discovery and Complete Genome Sequence of a Bacteriophage from an Obligate Intracellular Symbiont of a Cellulolytic Protist in the Termite Gut. <i>Microbes and Environments</i> , 2017, 32, 112-117.	0.7	37
45	Extremely low genomic diversity of <i>Rickettsia japonica</i> distributed in Japan. <i>Genome Biology and Evolution</i> , 2017, 9, evw304.	1.1	16
46	Population structure of <i>Escherichia coli</i> O26:H11 with recent and repeated stx2 acquisition in multiple lineages. <i>Microbial Genomics</i> , 2017, 3, .	1.0	29
47	The complete genome sequencing of <i>Prevotella intermedia</i> strain OMA14 and a subsequent fine-scale, intra-species genomic comparison reveal an unusual amplification of conjugative and mobile transposons and identify a novel <i>Prevotella</i> lineage-specific repeat. <i>DNA Research</i> , 2016, 23, dsv032.	1.5	17
48	Acute transcriptional up-regulation specific to osteoblasts/osteoclasts in medaka fish immediately after exposure to microgravity. <i>Scientific Reports</i> , 2016, 6, 39545.	1.6	42
49	Comparison of Intracellular <i>Ca.</i> Endomicrobium <i>Trichonympha</i> Genomovars Illuminates the Requirement and Decay of Defense Systems against Foreign DNA. <i>Genome Biology and Evolution</i> , 2016, 8, 3099-3107.	1.1	27
50	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
51	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	9.4	226
52	Next-generation sequencing analysis of lager brewing yeast strains reveals the evolutionary history of interspecies hybridization. <i>DNA Research</i> , 2016, 23, dsv037.	1.5	99
53	A genetic mechanism for female-limited Batesian mimicry in <i>Papilio</i> butterfly. <i>Nature Genetics</i> , 2015, 47, 405-409.	9.4	215
54	Comparative genome and transcriptome analyses of the social amoeba <i>Acytostelium subglobosum</i> that accomplishes multicellular development without germ-soma differentiation. <i>BMC Genomics</i> , 2015, 16, 80.	1.2	23

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55	STAP cells are derived from ES cells. <i>Nature</i> , 2015, 525, E4-E5.	13.7	8
56	The Thermotolerant Yeast <i>Kluyveromyces marxianus</i> Is a Useful Organism for Structural and Biochemical Studies of Autophagy. <i>Journal of Biological Chemistry</i> , 2015, 290, 29506-29518.	1.6	16
57	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep seafloor sedimentary metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 80.	1.5	61
58	Dimeric combinations of MafB, cFos and cJun control the apoptosis-survival balance in limb morphogenesis. <i>Development (Cambridge)</i> , 2014, 141, 2885-2894.	1.2	27
59	Efficient de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads. <i>Genome Research</i> , 2014, 24, 1384-1395.	2.4	1,000
60	Sensory-Neuron Subtype-Specific Transcriptional Programs Controlling Dendrite Morphogenesis: Genome-wide Analysis of Abrupt and Knot/Collier. <i>Developmental Cell</i> , 2013, 27, 530-544.	3.1	60
61	Transcriptomic analysis of four developmental stages of <i>Strongyloides venezuelensis</i> . <i>Parasitology International</i> , 2013, 62, 57-65.	0.6	15
62	Coelacanth genomes reveal signatures for evolutionary transition from water to land. <i>Genome Research</i> , 2013, 23, 1740-1748.	2.4	108
63	<sc>DROMPA</sc>: easy to handle peak calling and visualization software for the computational analysis and validation of ChIP-seq data. <i>Genes To Cells</i> , 2013, 18, 589-601.	0.5	67
64	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. <i>Nature</i> , 2012, 489, 313-317.	13.7	488
65	Replisome Stability at Defective DNA Replication Forks Is Independent of S Phase Checkpoint Kinases. <i>Molecular Cell</i> , 2012, 45, 696-704.	4.5	140
66	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. <i>PLoS ONE</i> , 2012, 7, e30559.	1.1	161
67	Typing of O26 enterohaemorrhagic and enteropathogenic <i>Escherichia coli</i> isolated from humans and cattle with IS621 multiplex PCR-based fingerprinting. <i>Journal of Applied Microbiology</i> , 2011, 111, 773-786.	1.4	6
68	A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. <i>EMBO Journal</i> , 2011, 30, 364-378.	3.5	69
69	Chromosome length influences replication-induced topological stress. <i>Nature</i> , 2011, 471, 392-396.	13.7	99
70	ATP Hydrolysis Is Required for Relocating Cohesin from Sites Occupied by Its Scc2/4 Loading Complex. <i>Current Biology</i> , 2011, 21, 12-24.	1.8	173
71	Histone and TKO471/TrmBL2 form a novel heterogeneous genome architecture in the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>Molecular Biology of the Cell</i> , 2011, 22, 386-398.	0.9	44
72	The Lifestyle of the Segmented Filamentous Bacterium: A Non-Culturable Gut-Associated Immunostimulating Microbe Inferred by Whole-Genome Sequencing. <i>DNA Research</i> , 2011, 18, 291-303.	1.5	93

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73	Draft Genome Sequencing and Comparative Analysis of <i>Aspergillus sojae</i> NBRC4239. <i>DNA Research</i> , 2011, 18, 165-176.	1.5	75
74	A Direct Role for Cohesin in Gene Regulation and Ecdysone Response in <i>Drosophila</i> Salivary Glands. <i>Current Biology</i> , 2010, 20, 1787-1798.	1.8	57
75	Receptor for activated C kinase 1 stimulates nascent polypeptide-dependent translation arrest. <i>EMBO Reports</i> , 2010, 11, 956-961.	2.0	151
76	Genome-wide DNA methylation analysis in cohesin mutant human cell lines. <i>Nucleic Acids Research</i> , 2010, 38, 5657-5671.	6.5	22
77	Csm3, Tof1, and Mrc1 Form a Heterotrimeric Mediator Complex That Associates with DNA Replication Forks. <i>Journal of Biological Chemistry</i> , 2009, 284, 34355-34365.	1.6	123
78	Rec8 Guides Canonical Spo11 Distribution along Yeast Meiotic Chromosomes. <i>Molecular Biology of the Cell</i> , 2009, 20, 3064-3076.	0.9	109
79	Transcriptional Dysregulation in NIPBL and Cohesin Mutant Human Cells. <i>PLoS Biology</i> , 2009, 7, e1000119.	2.6	199
80	The Defective Prophage Pool of <i>Escherichia coli</i> O157: Prophage-Prophage Interactions Potentiate Horizontal Transfer of Virulence Determinants. <i>PLoS Pathogens</i> , 2009, 5, e1000408.	2.1	227
81	Budding Yeast Wpl1(Rad61)-Pds5 Complex Counteracts Sister Chromatid Cohesion-Establishing Reaction. <i>Current Biology</i> , 2009, 19, 492-497.	1.8	200
82	Ctf4 coordinates the progression of helicase and DNA polymerase $\epsilon$ . <i>Genes To Cells</i> , 2009, 14, 807-820.	0.5	82
83	Genome Sequence of the Lager Brewing Yeast, an Interspecies Hybrid. <i>DNA Research</i> , 2009, 16, 115-129.	1.5	269
84	Rad51 suppresses gross chromosomal rearrangement at centromere in <i>Schizosaccharomyces pombe</i> . <i>EMBO Journal</i> , 2008, 27, 3036-3046.	3.5	58
85	Cohesin mediates transcriptional insulation by CCCTC-binding factor. <i>Nature</i> , 2008, 451, 796-801.	13.7	1,050
86	MetaGeneAnnotator: Detecting Species-Specific Patterns of Ribosomal Binding Site for Precise Gene Prediction in Anonymous Prokaryotic and Phage Genomes. <i>DNA Research</i> , 2008, 15, 387-396.	1.5	596
87	Identification of <i>cis</i> -acting sites for condensin loading onto budding yeast chromosomes. <i>Genes and Development</i> , 2008, 22, 2215-2227.	2.7	302
88	Nutrient-Regulated Antisense and Intragenic RNAs Modulate a Signal Transduction Pathway in Yeast. <i>PLoS Biology</i> , 2008, 6, e326.	2.6	57
89	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. <i>DNA Research</i> , 2007, 14, 169-181.	1.5	760
90	Genome-wide localization of pre-RC sites and identification of replication origins in fission yeast. <i>EMBO Journal</i> , 2007, 26, 1327-1339.	3.5	163

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91	Genome-wide localization of pre-RC sites and identification of replication origins in fission yeast. EMBO Journal, 2007, 26, 2821-2821.	3.5	7
92	Chromosomal Association of the Smc5/6 Complex Reveals that It Functions in Differently Regulated Pathways. Molecular Cell, 2006, 22, 755-767.	4.5	197
93	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. Nature Genetics, 2006, 38, 158-167.	9.4	110
94	Human chromosome 11 DNA sequence and analysis including novel gene identification. Nature, 2006, 440, 497-500.	13.7	74
95	Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. Nature, 2006, 441, 53-61.	13.7	419
96	Meiotic cohesins modulate chromosome compaction during meiotic prophase in fission yeast. Journal of Cell Biology, 2006, 174, 499-508.	2.3	91
97	Identification of large ancient duplications associated with human gene deserts. Nature Genetics, 2005, 37, 1041-1043.	9.4	5
98	DNA sequence and analysis of human chromosome 18. Nature, 2005, 437, 551-555.	13.7	53
99	Cohesin relocation from sites of chromosomal loading to places of convergent transcription. Nature, 2004, 430, 573-578.	13.7	544
100	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	13.7	4,232
101	Human Versus Chimpanzee Chromosome-wide Sequence Comparison and Its Evolutionary Implication. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 455-460.	2.0	8
102	Construction and Analysis of a Human-Chimpanzee Comparative Clone Map. Science, 2002, 295, 131-134.	6.0	228
103	Comparative Genomic Sequence Analysis of the Human Chromosome 21 Down Syndrome Critical Region. Genome Research, 2002, 12, 1323-1332.	2.4	48
104	GTOP: a database of protein structures predicted from genome sequences. Nucleic Acids Research, 2002, 30, 294-298.	6.5	69
105	Guide to HGREP (Human Genome REconstruction Project). Trends in Glycoscience and Glycotechnology, 2002, 14, 189-197.	0.0	0
106	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074