

Osamu Gotoh

List of Publications by Year in descending order

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71
papers

8,474
citations

147801

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102487

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all docs

71
docs citations

71
times ranked

6696
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic determinants impacting the clinical outcome of mogamulizumab treatment for adult T-cell leukemia/lymphoma. <i>Haematologica</i> , 2022, 107, 2418-2431.	3.5	14
2	Immunogenic characteristics of microsatellite instability-low esophagogastric junction adenocarcinoma based on clinicopathological, molecular, immunological and survival analyses. <i>International Journal of Cancer</i> , 2021, 148, 1260-1275.	5.1	4
3	Immunogenomic landscape of gynecologic carcinosarcoma. <i>Gynecologic Oncology</i> , 2021, 160, 547-556.	1.4	8
4	T-cell complexity and density are associated with sensitivity to neoadjuvant chemoradiotherapy in patients with rectal cancer. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 509-518.	4.2	25
5	Pathogenicity assessment of variants for breast cancer susceptibility genes based on BRCAness of tumor sample. <i>Cancer Science</i> , 2021, 112, 1310-1319.	3.9	3
6	Genomic alterations in gynecological malignancies: histotype-associated driver mutations, molecular subtyping schemes, and tumorigenic mechanisms. <i>Journal of Human Genetics</i> , 2021, 66, 853-868.	2.3	5
7	A method of sample-wise region-set enrichment analysis for DNA methylomics. <i>Epigenomics</i> , 2021, 13, 1081-1093.	2.1	1
8	Two Distinct Tumorigenic Processes in Endometrial Endometrioid Adenocarcinoma. <i>American Journal of Pathology</i> , 2020, 190, 234-251.	3.8	11
9	Sequencing artifacts derived from a library preparation method using enzymatic fragmentation. <i>PLoS ONE</i> , 2020, 15, e0227427.	2.5	24
10	Prevalence of disease-causing genes in Japanese patients with BRCA1/2-wildtype hereditary breast and ovarian cancer syndrome. <i>Npj Breast Cancer</i> , 2020, 6, 25.	5.2	21
11	Sequencing artifacts derived from a library preparation method using enzymatic fragmentation. , 2020, 15, e0227427.		0
12	Sequencing artifacts derived from a library preparation method using enzymatic fragmentation. , 2020, 15, e0227427.		0
13	Sequencing artifacts derived from a library preparation method using enzymatic fragmentation. , 2020, 15, e0227427.		0
14	Sequencing artifacts derived from a library preparation method using enzymatic fragmentation. , 2020, 15, e0227427.		0
15	Clinically relevant molecular subtypes and genomic alteration-independent differentiation in gynecologic carcinosarcoma. <i>Nature Communications</i> , 2019, 10, 4965.	12.8	82
16	Characterization of moss ent-kaurene oxidase (CYP701B1) using a highly purified preparation. <i>Journal of Biochemistry</i> , 2018, 163, 69-76.	1.7	2
17	Evolutionary origin of mitochondrial cytochrome P450. <i>Journal of Biochemistry</i> , 2017, 161, 399-407.	1.7	20
18	A multiplex RNA quantification method to determine the absolute amounts of mRNA without reverse transcription. <i>Analytical Biochemistry</i> , 2017, 539, 96-103.	2.4	2

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19	Tetrahedral Gray Code for Visualization of Genome Information. <i>PLoS ONE</i> , 2014, 9, e86133.	2.5	1
20	The Apoptotic Initiator Caspase-8: Its Functional Ubiquity and Genetic Diversity during Animal Evolution. <i>Molecular Biology and Evolution</i> , 2014, 31, 3282-3301.	8.9	25
21	Benchmarking spliced alignment programs including Spaln2, an extended version of Spaln that incorporates additional species-specific features. <i>Nucleic Acids Research</i> , 2012, 40, e161-e161.	14.5	155
22	Evolution of Cytochrome P450 Genes from the Viewpoint of Genome Informatics. <i>Biological and Pharmaceutical Bulletin</i> , 2012, 35, 812-817.	1.4	41
23	Identification of a new clock-related element EL-box involved in circadian regulation by BMAL1/CLOCK and HES1. <i>Gene</i> , 2012, 510, 118-125.	2.2	8
24	Multiplex cDNA quantification method that facilitates the standardization of gene expression data. <i>Nucleic Acids Research</i> , 2011, 39, e70-e70.	14.5	5
25	Transactivation activity of LBP proteins and their dimerization in living cells. <i>Genes To Cells</i> , 2009, 14, 1183-1196.	1.2	5
26	A space-efficient and accurate method for mapping and aligning cDNA sequences onto genomic sequence. <i>Nucleic Acids Research</i> , 2008, 36, 2630-2638.	14.5	91
27	1P487 Improvement in Software for Kinetics Analyses of Protein-Ligand Interaction(23. <i>Bioinformatics</i> ,) Tj ETQq1 1 0.784314 rgBT/O Butsuri, 2006, 46, S268.	0.1	0
28	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , 2005, 438, 1157-1161.	27.8	1,128
29	Species-specific variation of alternative splicing and transcriptional initiation in six eukaryotes. <i>Gene</i> , 2005, 364, 53-62.	2.2	92
30	A novel induction mechanism of the rat CYP1A2 gene mediated by Ah receptor Arnt heterodimer. <i>Biochemical and Biophysical Research Communications</i> , 2004, 318, 746-755.	2.1	93
31	Molecular Mechanism of Nuclear Translocation of an Orphan Nuclear Receptor, SXR. <i>Molecular Pharmacology</i> , 2003, 63, 524-531.	2.3	105
32	Emergence of Fluconazole-Resistant Sterol 14-Demethylase P450 (CYP51) in <i>Candida albicans</i> Is a Model Demonstrating the Diversification Mechanism of P450. <i>Archives of Biochemistry and Biophysics</i> , 2000, 379, 170-171.	3.0	12
33	Sterol 14-Demethylase P450 (CYP51) Provides a Breakthrough for the Discussion on the Evolution of Cytochrome P450 Gene Superfamily. <i>Biochemical and Biophysical Research Communications</i> , 2000, 273, 799-804.	2.1	103
34	Identification of Novel First Exons in Ad4BP/SF-1 (NR5A1) Gene and Their Tissue- and Species-Specific Usage. <i>Biochemical and Biophysical Research Communications</i> , 2000, 278, 63-71.	2.1	23
35	Formation of Azole-Resistant <i>Candida albicans</i> by Mutation of Sterol 14-Demethylase P450. <i>Antimicrobial Agents and Chemotherapy</i> , 1999, 43, 1163-1169.	3.2	103
36	Multiple sequence alignment: Algorithms and applications. <i>Advances in Biophysics</i> , 1999, 36, 159-206.	0.5	74

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37	CYP51-like gene of <i>Mycobacterium tuberculosis</i> actually encodes a P450 similar to eukaryotic CYP51. <i>Journal of Biochemistry</i> , 1998, 124, 694-696.	1.7	61
38	Molecular Cloning and Expression of Fatty Acid Δ^6 -Hydroxylase from <i>Sphingomonas paucimobilis</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 23592-23596.	3.4	74
39	Significant Improvement in Accuracy of Multiple Protein Sequence Alignments by Iterative Refinement as Assessed by Reference to Structural Alignments. <i>Journal of Molecular Biology</i> , 1996, 264, 823-838.	4.2	302
40	cDNA Cloning of a Murine Homologue of <i>Drosophila</i> Single-Minded, Its mRNA Expression in Mouse Development, and Chromosome Localization. <i>Biochemical and Biophysical Research Communications</i> , 1996, 218, 588-594.	2.1	50
41	P450 superfamily: update on new sequences, gene mapping, accession numbers and nomenclature. <i>Pharmacogenetics and Genomics</i> , 1996, 6, 1-42.	5.7	2,629
42	Cloning and Gene Mapping of the Mouse Homologue of the CBFA2T1 Gene Associated with Human Acute Myeloid Leukemia. <i>Genomics</i> , 1995, 29, 755-759.	2.9	15
43	Interindividual difference in expression of human Ah receptor and related P450 genes. <i>Carcinogenesis</i> , 1994, 15, 801-806.	2.8	92
44	Xenobiotic Responsive Element in the 5' Upstream Region of the Human P-450c Gene1. <i>Journal of Biochemistry</i> , 1991, 110, 232-236.	1.7	52
45	cDNA cloning of cytochrome P-450 related to P-450p-2 from the cDNA library of human placenta. Gene structure and expression. <i>FEBS Journal</i> , 1990, 187, 23-29.	0.2	29
46	Differentiation of restriction sites in ribosomal DNA in the genus <i>Apodemus</i> . <i>Biochemical Genetics</i> , 1990, 28, 137-149.	1.7	32
47	Molecular Cloning and Sequence Analysis of cDNA Coding for Rat Liver Hemoprotein H-4501. <i>Journal of Biochemistry</i> , 1990, 108, 899-902.	1.7	22
48	Human Thymidylate Synthase Gene: Isolation of Phage Clones Which Cover a Functionally Active Gene and Structural Analysis of the Region Upstream from the Translation Initiation Codon1. <i>Journal of Biochemistry</i> , 1989, 106, 575-583.	1.7	42
49	Molecular Cloning and Nucleotide Sequence of DNA of Mitochondrial Cytochrome P-450(11 β) of Bovine Adrenal Cortex1. <i>Journal of Biochemistry</i> , 1987, 102, 559-568.	1.7	79
50	Alignment of three biological sequences with an efficient traceback procedure. <i>Journal of Theoretical Biology</i> , 1986, 121, 327-337.	1.7	142
51	Structure and drug inducibility of the human cytochrome P-450c gene. <i>FEBS Journal</i> , 1986, 159, 219-225.	0.2	87
52	Sequence search on a supercomputer. <i>Nucleic Acids Research</i> , 1986, 14, 57-64.	14.5	14
53	Nucleotide sequence of a functional cDNA for human thymidylate synthase. <i>Nucleic Acids Research</i> , 1985, 13, 2035-2043.	14.5	144
54	Implications of the genetic divergence between European wild mice with Robertsonian translocations from the viewpoint of mitochondrial DNA. <i>Genetical Research</i> , 1984, 43, 277-287.	0.9	34

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55	Structural Characteristics of Cytochrome P-450. Possible Location of the Heme-Binding Cysteine in Determined Amino-Acid Sequences. <i>Journal of Biochemistry</i> , 1983, 93, 807-817.	1.7	148
56	Salt-Concentration Dependence of Thermal Denaturation of Restriction Fragment DNAs from Φ X1741. <i>Journal of Biochemistry</i> , 1982, 92, 623-635.	1.7	9
57	An improved algorithm for matching biological sequences. <i>Journal of Molecular Biology</i> , 1982, 162, 705-708.	4.2	1,486
58	Computer Analysis of the Sequence Relationships among 4.5S RNA Molecular Species from Various Sources. <i>Journal of Biochemistry</i> , 1982, 92, 1173-1177.	1.7	15
59	Mitochondrial DNA analysis of mouse-rat hybrid cells: Effect of chloramphenicol selection on the relative amounts of parental mitochondrial DNAs. <i>Somatic Cell Genetics</i> , 1982, 8, 67-81.	2.7	29
60	Origins of Laboratory Mice Deduced from Restriction Patterns of Mitochondrial DNA. <i>Differentiation</i> , 1982, 22, 222-226.	1.9	154
61	Analysis of mitochondrial DNA species in interspecific hybrid somatic cells using restriction endonucleases. Identification of recombinant mtDNA molecules. <i>Experimental Cell Research</i> , 1981, 131, 458-462.	2.6	12
62	Length polymorphisms of restriction fragments of rat mitochondrial DNAs. <i>Biochemical and Biophysical Research Communications</i> , 1981, 98, 936-941.	2.1	10
63	EVOLUTIONARY RELATIONSHIPS AMONG FIVE SUBSPECIES OF <i>MUS MUSCULUS</i> BASED ON RESTRICTION ENZYME CLEAVAGE PATTERNS OF MITOCHONDRIAL DNA. <i>Genetics</i> , 1981, 98, 801-816.	2.9	131
64	A general characteristic of tumor mitochondria: Leakage of endogenous Mg ²⁺ on incubation with uncoupler and resultant reduction of uncoupler-stimulated ATPase activity. <i>Archives of Biochemistry and Biophysics</i> , 1980, 205, 27-35.	3.0	15
65	Identification of mitochondrial DNA species in interspecific cybrids and reconstituted cells using restriction endonuclease. <i>FEBS Letters</i> , 1980, 117, 59-62.	2.8	28
66	Unique uncoupler-stimulation pattern of mitochondrial ATPase activity of tumor cells, brain, and fetal liver. <i>Biochemical and Biophysical Research Communications</i> , 1980, 92, 261-267.	2.1	9
67	An improved method for estimating sequence divergence between related DNAs from changes in restriction endonuclease cleavage sites. <i>Journal of Molecular Evolution</i> , 1979, 14, 301-310.	1.8	57
68	Two different molecular types of rat mitochondrial DNAs. <i>Biochemical and Biophysical Research Communications</i> , 1978, 81, 871-877.	2.1	33
69	Strictly maternal inheritance of rat mitochondrial DNA. <i>Biochemical and Biophysical Research Communications</i> , 1978, 83, 1032-1038.	2.1	90
70	The differences between the primary structures of mitochondrial DNAs from rat liver and ascites hepatoma (AH-130). <i>Cancer Letters</i> , 1978, 4, 125-130.	7.2	15
71	Long range homogeneity of physical stability in double-stranded DNA. <i>Nature</i> , 1976, 263, 439-440.	27.8	47