

Shujiro Okuda

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

20,419
citations

94433

37
h-index

25787

108
g-index

118
all docs

118
docs citations

118
times ranked

34935
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of Potential Markers for Lip Vermilion Epithelium in Japanese Macaques Based on the Results of Gene Expression Profile. , 2022, 1, 3-13.		2
2	Cyclin D1 Binding Protein 1 Responds to DNA Damage through the ATM-CHK2 Pathway. Journal of Clinical Medicine, 2022, 11, 851.	2.4	2
3	Putrescine Production by <i>Lactobacillus curvatus</i> KP 3-4 Isolated from Fermented Foods. Microorganisms, 2022, 10, 697.	3.6	6
4	Differing impact of phosphoglycerate mutase 1-deficiency on brown and white adipose tissue. IScience, 2022, 25, 104268.	4.1	2
5	Glycoprotein nonmetastatic melanoma protein B regulates lysosomal integrity and lifespan of senescent cells. Scientific Reports, 2022, 12, 6522.	3.3	24
6	The jPOST Repository as a Public Data Repository for Shotgun Proteomics. Methods in Molecular Biology, 2021, 2259, 309-322.	0.9	15
7	p62/SQSTM1-droplet serves as a platform for autophagosome formation and anti-oxidative stress response. Nature Communications, 2021, 12, 16.	12.8	137
8	Mutational signatures in squamous cell carcinoma of the lung. Journal of Thoracic Disease, 2021, 13, 1075-1082.	1.4	4
9	Adipose most abundant 2 protein is a predictive marker for cisplatin sensitivity in cancers. Scientific Reports, 2021, 11, 6255.	3.3	2
10	Histopathological characteristics and artificial intelligence for predicting tumor mutational burden-high colorectal cancer. Journal of Gastroenterology, 2021, 56, 547-559.	5.1	23
11	Three-dimensional understanding of the morphological complexity of the human uterine endometrium. IScience, 2021, 24, 102258.	4.1	59
12	Development of Novel PCR Assays for Improved Detection of Enterovirus D68. Journal of Clinical Microbiology, 2021, 59, e0115121.	3.9	10
13	Proposing a molecular classification associated with hypercoagulation in ovarian clear cell carcinoma. Gynecologic Oncology, 2021, 163, 327-333.	1.4	5
14	Altered microbiota by a high-fat diet accelerates lethal myeloid hematopoiesis associated with systemic SOCS3 deficiency. IScience, 2021, 24, 103117.	4.1	5
15	Activin A Receptor Type 2A Mutation Affects the Tumor Biology of Microsatellite Instability-High Gastric Cancer. Journal of Gastrointestinal Surgery, 2021, 25, 2231-2241.	1.7	4
16	Profiling of host genetic alterations and intra-tumor microbiomes in colorectal cancer. Computational and Structural Biotechnology Journal, 2021, 19, 3330-3338.	4.1	15
17	GlycoPOST realizes FAIR principles for glycomics mass spectrometry data. Nucleic Acids Research, 2021, 49, D1523-D1528.	14.5	78
18	Functional glyco-metagenomics elucidates the role of glycan-related genes in environments. BMC Bioinformatics, 2021, 22, 505.	2.6	1

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19	Senolytic vaccination improves normal and pathological age-related phenotypes and increases lifespan in progeroid mice. <i>Nature Aging</i> , 2021, 1, 1117-1126.	11.6	87
20	Plasma Sphingosine-1-Phosphate Levels Are Associated with Progression of Estrogen Receptor-Positive Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13367.	4.1	6
21	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	14.5	491
22	Genetic profiling for diffuse type and genomically stable subtypes in gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3301-3308.	4.1	12
23	Sphingosine Kinase 1 is Associated With Immune Cell-Related Gene Expressions in Human Breast Cancer. <i>Journal of Surgical Research</i> , 2020, 256, 645-656.	1.6	8
24	Frequent Germline and Somatic Single Nucleotide Variants in the Promoter Region of the Ribosomal RNA Gene in Japanese Lung Adenocarcinoma Patients. <i>Cells</i> , 2020, 9, 2409.	4.1	4
25	The GlyCosmos Portal: a unified and comprehensive web resource for the glycosciences. <i>Nature Methods</i> , 2020, 17, 649-650.	19.0	71
26	XCL1 expression correlates with CD8-positive T cells infiltration and PD-L1 expression in squamous cell carcinoma arising from mature cystic teratoma of the ovary. <i>Oncogene</i> , 2020, 39, 3541-3554.	5.9	26
27	Phosphoproteomic and bioinformatic methods for analyzing signaling in vertebrate axon growth and regeneration. <i>Journal of Neuroscience Methods</i> , 2020, 339, 108723.	2.5	7
28	Verification of the Japanese staging system for rectal cancer, focusing on differences with the TNM classification. <i>Surgery Today</i> , 2020, 50, 1443-1451.	1.5	4
29	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020, 9, 136.	1.6	5
30	RNF43 mutation is associated with aggressive tumor biology along with BRAF V600E mutation in right-sided colorectal cancer. <i>Oncology Reports</i> , 2020, 43, 1853-1862.	2.6	15
31	The Human Gut Microbiome is Structured to Optimize Molecular Interaction Networks. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1040-1046.	4.1	6
32	Towards a standardized bioinformatics infrastructure for N- and O-glycomics. <i>Nature Communications</i> , 2019, 10, 3275.	12.8	70
33	Evolutionary analysis of proline-directed phosphorylation sites in the mammalian growth cone identified using phosphoproteomics. <i>Molecular Brain</i> , 2019, 12, 53.	2.6	9
34	Open Agile text mining for bioinformatics: the PubAnnotation ecosystem. <i>Bioinformatics</i> , 2019, 35, 4372-4380.	4.1	16
35	Autophagy regulates lipid metabolism through selective turnover of NCoR1. <i>Nature Communications</i> , 2019, 10, 1567.	12.8	143
36	BRAF V600E and SRC mutations as molecular markers for predicting prognosis and conversion surgery in Stage IV colorectal cancer. <i>Scientific Reports</i> , 2019, 9, 2466.	3.3	16

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37	Characterisation of N-glycans in the epithelial-like tissue of the rat cochlea. <i>Scientific Reports</i> , 2019, 9, 1551.	3.3	4
38	Rice Endosperm Protein Administration to Juvenile Mice Regulates Gut Microbiota and Suppresses the Development of High-Fat Diet-Induced Obesity and Related Disorders in Adulthood. <i>Nutrients</i> , 2019, 11, 2919.	4.1	19
39	Knowledge base toward understanding actionable alterations and realizing precision oncology. <i>International Journal of Clinical Oncology</i> , 2019, 24, 123-130.	2.2	9
40	<i>SMAD4</i> alteration associates with invasive front pathological markers and poor prognosis in colorectal cancer. <i>Histopathology</i> , 2019, 74, 873-882.	2.9	37
41	Next generation sequencing-based gene panel tests for the management of solid tumors. <i>Cancer Science</i> , 2019, 110, 6-15.	3.9	107
42	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	14.5	94
43	Clinical and Genetic Implications of Mutation Burden in Squamous Cell Carcinoma of the Lung. <i>Annals of Surgical Oncology</i> , 2018, 25, 1564-1571.	1.5	23
44	AldB controls persister formation in <i>Escherichia coli</i> depending on environmental stress. <i>Microbiology and Immunology</i> , 2018, 62, 299-309.	1.4	8
45	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis. <i>Scientific Reports</i> , 2018, 8, 5608.	3.3	20
46	Impact of Concurrent Genomic Alterations Detected by Comprehensive Genomic Sequencing on Clinical Outcomes in East-Asian Patients with EGFR-Mutated Lung Adenocarcinoma. <i>Scientific Reports</i> , 2018, 8, 1005.	3.3	22
47	Novel therapeutic strategy for cervical cancer harboring FGFR3-TACC3 fusions. <i>Oncogenesis</i> , 2018, 7, 4.	4.9	41
48	Unique transcriptional profile of native persisters in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 15-22.	2.2	14
49	Identification of TRA-60-positive cells as a potent refractory population in follicular lymphomas. <i>Cancer Science</i> , 2018, 110, 443-457.	3.9	7
50	Actionable Gene Alterations in an Asian Population With Triple-Negative Breast Cancer. <i>JCO Precision Oncology</i> , 2018, 2, 1-13.	3.0	3
51	Novel gene fusions found in cervical cancer. <i>EBioMedicine</i> , 2018, 38, 13-14.	6.1	0
52	Novel <i>MXD4-NUTM1</i> fusion transcript identified in primary ovarian undifferentiated small round cell sarcoma. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 557-563.	2.8	28
53	Sharing of human milk oligosaccharides degradants within bifidobacterial communities in faecal cultures supplemented with <i>Bifidobacterium bifidum</i> . <i>Scientific Reports</i> , 2018, 8, 13958.	3.3	121
54	Analysis of polyamine biosynthetic- and transport ability of human indigenous <i>Bifidobacterium</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2018, 82, 1606-1614.	1.3	12

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55	Growth Cone Phosphoproteomics Reveals that GAP-43 Phosphorylated by JNK Is a Marker of Axon Growth and Regeneration. <i>IScience</i> , 2018, 4, 190-203.	4.1	44
56	Common driver mutations and smoking history affect tumor mutation burden in lung adenocarcinoma. <i>Journal of Surgical Research</i> , 2018, 230, 181-185.	1.6	55
57	Clinical Significance of BRAF Non-V600E Mutations in Colorectal Cancer: A Retrospective Study of Two Institutions. <i>Journal of Surgical Research</i> , 2018, 232, 72-81.	1.6	19
58	Genome-wide analysis of single nucleotide variants on phosphorylation motifs. <i>FASEB Journal</i> , 2018, 32, lb113.	0.5	0
59	jPOSTrepo: an international standard data repository for proteomes. <i>Nucleic Acids Research</i> , 2017, 45, D1107-D1111.	14.5	451
60	Cost-effectiveness analysis of the use of comprehensive molecular profiling before initiating monoclonal antibody therapy against metastatic colorectal cancer in Japan. <i>Journal of Cancer Policy</i> , 2017, 12, 61-66.	1.4	7
61	Molecular Insight into Evolution of Symbiosis between Breast-Fed Infants and a Member of the Human Gut Microbiome <i>Bifidobacterium longum</i> . <i>Cell Chemical Biology</i> , 2017, 24, 515-524.e5.	5.2	102
62	Utility of comprehensive genomic sequencing for detecting HER2-positive colorectal cancer. <i>Human Pathology</i> , 2017, 66, 1-9.	2.0	31
63	Use of Gifu Anaerobic Medium for culturing 32 dominant species of human gut microbes and its evaluation based on short-chain fatty acids fermentation profiles. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 2009-2017.	1.3	50
64	Actionable gene-based classification toward precision medicine in gastric cancer. <i>Genome Medicine</i> , 2017, 9, 93.	8.2	59
65	Comprehensive analysis of polyamine transport and biosynthesis in the dominant human gut bacteria: Potential presence of novel polyamine metabolism and transport genes. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 93, 52-61.	2.8	37
66	Mutations in SDR9C7 gene encoding an enzyme for vitamin A metabolism underlie autosomal recessive congenital ichthyosis. <i>Journal of Dermatological Science</i> , 2017, 86, e50.	1.9	3
67	Rare <i>PDCD11</i> variations are not associated with risk of schizophrenia in Japan. <i>Psychiatry and Clinical Neurosciences</i> , 2017, 71, 780-788.	1.8	6
68	Latest developments in Semantic Web technologies applied to the glycosciences. <i>Perspectives in Science</i> , 2017, 11, 18-23.	0.6	2
69	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	14.5	860
70	Comprehensive genomic sequencing detects important genetic differences between right-sided and left-sided colorectal cancer. <i>Oncotarget</i> , 2017, 8, 93567-93579.	1.8	26
71	Inhibition of dipeptidyl peptidase-4 ameliorates cardiac ischemia and systolic dysfunction by up-regulating the FGF-2/EGR-1 pathway. <i>PLoS ONE</i> , 2017, 12, e0182422.	2.5	17
72	An adenylyl cyclase with a phosphodiesterase domain in basal plants with a motile sperm system. <i>Scientific Reports</i> , 2016, 6, 39232.	3.3	42

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73	Genomic landscape of colorectal cancer in Japan: clinical implications of comprehensive genomic sequencing for precision medicine. <i>Genome Medicine</i> , 2016, 8, 136.	8.2	64
74	Mutations in <i>SDR9C7</i> gene encoding an enzyme for vitamin A metabolism underlie autosomal recessive congenital ichthyosis. <i>Human Molecular Genetics</i> , 2016, 25, dww277.	2.9	40
75	Species–function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	13.3	279
76	Novel kinase fusion transcripts found in endometrial cancer. <i>Scientific Reports</i> , 2016, 5, 18657.	3.3	11
77	p62/Sqstm1 promotes malignancy of HCV-positive hepatocellular carcinoma through Nrf2-dependent metabolic reprogramming. <i>Nature Communications</i> , 2016, 7, 12030.	12.8	253
78	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate–Product Pairs. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 510-516.	5.4	17
79	GlyYouCan 1.0 – The international glycan structure repository. <i>Nucleic Acids Research</i> , 2016, 44, D1237-D1242.	14.5	83
80	Human <i>T</i> cell leukemia virus type 1 tax oncoprotein represses the expression of the <i>BCL11B</i> tumor suppressor in <i>T</i> cells. <i>Cancer Science</i> , 2015, 106, 461-465.	3.9	15
81	Large-scale analysis of the evolutionary histories of phosphorylation motifs in the human genome. <i>GigaScience</i> , 2015, 4, 21.	6.4	6
82	Cytotoxic Glycosylated Fatty Acid Amides from a <i>Stelletta</i> sp. Marine Sponge. <i>Journal of Natural Products</i> , 2015, 78, 2808-2813.	3.0	10
83	GlycoRDF: an ontology to standardize glycomics data in RDF. <i>Bioinformatics</i> , 2015, 31, 919-925.	4.1	51
84	GlycoEpitope: Database for Carbohydrate Antigen and Antibody. , 2015, , 267-273.		4
85	RNA Sequencing Revealed Numerous Polyketide Synthase Genes in the Harmful Dinoflagellate <i>Karenia mikimotoi</i> . <i>PLoS ONE</i> , 2015, 10, e0142731.	2.5	37
86	Resequencing and Association Analysis of CLN8 with Autism Spectrum Disorder in a Japanese Population. <i>PLoS ONE</i> , 2015, 10, e0144624.	2.5	2
87	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	1.6	47
88	Elucidation of the evolutionary expansion of phosphorylation signaling networks using comparative phosphomotif analysis. <i>BMC Genomics</i> , 2014, 15, 546.	2.8	8
89	Enhanced Translocation and Growth of <i>Rhodococcus erythropolis</i> PR4 in the Alkane Phase of Aqueous-Alkane Two Phase Cultures Were Mediated by GroEL2 Overexpression. <i>Microbes and Environments</i> , 2014, 29, 346-352.	1.6	14
90	GlycoEpitope: A Database for Carbohydrate Antigen and Antibody. , 2014, , 1-7.		2

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91	Introducing glycomics data into the Semantic Web. <i>Journal of Biomedical Semantics</i> , 2013, 4, 39.	1.6	46
92	The Fifth ACGG-DB Meeting Report: Towards an International Glycan Structure Repository. <i>Glycobiology</i> , 2013, 23, 1422-1424.	2.5	8
93	KEGG OC: a large-scale automatic construction of taxonomy-based ortholog clusters. <i>Nucleic Acids Research</i> , 2012, 41, D353-D357.	14.5	96
94	Virtual metagenome reconstruction from 16S rRNA gene sequences. <i>Nature Communications</i> , 2012, 3, 1203.	12.8	24
95	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	27.8	5,345
96	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011, 2, 4.	1.6	19
97	In silico study on the substrate binding manner in human myo-inositol monophosphatase 2. <i>Journal of Molecular Modeling</i> , 2011, 17, 2559-2567.	1.8	5
98	ODB: a database for operon organizations, 2011 update. <i>Nucleic Acids Research</i> , 2011, 39, D552-D555.	14.5	38
99	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011, 39, W412-W415.	14.5	322
100	Direct Observation and Analysis of Bacterial Growth on an Antimicrobial Surface. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5409-5414.	3.1	16
101	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. <i>Carbohydrate Research</i> , 2009, 344, 881-887.	2.3	37
102	Extraction and Analysis of Chemical Modification Patterns in Drug Development. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 1122-1129.	5.4	12
103	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	14.5	445
104	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. <i>Journal of Lipid Research</i> , 2008, 49, 183-191.	4.2	150
105	Network analysis of adverse drug interactions. <i>Genome Informatics</i> , 2008, 20, 252-9.	0.4	6
106	KEGG for linking genomes to life and the environment. <i>Nucleic Acids Research</i> , 2007, 36, D480-D484.	14.5	5,451
107	KAAS: an automatic genome annotation and pathway reconstruction server. <i>Nucleic Acids Research</i> , 2007, 35, W182-W185.	14.5	3,517
108	Characterization of relationships between transcriptional units and operon structures in <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2007, 8, 48.	2.8	51

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109	Extracting Sequence Motifs and the Phylogenetic Features of SNARE-Dependent Membrane Traffic. <i>Traffic</i> , 2006, 7, 1104-1118.	2.7	44
110	ODB: a database of operons accumulating known operons across multiple genomes. <i>Nucleic Acids Research</i> , 2006, 34, D358-D362.	14.5	46
111	Analysis of the differences in metabolic network expansion between prokaryotes and eukaryotes. <i>Genome Informatics</i> , 2006, 17, 230-9.	0.4	2
112	Conservation of gene co-regulation between two prokaryotes: <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>Genome Informatics</i> , 2005, 16, 116-24.	0.4	3
113	Electrophoretic Mobility of <i>Bacillus subtilis</i> Knockout Mutants with and without Flagella. <i>Journal of Bacteriology</i> , 2003, 185, 3711-3717.	2.2	17
114	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	1.6	0