

Shigehiko Kanaya

List of Publications by Year in descending order

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75
papers

1,693
citations

448610

19
h-index

340414

39
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79
all docs

79
docs citations

79
times ranked

2870
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating cepharanthine analogues as natural drugs against SARS-CoV-2. FEBS Open Bio, 2022, 12, 285-294.	1.0	20
2	Recent Trends in Computational Biomedical Research. Life, 2022, 12, 27.	1.1	2
3	Algorithm Cocktail Approach for Predicting Body Constitution and Bias Recovery. , 2022, , .		0
4	Reconciling of the distances in physical space and latent feature space for complex activity modeling. , 2022, , .		0
5	Deep Learning-Based Sleep Staging with Acceleration and Heart Rate Data of a Consumer Wearable Device. , 2022, , .		1
6	Very short-term beat-by-beat blood pressure variability in the supine position at rest correlates well with the nocturnal blood pressure variability assessed by ambulatory blood pressure monitoring. Hypertension Research, 2022, 45, 1008-1017.	1.5	3
7	Embedding of Molecular Structure Using Molecular Hypergraph Variational Autoencoder with Metric Learning. Molecular Informatics, 2021, 40, e2000203.	1.4	14
8	Development of a biomarker database toward performing disease classification and finding disease interrelations. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	2
9	Prediction of Body Constitutions through Life-Style for Health Guidance. , 2021, , .		1
10	An Approach to Construct and Validate TCM Dataset Effective against Bacterial Pneumonia. , 2021, , .		0
11	Potential anti-COVID-19 agents, cepharanthine and nelfinavir, and their usage for combination treatment. IScience, 2021, 24, 102367.	1.9	126
12	A Real-Time Portable IoT System for Telework Tracking. Frontiers in Digital Health, 2021, 3, 643042.	1.5	2
13	Examination of a Regression Model to Quantify the Severities of Low Back Pain and Lower Limb Symptoms in Patients with Lumbar Spinal Stenosis. The Japanese Journal of Rehabilitation Medicine, 2021, 58, 680-691.	0.0	0
14	Identification of Targeted Proteins by Jamu Formulas for Different Efficacies Using Machine Learning Approach. Life, 2021, 11, 866.	1.1	3
15	Current status of structure-based drug repurposing against COVID-19 by targeting SARS-CoV-2 proteins. Biophysics and Physicobiology, 2021, 18, 226-240.	0.5	6
16	Evaluation of intercellular lipid lamellae in the stratum corneum by polarized microscopy. Skin Research and Technology, 2021, , .	0.8	1
17	Comprehensive Exploration of Target-specific Ligands Using a Graph Convolution Neural Network. Molecular Informatics, 2020, 39, e1900095.	1.4	26
18	Knowledge-based structural models of SARS-CoV-2 proteins and their complexes with potential drugs. FEBS Letters, 2020, 594, 1960-1973.	1.3	21

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19	Examination of the regression model to quantify the degree of low back pain and lower limb symptoms in patients with lumbar disc herniation by the Japanese Orthopaedic Association Back Pain Evaluation Questionnaire (JOABPEQ). PLoS ONE, 2020, 15, e0243861.	1.1	2
20	Data Analysis of Health-related Information of Kurobe Local Resident by Constitution Theory of Traditional Chinese Medicine. Japanese Journal of Complementary and Alternative Medicine, 2020, 17, 145-153.	1.0	0
21	Classification of alkaloids according to the starting substances of their biosynthetic pathways using graph convolutional neural networks. BMC Bioinformatics, 2019, 20, 380.	1.2	45
22	Pentagamavunon-1 (PGV-1) inhibits ROS metabolic enzymes and suppresses tumor cell growth by inducing M phase (prometaphase) arrest and cell senescence. Scientific Reports, 2019, 9, 14867.	1.6	20
23	Evaluation of microbial communities in peels of Brazilian tropical fruits by amplicon sequence analysis. Brazilian Journal of Microbiology, 2019, 50, 739-748.	0.8	12
24	A Novel CNN-Based Framework for Classification of Signal Quality and Sleep Position from a Capacitive ECG Measurement. Sensors, 2019, 19, 1731.	2.1	24
25	[Special Issue for Honor Award dedicating to Prof Kimito Funatsu](Mini-review)Meanings of the Honor Award for Prof Kimito Funatsu. Journal of Computer Aided Chemistry, 2019, 20, 23-28.	0.3	0
26	Curcumin Derivatives Verify the Essentiality of ROS Upregulation in Tumor Suppression. Molecules, 2019, 24, 4067.	1.7	29
27	Determination of Optimum Number of Groups on the Crowdsourcing Survey in Japanese People Interpreted by Physical Constitution Defined by CCMQ-J. Japanese Journal of Complementary and Alternative Medicine, 2019, 16, 105-112.	1.0	0
28	UC2 search: using unique connectivity of uncharged compounds for metabolite annotation by database searching in mass spectrometry-based metabolomics. Bioinformatics, 2018, 34, 698-700.	1.8	17
29	Molecular components of Arabidopsis intact vacuoles clarified with metabolomic and proteomic analyses. Plant and Cell Physiology, 2018, 59, 1353-1362.	1.5	11
30	Oviposition inhibitor in umbelliferous medicinal plants for the common yellow swallowtail (Papilio Tj ETQq0 0 0 rgBT/Overlock 10 Tf 00	1.1	0
31	System evaluation of automated production and inhalation of 15O-labeled gaseous radiopharmaceuticals for the rapid 15O-oxygen PET examinations. EJNMMI Physics, 2018, 5, 37.	1.3	11
32	Co-ordinated Regulations of mRNA Synthesis and Decay during Cold Acclimation in Arabidopsis Cells. Plant and Cell Physiology, 2017, 58, 1090-1102.	1.5	10
33	Metabolomic Studies of Indonesian Jamu Medicines: Prediction of Jamu Efficacy and Identification of Important Metabolites. Molecular Informatics, 2017, 36, 1700050.	1.4	17
34	[Dedicated to Prof. T. Okada and Prof. T. Nishioka: data science in chemistry]Classification of Alkaloid Compounds Based on Subring Skeleton (SRS) Profiling: On Finding Relationship of Compounds with Metabolic Pathways. Journal of Computer Aided Chemistry, 2017, 18, 58-75.	0.3	4
35	Novel Approach to Classify Plants Based on Metabolite-Content Similarity. BioMed Research International, 2017, 2017, 1-12.	0.9	30
36	Big Data and Network Biology 2016. BioMed Research International, 2017, 2017, 1-2.	0.9	1

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37	[Dedicated to Prof. T. Okada and Prof. T. Nishioka: data science in chemistry]Centrality Values of Yeast Proteins in a PPI Network Are Related to Their Essentiality and Functions. Journal of Computer Aided Chemistry, 2017, 18, 94-109.	0.3	2
38	Structural Optimization of a Wearable Deep Body Thermometer: From Theoretical Simulation to Experimental Verification. Journal of Sensors, 2016, 2016, 1-7.	0.6	13
39	Critical Involvement of Environmental Carbon Dioxide Fixation to Drive Wax Ester Fermentation in Euglena. PLoS ONE, 2016, 11, e0162827.	1.1	8
40	Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles. Journal of Biomedical Informatics, 2016, 61, 194-202.	2.5	6
41	Comparative analysis of transcriptomes in aerial stems and roots of Ephedra sinica based on high-throughput mRNA sequencing. Genomics Data, 2016, 10, 4-11.	1.3	6
42	Utilization of KNApSACK Family Databases for Developing Herbal Medicine Systems. Journal of Computer Aided Chemistry, 2016, 17, 1-7.	0.3	8
43	Finding an appropriate equation to measure similarity between binary vectors: case studies on Indonesian and Japanese herbal medicines. BMC Bioinformatics, 2016, 17, 520.	1.2	15
44	Development of high-resolution brain SPECT system using full-digital gamma camera with multiple position-sensitive PMTs. , 2015, , .		0
45	Metabolomic Characterization of a Low Phytic Acid and High Anti-oxidative Cultivar of Turmeric. Natural Product Communications, 2015, 10, 1934578X1501000.	0.2	2
46	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. Frontiers in Bioengineering and Biotechnology, 2015, 3, 38.	2.0	39
47	A Glimpse to Background and Characteristics of Major Molecular Biological Networks. BioMed Research International, 2015, 2015, 1-14.	0.9	12
48	Development and Mining of a Volatile Organic Compound Database. BioMed Research International, 2015, 2015, 1-13.	0.9	30
49	Targeted Integration of RNA-Seq and Metabolite Data to Elucidate Curcuminoid Biosynthesis in Four Curcuma Species. Plant and Cell Physiology, 2015, 56, 843-851.	1.5	9
50	The dynamic balance of import and export of zinc in <i>Escherichia coli</i> suggests a heterogeneous population response to stress. Journal of the Royal Society Interface, 2015, 12, 20150069.	1.5	19
51	Evaluation of structural and thermophysical effects on the measurement accuracy of deep body thermometers based on dual-heat-flux method. Journal of Thermal Biology, 2015, 47, 26-31.	1.1	23
52	Integration of Residue Attributes for Sequence Diversity Characterization of Terpenoid Enzymes. BioMed Research International, 2014, 2014, 1-10.	0.9	2
53	KEGGscape: a Cytoscape app for pathway data integration. F1000Research, 2014, 3, 144.	0.8	65
54	Clustering of 3D π -Structure Similarity Based Network of Secondary Metabolites Reveals Their Relationships with Biological Activities. Molecular Informatics, 2014, 33, 790-801.	1.4	18

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55	Integrated network analysis and effective tools in plant systems biology. <i>Frontiers in Plant Science</i> , 2014, 5, 598.	1.7	55
56	A Novel Bioinformatics Method for Efficient Knowledge Discovery by BLSOM from Big Genomic Sequence Data. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	3
57	An Unsupervised Approach to Predict Functional Relations between Genes Based on Expression Data. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	5
58	Systems Biology in the Context of Big Data and Networks. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	75
59	Supervised Clustering Based on DPCLUSO: Prediction of Plant-Disease Relations Using Jamu Formulas of KNAPSAcK Database. <i>BioMed Research International</i> , 2014, 2014, 1-15.	0.9	21
60	KNAPSAcK Metabolite Activity Database for Retrieving the Relationships Between Metabolites and Biological Activities. <i>Plant and Cell Physiology</i> , 2014, 55, e7-e7.	1.5	92
61	DATA MINING METHODS FOR OMICS AND KNOWLEDGE OF CRUDE MEDICINAL PLANTS TOWARD BIG DATA BIOLOGY. <i>Computational and Structural Biotechnology Journal</i> , 2013, 4, e201301010.	1.9	46
62	Systematization of the Protein Sequence Diversity in Enzymes Related to Secondary Metabolic Pathways in Plants, in the Context of Big Data Biology Inspired by the KNAPSAcK Motorcycle Database. <i>Plant and Cell Physiology</i> , 2013, 54, 711-727.	1.5	18
63	KNAPSAcK Family Databases: Integrated Metabolite-Plant Species Databases for Multifaceted Plant Research. <i>Plant and Cell Physiology</i> , 2012, 53, e1-e1.	1.5	529
64	Partitioning a PPI Network into Overlapping Modules Constrained by High-Density and Periphery Tracking. , 2012, 2012, 1-11.		25
65	Protein function prediction based on k-cores of interaction networks. , 2010, , .		0
66	System Biology Approach for Elucidating the Relationship Between Indonesian Herbal Plants and the Efficacy of Jamu. , 2010, , .		9
67	An approach to peak detection in GC-MS chromatograms and application of KNAPSAcK database in prediction of candidate metabolites. <i>Plant Biotechnology</i> , 2009, 26, 167-174.	0.5	9
68	Metabolic pathway prediction based on inclusive relation between cyclic substructures. <i>Plant Biotechnology</i> , 2009, 26, 459-468.	0.5	9
69	Visualization of metabolite identifier information. <i>Plant Biotechnology</i> , 2009, 26, 479-483.	0.5	6
70	Characterizing gene coexpression modules in <i>Oryza sativa</i> based on a graph-clustering approach. <i>Plant Biotechnology</i> , 2009, 26, 485-493.	0.5	12
71	Bioinformatics from MOURA to SHIKKAI. <i>Plant Biotechnology</i> , 2009, 26, 443-444.	0.5	0
72	A tool for high-throughput prediction of molecular formulas and identification of isotopic peaks from large-scale mass spectrometry data. <i>Plant Biotechnology</i> , 2008, 25, 377-380.	0.5	10

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73	A density-periphery based graph clustering software developed for detection of protein complexes in interaction networks. , 2007, , .		1
74	[Special Issue: Fact Databases and Freewares] DPPlus: A Density-periphery Based Graph Clustering Software Mainly Focused on Detection of Protein Complexes in Interaction Networks. Journal of Computer Aided Chemistry, 2006, 7, 150-156.	0.3	24
75	Comparative Genome Analysis Focused on Periodicity from Prokaryote to Higher Eukaryote Genomes Based on Power Spectrum. Journal of Computer Chemistry Japan, 2003, 2, 95-110.	0.0	1