Sungroh Yoon

List of Publications by Year in descending order

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106 4,028 27 56
papers citations h-index g-index

109 109 109 5050 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Deep learning in bioinformatics. Briefings in Bioinformatics, 2017, 18, bbw068.	3.2	865
2	Deep learning improves prediction of CRISPR–Cpf1 guide RNA activity. Nature Biotechnology, 2018, 36, 239-241.	9.4	252
3	How Generative Adversarial Networks and Their Variants Work. ACM Computing Surveys, 2020, 52, 1-43.	16.1	185
4	Predicting the efficiency of prime editing guide RNAs in human cells. Nature Biotechnology, 2021, 39, 198-206.	9.4	160
5	Got target?: computational methods for microRNA target prediction and their extension. Experimental and Molecular Medicine, 2010, 42, 233.	3.2	156
6	Deep Learning for Anomaly Detection in Time-Series Data: Review, Analysis, and Guidelines. IEEE Access, 2021, 9, 120043-120065.	2.6	137
7	Prediction of the sequence-specific cleavage activity of Cas9 variants. Nature Biotechnology, 2020, 38, 1328-1336.	9.4	133
8	SpCas9 activity prediction by DeepSpCas9, a deep learning–based model with high generalization performance. Science Advances, 2019, 5, eaax9249.	4.7	130
9	Prediction of regulatory modules comprising microRNAs and target genes. Bioinformatics, 2005, 21, ii93-ii100.	1.8	109
10	Comprehensive ensemble in QSAR prediction for drug discovery. BMC Bioinformatics, 2019, 20, 521.	1.2	104
11	High-throughput analysis of the activities of xCas9, SpCas9-NG and SpCas9 at matched and mismatched target sequences in human cells. Nature Biomedical Engineering, 2020, 4, 111-124.	11.6	98
12	Biometric Authentication Using Noisy Electrocardiograms Acquired by Mobile Sensors. IEEE Access, 2016, 4, 1266-1273.	2.6	86
13	LncRNAnet: long non-coding RNA identification using deep learning. Bioinformatics, 2018, 34, 3889-3897.	1.8	80
14	Sequence-specific prediction of the efficiencies of adenine and cytosine base editors. Nature Biotechnology, 2020, 38, 1037-1043.	9.4	73
15	Patch SVDD: Patch-Level SVDD for Anomaly Detection and Segmentation. Lecture Notes in Computer Science, 2021, , 375-390.	1.0	72
16	deepTarget., 2016,,.		66
17	End-to-End Blood Pressure Prediction via Fully Convolutional Networks. IEEE Access, 2019, 7, 185458-185468.	2.6	61
18	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. Current Protocols, 2021, 1, e113.	1.3	61

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19	Computational identification of microRNAs and their targets. Birth Defects Research Part C: Embryo Today Reviews, 2006, 78, 118-128.	3.6	59
20	CASPER: context-aware scheme for paired-end reads from high-throughput amplicon sequencing. BMC Bioinformatics, 2014, 15, S10.	1.2	56
21	Fast and Efficient Information Transmission with Burst Spikes in Deep Spiking Neural Networks. , 2019, ,		52
22	T2FSNN: Deep Spiking Neural Networks with Time-to-first-spike Coding. , 2020, , .		51
23	Discovering Coherent Biclusters from Gene Expression Data Using Zero-Suppressed Binary Decision Diagrams. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 339-354.	1.9	50
24	Single-image deblurring with neural networks: A comparative survey. Computer Vision and Image Understanding, 2021, 203, 103134.	3.0	47
25	Generation of a more efficient prime editor 2 by addition of the Rad51 DNA-binding domain. Nature Communications, 2021, 12, 5617.	5.8	47
26	DUDE-Seq: Fast, flexible, and robust denoising for targeted amplicon sequencing. PLoS ONE, 2017, 12, e0181463.	1.1	47
27	Adversarial Vertex Mixup: Toward Better Adversarially Robust Generalization. , 2020, , .		45
28	Large-scale machine learning of media outlets for understanding public reactions to nation-wide viral infection outbreaks. Methods, 2017, 129, 50-59.	1.9	43
29	PuVAE: A Variational Autoencoder to Purify Adversarial Examples. IEEE Access, 2019, 7, 126582-126593.	2.6	36
30	DeepCCI., 2017,,.		30
31	Clustering protein environments for function prediction: finding PROSITE motifs in 3D. BMC Bioinformatics, 2007, 8, S10.	1.2	29
32	The message passing neural networks for chemical property prediction on SMILES. Methods, 2020, 179, 65-72.	1.9	29
33	Recording of elapsed time and temporal information about biological events using Cas9. Cell, 2021, 184, 1047-1063.e23.	13.5	29
34	IO Workload Characterization Revisited: A Data-Mining Approach. IEEE Transactions on Computers, 2014, 63, 3026-3038.	2.4	28
35	Frame-to-Frame Aggregation of Active Regions in Web Videos for Weakly Supervised Semantic Segmentation. , 2019, , .		27
36	High-Dimensional Fused Lasso Regression Using Majorization–Minimization and Parallel Processing. Journal of Computational and Graphical Statistics, 2015, 24, 121-153.	0.9	21

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37	Prediction of pathologic femoral fractures in patients with lung cancer using machine learning algorithms: Comparison of computed tomography-based radiological features with clinical features versus without clinical features. Journal of Orthopaedic Surgery, 2017, 25, 230949901771624.	0.4	21
38	Pre-Training of Deep Bidirectional Protein Sequence Representations With Structural Information. IEEE Access, 2021, 9, 123912-123926.	2.6	20
39	Entropy-Based Analysis and Bioinformatics-Inspired Integration of Global Economic Information Transfer. PLoS ONE, 2013, 8, e51986.	1.1	20
40	Ensemble learning can significantly improve human microRNA target prediction. Methods, 2014, 69, 220-229.	1.9	18
41	Deep learning based low-cost high-accuracy diagnostic framework for dementia using comprehensive neuropsychological assessment profiles. BMC Geriatrics, 2018, 18, 234.	1.1	18
42	Pediatric Sleep Stage Classification Using Multi-Domain Hybrid Neural Networks. IEEE Access, 2019, 7, 96495-96505.	2.6	17
43	End-to-End Representation Learning for Chemical-Chemical Interaction Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1436-1447.	1.9	14
44	Learning-Based Instantaneous Drowsiness Detection Using Wired and Wireless Electroencephalography. IEEE Access, 2019, 7, 146390-146402.	2.6	14
45	Interpretation of NLP models through input marginalization. , 2020, , .		14
46	Co-clustering: A Versatile Tool for Data Analysis in Biomedical Informatics. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 493-494.	3.6	13
47	Multi-Threaded Hierarchical Clustering by Parallel Nearest-Neighbor Chaining. IEEE Transactions on Parallel and Distributed Systems, 2015, 26, 2534-2548.	4.0	13
48	HiComet: a high-throughput comet analysis tool for large-scale DNA damage assessment. BMC Bioinformatics, 2018, 19, 44.	1.2	13
49	Electroencephalographic Resting-State Functional Connectivity of Benign Epilepsy with		

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55	AnomiGAN: Generative Adversarial Networks for Anonymizing Private Medical Data., 2019, , .		11
56	GPU-based acceleration of an RNA tertiary structure prediction algorithm. Computers in Biology and Medicine, 2013, 43, 1011-1022.	3.9	10
57	NC-link: A New Linkage Method for Efficient Hierarchical Clustering of Large-Scale Data. IEEE Access, 2017, , 1-1.	2.6	9
58	Imbalanced Data Classification via Cooperative Interaction Between Classifier and Generator. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 3343-3356.	7.2	9
59	Feature Concentration for Supervised and Semisupervised Learning With Unbalanced Datasets in Visual Inspection. IEEE Transactions on Industrial Electronics, 2021, 68, 7620-7630.	5.2	8
60	Learn2Evade: Learning-Based Generative Model for Evading PDF Malware Classifiers. IEEE Transactions on Artificial Intelligence, 2021, 2, 299-313.	3.4	8
61	Gradient Masking of Label Smoothing in Adversarial Robustness. IEEE Access, 2021, 9, 6453-6464.	2.6	8
62	NAND Flash Memory With Multiple Page Sizes for High-Performance Storage Devices. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2016, 24, 764-768.	2.1	7
63	Large-Scale Structured Sparsity via Parallel Fused Lasso on Multiple GPUs. Journal of Computational and Graphical Statistics, 2017, 26, 851-864.	0.9	7
64	Development and External Validation of the Korean Prostate Cancer Risk Calculator for High-Grade Prostate Cancer: Comparison with Two Western Risk Calculators in an Asian Cohort. PLoS ONE, 2017, 12, e0168917.	1.1	7
65	Exome-based genome-wide association study and risk assessment using genetic risk score to prostate cancer in the Korean population. Oncotarget, 2017, 8, 43934-43943.	0.8	7
66	Flexible Dual-Branched Message-Passing Neural Network for a Molecular Property Prediction. ACS Omega, 2022, 7, 4234-4244.	1.6	7
67	Prediction and Analysis of Human microRNA Regulatory Modules. , 2005, 2005, 4799-802.		6
68	XGBoost-Based Instantaneous Drowsiness Detection Framework Using Multitaper Spectral Information of Electroencephalography. , 2018, , .		6
69	Development and Validation of a Next-Generation Sequencing–Based Multigene Assay to Predict the Prognosis of Estrogen Receptor–Positive, HER2-Negative Breast Cancer. Clinical Cancer Research, 2020, 26, 6513-6522.	3.2	6
70	The Use of Exome Genotyping to Predict Pathological Gleason Score Upgrade after Radical Prostatectomy in Low-Risk Prostate Cancer Patients. PLoS ONE, 2014, 9, e104146.	1.1	6
71	Genetic risk score to predict biochemical recurrence after radical prostatectomy in prostate cancer: prospective cohort study. Oncotarget, 2017, 8, 75979-75988.	0.8	6
72	Prediction of clinically significant prostate cancer using polygenic risk models in Asians. Investigative and Clinical Urology, 2022, 63, 42.	1.0	6

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73	Regularization and Kernelization of the Maximin Correlation Approach. IEEE Access, 2016, 4, 1385-1392.	2.6	5
74	DNA Steganalysis Using Deep Recurrent Neural Networks., 2018,,.		5
75	TensorLightning: A Traffic-Efficient Distributed Deep Learning on Commodity Spark Clusters. IEEE Access, 2018, 6, 27671-27680.	2.6	5
76	Anomaly Detection by Learning Dynamics From a Graph. IEEE Access, 2020, 8, 64356-64365.	2.6	5
77	PixelSteganalysis: Pixel-Wise Hidden Information Removal With Low Visual Degradation. IEEE Transactions on Dependable and Secure Computing, 2023, 20, 331-342.	3.7	5
78	Energy-Efficient Inference Accelerator for Memory-Augmented Neural Networks on an FPGA. , 2019, , .		4
79	DNA Privacy: Analyzing Malicious DNA Sequences using Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	4
80	A genetic variant in SLC28A3, rs56350726, is associated with progression to castration-resistant prostate cancer in a Korean population with metastatic prostate cancer. Oncotarget, 2017, 8, 96893-96902.	0.8	4
81	Methodology for Big Data Analysis Using Data from National Health Insurance Service: Preliminary Methodologic Study and Review about the Relationship between Sinus Surgery and Asthma. Journal of Rhinology, 2015, 22, 28.	0.1	3
82	A clinicogenetic model to predict lymph node invasion by use of genome-based biomarkers from exome arrays in prostate cancer patients. Korean Journal of Urology, 2015, 56, 109.	1,2	3
83	Mining internet media for monitoring changes of public emotions about infectious diseases. , 2016, , .		3
84	Machine learning-based identification of endogenous cellular microRNA sponges against viral microRNAs. Methods, 2017, 129, 33-40.	1.9	3
85	CloudSocket: Fine-Grained Power Sensing System for Datacenters. IEEE Access, 2018, 6, 49601-49610.	2.6	3
86	Prediction of Drug Classes with a Deep Neural Network using Drug Targets and Chemical Structure Data. , 2019, , .		3
87	Accelerating Neural Architecture Search via Proxy Data. , 2021, , .		3
88	Measuring Large-Scale Dynamic Graph Similarity by RICom: RWR with Intergraph Compression., 2015,,.		2
89	CloudSocket: Smart grid platform for datacenters. , 2016, , .		2
90	Memory-Augmented Neural Networks on FPGA for Real-Time and Energy-Efficient Question Answering. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2021, 29, 162-175.	2.1	2

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91	Compensating Nonuniform OLED Pixel Brightness in a Vertical Blanking Interval by Learning TFT Characteristics. IEEE Transactions on Electron Devices, 2021, 68, 3396-3402.	1.6	2
92	Rapid and Robust Denoising of Pyrosequenced Amplicons for Metagenomics., 2012,,.		1
93	Ensemble learning for robust prediction of microRNA-mRNA interactions. , 2014, , .		1
94	Genome-wide detection of allelic genetic variation to predict biochemical recurrence after radical prostatectomy among prostate cancer patients using an exome SNP chip. Journal of Cancer Research and Clinical Oncology, 2015, 141, 1493-1501.	1,2	1
95	An effective pre-store/pre-load method exploiting intra-request idle time of NAND flash-based storage devices. Microprocessors and Microsystems, 2017, 50, 222-236.	1.8	1
96	Machine learning methods and systems for data-driven discovery in biomedical informatics. Methods, 2017, 129, 1-2.	1.9	1
97	MUGAN: multi-GPU accelerated AmpliconNoise server for rapid microbial diversity assessment. Bioinformatics, 2021, 37, 1562-1570.	1.8	1
98	65â€2: A Light and Fast Branched Neural Network using Perceptual Optimization for Highâ€Quality Visual Restoration of UDC images. Digest of Technical Papers SID International Symposium, 2022, 53, 861-864.	0.1	1
99	Design of a bitmap-based QoS-aware memory controller for a packet memory. IEICE Electronics Express, 2014, 11, 20130983-20130983.	0.3	0
100	Computational prediction of competitive endogenous RNA. , 2015, , .		0
101	Genome-wide detection of allelic genetic variation to predict advanced-stage prostate cancer after radical prostatectomy using an exome SNP chip. Urologic Oncology: Seminars and Original Investigations, 2015, 33, 385.e7-385.e13.	0.8	0
102	60â€2: Selfâ€supervised Perceptual Motion Deblurring using a Conditional Generative Neural Network Guided by Optical Flow. Digest of Technical Papers SID International Symposium, 2020, 51, 893-896.	0.1	0
103	Energy-aware Placement for SRAM-NVM Hybrid FPGAs. , 2020, , .		O
104	NASCUP: Nucleic Acid Sequence Classification by Universal Probability. IEEE Access, 2021, 9, 162779-162791.	2.6	0
105	Exploiting Binary Abstractions in Deciphering Gene Interactions. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0
106	Data Embedding Scheme for Efficient Program Behavior Modeling With Neural Networks. IEEE Transactions on Emerging Topics in Computational Intelligence, 2022, 6, 982-993.	3.4	0