Yoshihiro Yamanishi

List of Publications by Year
in descending order

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Version: 2024-02-01

54	8,601	304368 22	182168 51
papers	citations	h-index	g-index

54	54	54	11136
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Epigenetic landscape of drug responses revealed through large-scale ChIP-seq data analyses. BMC Bioinformatics, 2022, 23, 51.	1.2	7
2	Scaffold-Retained Structure Generator to Exhaustively Create Molecules in an Arbitrary Chemical Space. Journal of Chemical Information and Modeling, 2022, 62, 2212-2225.	2.5	9
3	A Web Server for GPCR-GPCR Interaction Pair Prediction. Frontiers in Endocrinology, 2022, 13, 825195.	1.5	3
4	From drug repositioning to target repositioning: prediction of therapeutic targets using genetically perturbed transcriptomic signatures. Bioinformatics, 2022, 38, i68-i76.	1.8	3
5	TRANSDIRE: data-driven direct reprogramming by a pioneer factor-guided trans-omics approach. Bioinformatics, 2022, 38, 2839-2846.	1.8	4
6	The novel driver gene ASAP2 is a potential druggable target in pancreatic cancer. Cancer Science, 2021, 112, 1655-1668.	1.7	18
7	Prediction of single-cell mechanisms for disease progression in hypertrophic remodelling by a trans-omics approach. Scientific Reports, 2021, 11, 8112.	1.6	4
8	Lean-Docking: Exploiting Ligandsâ€™ Predicted Docking Scores to Accelerate Molecular Docking. Journal of Chemical Information and Modeling, 2021, 61, 2341-2352.	2.5	38
9	TRIOMPHE: Transcriptome-Based Inference and Generation of Molecules with Desired Phenotypes by Machine Learning. Journal of Chemical Information and Modeling, 2021, 61, 4303-4320.	2.5	7
10	Omicsâ€based Identification of Glycan Structures as Biomarkers for a Variety of Diseases. Molecular Informatics, 2020, 39, 1900112.	1.4	5
11	Prediction of the Health Effects of Food Peptides and Elucidation of the Modeâ€ofâ€action Using Multiâ€task Graph Convolutional Neural Network. Molecular Informatics, 2020, 39, e1900134.	1.4	8
12	Network-based characterization of diseaseâ€“disease relationships in terms of drugs and therapeutic targets. Bioinformatics, 2020, 36, i516-i524.	1.8	13
13	Space-Efficient Feature Maps for String Alignment Kernels. Data Science and Engineering, 2020, 5, 168-179.	4.6	0
14	Ranking Molecules with Vanishing Kernels and a Single Parameter: Active Applicability DomainIncluded. Journal of Chemical Information and Modeling, 2020, 60, 4376-4387.	2.5	2
15	Predicting drug-induced transcriptome responses of a wide range of human cell lines by a novel tensor-train decomposition algorithm. Bioinformatics, 2019, 35, i191-i199.	1.8	24
16	Chemoinformatics and structural bioinformatics in OCaml. Journal of Cheminformatics, 2019, 11, 10.	2.8	5
17	Network-based characterization of drug-protein interaction signatures with a space-efficient approach. BMC Systems Biology, 2019, 13, 39.	3.0	13
18	A Distance-Based Boolean Applicability Domain for Classification of High Throughput Screening Data. Journal of Chemical Information and Modeling, 2019, 59, 463-476.	2.5	13

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19	MIBG myocardial scintigraphy in progressive supranuclear palsy. Journal of the Neurological Sciences, 2019, 396, 3-7.	0.3	4
20	The Use of Large-Scale Chemically-Induced Transcriptome Data Acquired from LINCS to Study Small Molecules. Methods in Molecular Biology, 2019, 1888, 189-203.	0.4	2
21	Predicting inhibitory and activatory drug targets by chemically and genetically perturbed transcriptome signatures. Scientific Reports, 2018, 8, 156.	1.6	43
22	Linear and Kernel Model Construction Methods for Predicting Drugâ€“Target Interactions in a Chemogenomic Framework. Methods in Molecular Biology, 2018, 1825, 355-368.	0.4	3
23	Pathway-Based Drug Repositioning for Cancers: Computational Prediction and Experimental Validation. Journal of Medicinal Chemistry, 2018, 61, 9583-9595.	2.9	19
24	Sparse Modeling to Analyze Drugâ€“Target Interaction Networks. Methods in Molecular Biology, 2018, 1807, 181-193.	0.4	1
25	KampoDB, database of predicted targets and functional annotations of natural medicines. Scientific Reports, 2018, 8, 11216.	1.6	11
26	Elucidating the modes of action for bioactive compounds in a cell-specific manner by large-scale chemically-induced transcriptomics. Scientific Reports, 2017, 7, 40164.	1.6	50
27	GGIP: Structure and sequence-based GPCR-GPCR interaction pair predictor. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1224-1233.	1.5	13
28	Simultaneous prediction of enzyme orthologs from chemical transformation patterns for de novo metabolic pathway reconstruction. Bioinformatics, 2016, 32, i278-i287.	1.8	15
29	Predicting target proteins for drug candidate compounds based on drug-induced gene expression data in a chemical structure-independent manner. BMC Medical Genomics, 2015, 8, 82.	0.7	35
30	Large-Scale Prediction of Beneficial Drug Combinations Using Drug Efficacy and Target Profiles. Journal of Chemical Information and Modeling, 2015, 55, 2705-2716.	2.5	29
31	Metabolome-scale de novo pathway reconstruction using regioisomer-sensitive graph alignments. Bioinformatics, 2015, 31, i161-i170.	1.8	14
32	Mining Discriminative Patterns from Graph Data with Multiple Labels and Its Application to Quantitative Structureâ€“Activity Relationship (QSAR) Models. Journal of Chemical Information and Modeling, 2015, 55, 2519-2527.	2.5	8
33	Systematic Drug Repositioning for a Wide Range of Diseases with Integrative Analyses of Phenotypic and Molecular Data. Journal of Chemical Information and Modeling, 2015, 55, 446-459.	2.5	63
34	Target-Based Drug Repositioning Using Large-Scale Chemicalâ€“Protein Interactome Data. Journal of Chemical Information and Modeling, 2015, 55, 2717-2730.	2.5	52
35	Metabolome-scale prediction of intermediate compounds in multistep metabolic pathways with a recursive supervised approach. Bioinformatics, 2014, 30, i165-i174.	1.8	15
36	DINIES: drugâ€“target interaction network inference engine based on supervised analysis. Nucleic Acids Research, 2014, 42, W39-W45.	6.5	97

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37	Benchmarking a Wide Range of Chemical Descriptors for Drugâ€Target Interaction Prediction Using a Chemogenomic Approach. Molecular Informatics, 2014, 33, 719-731.	1.4	49
38	KCF-S: KEGG Chemical Function and Substructure for improved interpretability and prediction in chemical bioinformatics. BMC Systems Biology, 2013, 7, S2.	3.0	25
39	Scalable prediction of compound-protein interactions using minwise hashing. BMC Systems Biology, 2013, 7, S3.	3.0	37
40	Inferring Chemogenomic Features from Drugâ€Target Interaction Networks. Molecular Informatics, 2013, 32, 991-999.	1.4	8
41	Supervised de novo reconstruction of metabolic pathways from metabolome-scale compound sets. Bioinformatics, 2013, 29, i135-i144.	1.8	31
42	Identification of chemogenomic features from drugâ€“target interaction networks using interpretable classifiers. Bioinformatics, 2012, 28, i487-i494.	1.8	78
43	Relating drugâ€“protein interaction network with drug side effects. Bioinformatics, 2012, 28, i522-i528.	1.8	176
44	Drug Side-Effect Prediction Based on the Integration of Chemical and Biological Spaces. Journal of Chemical Information and Modeling, 2012, 52, 3284-3292.	2.5	125
45	Extracting Sets of Chemical Substructures and Protein Domains Governing Drug-Target Interactions. Journal of Chemical Information and Modeling, 2011, 51, 1183-1194.	2.5	71
46	INTEGER PROGRAMMING-BASED METHOD FOR COMPLETING SIGNALING PATHWAYS AND ITS APPLICATION TO ANALYSIS OF COLORECTAL CANCER. , 2010, , .		0
47	Cartesian Kernel: An Efficient Alternative to the Pairwise Kernel. IEICE Transactions on Information and Systems, 2010, E93-D, 2672-2679.	0.4	8
48	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. Bioinformatics, 2010, 26, i246-i254.	1.8	396
49	Supervised prediction of drugâ€“target interactions using bipartite local models. Bioinformatics, 2009, 25, 2397-2403.	1.8	527
50	Prediction of drugâ€“target interaction networks from the integration of chemical and genomic spaces. Bioinformatics, 2008, 24, i232-i240.	1.8	864
51	KEGG for linking genomes to life and the environment. Nucleic Acids Research, 2007, 36, D480-D484.	6.5	5,451
52	Glycan classification with tree kernels. Bioinformatics, 2007, 23, 1211-1216.	1.8	43
53	AN IMPROVED SCORING SCHEME FOR PREDICTING GLYCAN STRUCTURES FROM GENE EXPRESSION DATA. , 2007, , .		18
54	Extraction of leukemia specific glycan motifs in humans by computational glycomics. Carbohydrate Research, 2005, 340, 2270-2278.	1.1	44