## Yoshihiro Yamanishi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	KEGC for linking genomes to life and the environment. Nucleic Acids Research, 2007, 36, D480-D484.	14.5	5,451
2	Prediction of drug–target interaction networks from the integration of chemical and genomic spaces. Bioinformatics, 2008, 24, i232-i240.	4.1	864
3	Supervised prediction of drug–target interactions using bipartite local models. Bioinformatics, 2009, 25, 2397-2403.	4.1	527
4	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. Bioinformatics, 2010, 26, i246-i254.	4.1	396
5	Relating drug–protein interaction network with drug side effects. Bioinformatics, 2012, 28, i522-i528.	4.1	176
6	Drug Side-Effect Prediction Based on the Integration of Chemical and Biological Spaces. Journal of Chemical Information and Modeling, 2012, 52, 3284-3292.	5.4	125
7	DINIES: drug–target interaction network inference engine based on supervised analysis. Nucleic Acids Research, 2014, 42, W39-W45.	14.5	97
8	ldentification of chemogenomic features from drug–target interaction networks using interpretable classifiers. Bioinformatics, 2012, 28, i487-i494.	4.1	78
9	Extracting Sets of Chemical Substructures and Protein Domains Governing Drug-Target Interactions. Journal of Chemical Information and Modeling, 2011, 51, 1183-1194.	5.4	71
10	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.	5.4	63
11	Target-Based Drug Repositioning Using Large-Scale Chemical–Protein Interactome Data. Journal of Chemical Information and Modeling, 2015, 55, 2717-2730.	5.4	52
12	Elucidating the modes of action for bioactive compounds in a cell-specific manner by large-scale chemically-induced transcriptomics. Scientific Reports, 2017, 7, 40164.	3.3	50
13	Benchmarking a Wide Range of Chemical Descriptors for Drugâ€Target Interaction Prediction Using a Chemogenomic Approach. Molecular Informatics, 2014, 33, 719-731.	2.5	49
14	Extraction of leukemia specific glycan motifs in humans by computational glycomics. Carbohydrate Research, 2005, 340, 2270-2278.	2.3	44
15	Glycan classification with tree kernels. Bioinformatics, 2007, 23, 1211-1216.	4.1	43
16	Predicting inhibitory and activatory drug targets by chemically and genetically perturbed transcriptome signatures. Scientific Reports, 2018, 8, 156.	3.3	43
17	Lean-Docking: Exploiting Ligands' Predicted Docking Scores to Accelerate Molecular Docking. Journal of Chemical Information and Modeling, 2021, 61, 2341-2352.	5.4	38
18	Scalable prediction of compound-protein interactions using minwise hashing. BMC Systems Biology, 2013, 7, S3.	3.0	37

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19	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.	1.5	35
20	Supervised <i>de novo</i> reconstruction of metabolic pathways from metabolome-scale compound sets. Bioinformatics, 2013, 29, i135-i144.	4.1	31
21	Large-Scale Prediction of Beneficial Drug Combinations Using Drug Efficacy and Target Profiles. Journal of Chemical Information and Modeling, 2015, 55, 2705-2716.	5.4	29
22	KCF-S: KEGG Chemical Function and Substructure for improved interpretability and prediction in chemical bioinformatics. BMC Systems Biology, 2013, 7, S2.	3.0	25
23	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.	4.1	24
24	Pathway-Based Drug Repositioning for Cancers: Computational Prediction and Experimental Validation. Journal of Medicinal Chemistry, 2018, 61, 9583-9595.	6.4	19
25	The novel driver gene <i>ASAP2</i> is a potential druggable target in pancreatic cancer. Cancer Science, 2021, 112, 1655-1668.	3.9	18
26	AN IMPROVED SCORING SCHEME FOR PREDICTING GLYCAN STRUCTURES FROM GENE EXPRESSION DATA. , 2007, , .		18
27	Metabolome-scale prediction of intermediate compounds in multistep metabolic pathways with a recursive supervised approach. Bioinformatics, 2014, 30, i165-i174.	4.1	15
28	Simultaneous prediction of enzyme orthologs from chemical transformation patterns for <i>de novo</i> metabolic pathway reconstruction. Bioinformatics, 2016, 32, i278-i287.	4.1	15
29	Metabolome-scale <i>de novo</i> pathway reconstruction using regioisomer-sensitive graph alignments. Bioinformatics, 2015, 31, i161-i170.	4.1	14
30	GGIP: Structure and sequence-based GPCR-GPCR interaction pair predictor. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1224-1233.	2.6	13
31	Network-based characterization of drug-protein interaction signatures with a space-efficient approach. BMC Systems Biology, 2019, 13, 39.	3.0	13
32	A Distance-Based Boolean Applicability Domain for Classification of High Throughput Screening Data. Journal of Chemical Information and Modeling, 2019, 59, 463-476.	5.4	13
33	Network-based characterization of disease–disease relationships in terms of drugs and therapeutic targets. Bioinformatics, 2020, 36, i516-i524.	4.1	13
34	KampoDB, database of predicted targets and functional annotations of natural medicines. Scientific Reports, 2018, 8, 11216.	3.3	11
35	Scaffold-Retained Structure Generator to Exhaustively Create Molecules in an Arbitrary Chemical Space. Journal of Chemical Information and Modeling, 2022, 62, 2212-2225.	5.4	9
36	Cartesian Kernel: An Efficient Alternative to the Pairwise Kernel. IEICE Transactions on Information and Systems, 2010, E93-D, 2672-2679.	0.7	8

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37	Inferring Chemogenomic Features from Drugâ€Target Interaction Networks. Molecular Informatics, 2013, 32, 991-999.	2.5	8
38	Mining Discriminative Patterns from Graph Data with Multiple Labels and Its Application to Quantitative Structure–Activity Relationship (QSAR) Models. Journal of Chemical Information and Modeling, 2015, 55, 2519-2527.	5.4	8
39	Prediction of the Health Effects of Food Peptides and Elucidation of the Modeâ€ofâ€action Using Multiâ€ŧask Graph Convolutional Neural Network. Molecular Informatics, 2020, 39, e1900134.	2.5	8
40	TRIOMPHE: Transcriptome-Based Inference and Generation of Molecules with Desired Phenotypes by Machine Learning. Journal of Chemical Information and Modeling, 2021, 61, 4303-4320.	5.4	7
41	Epigenetic landscape of drug responses revealed through large-scale ChIP-seq data analyses. BMC Bioinformatics, 2022, 23, 51.	2.6	7
42	Chemoinformatics and structural bioinformatics in OCaml. Journal of Cheminformatics, 2019, 11, 10.	6.1	5
43	Omicsâ€based Identification of Glycan Structures as Biomarkers for a Variety of Diseases. Molecular Informatics, 2020, 39, 1900112.	2.5	5
44	MIBC myocardial scintigraphy in progressive supranuclear palsy. Journal of the Neurological Sciences, 2019, 396, 3-7.	0.6	4
45	Prediction of single-cell mechanisms for disease progression in hypertrophic remodelling by a trans-omics approach. Scientific Reports, 2021, 11, 8112.	3.3	4
46	TRANSDIRE: data-driven direct reprogramming by a pioneer factor-guided trans-omics approach. Bioinformatics, 2022, 38, 2839-2846.	4.1	4
47	Linear and Kernel Model Construction Methods for Predicting Drug–Target Interactions in a Chemogenomic Framework. Methods in Molecular Biology, 2018, 1825, 355-368.	0.9	3
48	A Web Server for GPCR-GPCR Interaction Pair Prediction. Frontiers in Endocrinology, 2022, 13, 825195.	3.5	3
49	From drug repositioning to target repositioning: prediction of therapeutic targets using genetically perturbed transcriptomic signatures. Bioinformatics, 2022, 38, i68-i76.	4.1	3
50	The Use of Large-Scale Chemically-Induced Transcriptome Data Acquired from LINCS to Study Small Molecules. Methods in Molecular Biology, 2019, 1888, 189-203.	0.9	2
51	Ranking Molecules with Vanishing Kernels and a Single Parameter: Active Applicability Domain <i>Included</i> . Journal of Chemical Information and Modeling, 2020, 60, 4376-4387.	5.4	2
52	Sparse Modeling to Analyze Drug–Target Interaction Networks. Methods in Molecular Biology, 2018, 1807, 181-193.	0.9	1
53	INTEGER PROGRAMMING-BASED METHOD FOR COMPLETING SIGNALING PATHWAYS AND ITS APPLICATION TO ANALYSIS OF COLORECTAL CANCER. , 2010, , .		0
54	Space-Efficient Feature Maps for String Alignment Kernels. Data Science and Engineering, 2020, 5, 168-179.	6.4	0