Takashi Ishida

List of Publications by Year
in descending order

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49 papers	2,461 citations	430874 18 h-index	265206 42 g-index
52 all docs	52 docs citations	52 times ranked	4137 citing authors

#	Article	IF	Citations
1	A Benchmark Dataset for Evaluating Practical Performance of Model Quality Assessment of Homology Models. Bioengineering, 2022, 9, 118.	3.5	1
2	Protein Model Quality Estimation Using Molecular Dynamics Simulation. ACS Omega, 2022, 7, 24274-24281.	3.5	0
3	Single-Step Retrosynthesis Prediction Based on the Identification of Potential Disconnection Sites Using Molecular Substructure Fingerprints. Journal of Chemical Information and Modeling, 2021, 61, 641-652.	5.4	11
4	P3CMQA: Single-Model Quality Assessment Using 3DCNN with Profile-Based Features. Bioengineering, 2021, 8, 40.	3.5	7
5	Taxonomic and Gene Category Analyses of Subgingival Plaques from a Group of Japanese Individuals with and without Periodontitis. International Journal of Molecular Sciences, 2021, 22, 5298.	4.1	3
6	Computer aided drug discovery review for infectious diseases with case study of anti-Chagas project. Parasitology International, 2021, 83, 102366.	1.3	3
7	End-to-end learning for compound activity prediction based on binding pocket information. BMC Bioinformatics, 2021, 22, 529.	2.6	0
8	Sequence alignment using machine learning for accurate template-based protein structure prediction. Bioinformatics, 2020, 36, 104-111.	4.1	13
9	Mathematical proof of the third order accuracy of the speedy double bootstrap method. Communications in Statistics - Theory and Methods, 2020, 49, 3950-3964.	1.0	0
10	Sequence alignment generation using intermediate sequence search for homology modeling. Computational and Structural Biotechnology Journal, 2020, 18, 2043-2050.	4.1	2
11	Protein model accuracy estimation based on local structure quality assessment using 3D convolutional neural network. PLoS ONE, 2019, 14, e0221347.	2.5	28
12	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	3.3	15
13	In Silico Prediction of Major Clearance Pathways of Drugs among 9 Routes with Two-Step Support Vector Machines. Pharmaceutical Research, 2018, 35, 197.	3.5	10
14	Stacking Multiple Molecular Fingerprints for Improving Ligand-Based Virtual Screening. Lecture Notes in Computer Science, 2018, , 279-288.	1.3	5
15	GHOSTX: A Fast Sequence Homology Search Tool for Functional Annotation of Metagenomic Data. Methods in Molecular Biology, 2017, 1611, 15-25.	0.9	8
16	Spresso: an ultrafast compound pre-screening method based on compound decomposition. Bioinformatics, 2017, 33, 3836-3843.	4.1	11
17	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. Scientific Reports, 2017, 7, 12038.	3.3	28
18	In silico, in vitro, X-ray crystallography, and integrated strategies for discovering spermidine synthase inhibitors for Chagas disease. Scientific Reports, 2017, 7, 6666.	3.3	21

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19	A Massively Parallel Sequence Similarity Search for Metagenomic Sequencing Data. International Journal of Molecular Sciences, 2017, 18, 2124.	4.1	4
20	GPU-Acceleration of Sequence Homology Searches with Database Subsequence Clustering. PLoS ONE, 2016, 11, e0157338.	2.5	8
21	Development of a Support Vector Machine-Based System to Predict Whether a Compound Is a Substrate of a Given Drug Transporter Using Its Chemical Structure. Journal of Pharmaceutical Sciences, 2016, 105, 2222-2230.	3.3	13
22	Reliable dn/dc Values of Cellulose, Chitin, and Cellulose Triacetate Dissolved in LiCl/N,N-Dimethylacetamide for Molecular Mass Analysis. Biomacromolecules, 2016, 17, 192-199.	5.4	43
23	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. Scientific Reports, 2015, 5, 17209.	3.3	33
24	Drug Clearance Pathway Prediction Based on Semi-supervised Learning. IPSJ Transactions on Bioinformatics, 2015, 8, 21-27.	0.2	0
25	Protein-protein docking on hardware accelerators: comparison of GPU and MIC architectures. BMC Systems Biology, 2015, 9, S6.	3.0	11
26	Faster sequence homology searches by clustering subsequences. Bioinformatics, 2015, 31, 1183-1190.	4.1	64
27	MEGADOCK 4.0: an ultraâ€“high-performance proteinâ€“protein docking software for heterogeneous supercomputers. Bioinformatics, 2014, 30, 3281-3283.	4.1	69
28	GHOSTX: An Improved Sequence Homology Search Algorithm Using a Query Suffix Array and a Database Suffix Array. PLoS ONE, 2014, 9, e103833.	2.5	76
29	Acceleration of sequence clustering using longest common subsequence filtering. BMC Bioinformatics, 2013, 14, S7.	2.6	9
30	MEGADOCK 3.0: a high-performance protein-protein interaction prediction software using hybrid parallel computing for petascale supercomputing environments. Source Code for Biology and Medicine, 2013, 8, 18.	1.7	22
31	Highly precise protein-protein interaction prediction based on consensus between template-based and de novo docking methods. BMC Proceedings, 2013, 7, S6.	1.6	37
32	Improvement of Protein-Protein Interaction Prediction by Integrating Template-Based and Template-Free Protein Docking. , 2013, , .		0
33	Assessing statistical reliability of phylogenetic trees via a speedy double bootstrap method. Molecular Phylogenetics and Evolution, 2013, 67, 429-435.	2.7	5
34	MEGADOCK: An All-to-All Protein-Protein Interaction Prediction System Using Tertiary Structure Data. Protein and Peptide Letters, 2013, 21, 766-778.	0.9	48
35	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	14.5	570
36	An Ultra-Fast Computing Pipeline for Metagenome Analysis with Next-Generation DNA Sequencers. , 2012, , .		1

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37	GHOSTM: A GPU-Accelerated Homology Search Tool for Metagenomics. PLoS ONE, 2012, 7, e36060.	2.5	22
38	Improvement of the Proteinâ€“Protein Docking Prediction by Introducing a Simple Hydrophobic Interaction Model: An Application to Interaction Pathway Analysis. Lecture Notes in Computer Science, 2012, , 178-187.	1.3	10
39	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
40	A Combined Approach for de novo DNA Sequence Assembly of Very Short Reads. IPSJ Transactions on Bioinformatics, 2011, 4, 21-33.	0.2	2
41	Absolute quality evaluation of protein model structures using statistical potentials with respect to the native and reference states. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1550-1563.	2.6	2
42	PiSite: a database of protein interaction sites using multiple binding states in the PDB. Nucleic Acids Research, 2009, 37, D360-D364.	14.5	47
43	Analyses on hydrophobicity and attractiveness of allâ€atom distanceâ€dependent potentials. Protein Science, 2009, 18, 1906-1915.	7.6	3
44	Identification of transient hub proteins and the possible structural basis for their multiple interactions. Protein Science, 2008, 17, 72-78.	7.6	63
45	Prediction of disordered regions in proteins based on the meta approach. Bioinformatics, 2008, 24, 1344-1348.	4.1	229
46	PrDOS: prediction of disordered protein regions from amino acid sequence. Nucleic Acids Research, 2007, 35, W460-W464.	14.5	733
47	Potential for assessing quality of protein structure based on contact number prediction. Proteins: Structure, Function and Bioinformatics, 2006, 64, 940-947.	2.6	13
48	Aggregation mechanism of polyglutamine diseases revealed using quantum chemical calculations, fragment molecular orbital calculations, molecular dynamics simulations, and binding free energy calculations. Computational and Theoretical Chemistry, 2006, 778, 85-95.	1.5	9
49	Development of an ab initio protein structure prediction system ABLE. Genome Informatics, 2003, 14, 228-37.	0.4	7