Takashi Ishida

List of Publications by Year
in descending order

49	2,461	430874	265206
papers	citations	18	42
		h-index	g-index

52	52	52	4137
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PrDOS: prediction of disordered protein regions from amino acid sequence. Nucleic Acids Research, 2007, 35, W460-W464.	14.5	733
2	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	14.5	570
3	Prediction of disordered regions in proteins based on the meta approach. Bioinformatics, 2008, 24, 1344-1348.	4.1	229
4	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
5	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
6	MEGADOCK 4.0: an ultra–high-performance protein–protein docking software for heterogeneous supercomputers. Bioinformatics, 2014, 30, 3281-3283.	4.1	69
7	Faster sequence homology searches by clustering subsequences. Bioinformatics, 2015, 31, 1183-1190.	4.1	64
8	Identification of transient hub proteins and the possible structural basis for their multiple interactions. Protein Science, 2008, 17, 72-78.	7.6	63
9	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
10	PiSite: a database of protein interaction sites using multiple binding states in the PDB. Nucleic Acids Research, 2009, 37, D360-D364.	14.5	47
11	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
12	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
13	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. Scientific Reports, 2015, 5, 17209.	3.3	33
14	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
15	Protein model accuracy estimation based on local structure quality assessment using 3D convolutional neural network. PLoS ONE, 2019, 14, e0221347.	2.5	28
16	GHOSTM: A GPU-Accelerated Homology Search Tool for Metagenomics. PLoS ONE, 2012, 7, e36060.	2.5	22
17	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
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

#	Article	IF	Citations
19	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	3.3	15
20	Potential for assessing quality of protein structure based on contact number prediction. Proteins: Structure, Function and Bioinformatics, 2006, 64, 940-947.	2.6	13
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	Sequence alignment using machine learning for accurate template-based protein structure prediction. Bioinformatics, 2020, 36, 104-111.	4.1	13
23	Protein-protein docking on hardware accelerators: comparison of GPU and MIC architectures. BMC Systems Biology, 2015, 9, S6.	3.0	11
24	Spresso: an ultrafast compound pre-screening method based on compound decomposition. Bioinformatics, 2017, 33, 3836-3843.	4.1	11
25	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
26	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
27	Improvement of the Protein–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
28	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
29	Acceleration of sequence clustering using longest common subsequence filtering. BMC Bioinformatics, 2013, 14, S7.	2.6	9
30	GPU-Acceleration of Sequence Homology Searches with Database Subsequence Clustering. PLoS ONE, 2016, 11, e0157338.	2.5	8
31	GHOSTX: A Fast Sequence Homology Search Tool for Functional Annotation of Metagenomic Data. Methods in Molecular Biology, 2017, 1611, 15-25.	0.9	8
32	P3CMQA: Single-Model Quality Assessment Using 3DCNN with Profile-Based Features. Bioengineering, 2021, 8, 40.	3.5	7
33	Development of an ab initio protein structure prediction system ABLE. Genome Informatics, 2003, 14, 228-37.	0.4	7
34	Assessing statistical reliability of phylogenetic trees via a speedy double bootstrap method. Molecular Phylogenetics and Evolution, 2013, 67, 429-435.	2.7	5
35	Stacking Multiple Molecular Fingerprints for Improving Ligand-Based Virtual Screening. Lecture Notes in Computer Science, 2018, , 279-288.	1.3	5
36	A Massively Parallel Sequence Similarity Search for Metagenomic Sequencing Data. International Journal of Molecular Sciences, 2017, 18, 2124.	4.1	4

#	ARTICLE	IF	CITATIONS
37	Analyses on hydrophobicity and attractiveness of all‑atom distance‑dependent potentials. Protein Science, 2009, 18, 1906-1915.	7.6	3
38	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
39	Computer aided drug discovery review for infectious diseases with case study of anti-Chagas project. Parasitology International, 2021, 83, 102366.	1.3	3
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	Sequence alignment generation using intermediate sequence search for homology modeling. Computational and Structural Biotechnology Journal, 2020, 18, 2043-2050.	4.1	2
43	An Ultra-Fast Computing Pipeline for Metagenome Analysis with Next-Generation DNA Sequencers. , 2012, , .		1
44	A Benchmark Dataset for Evaluating Practical Performance of Model Quality Assessment of Homology Models. Bioengineering, 2022, 9, 118.	3.5	1
45	Improvement of Protein-Protein Interaction Prediction by Integrating Template-Based and Template-Free Protein Docking. , 2013, , .		0
46	Drug Clearance Pathway Prediction Based on Semi-supervised Learning. IPSJ Transactions on Bioinformatics, 2015, 8, 21-27.	0.2	0
47	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
48	End-to-end learning for compound activity prediction based on binding pocket information. BMC Bioinformatics, 2021, 22, 529.	2.6	0
49	Protein Model Quality Estimation Using Molecular Dynamics Simulation. ACS Omega, 2022, 7, 24274-24281.	3.5	0