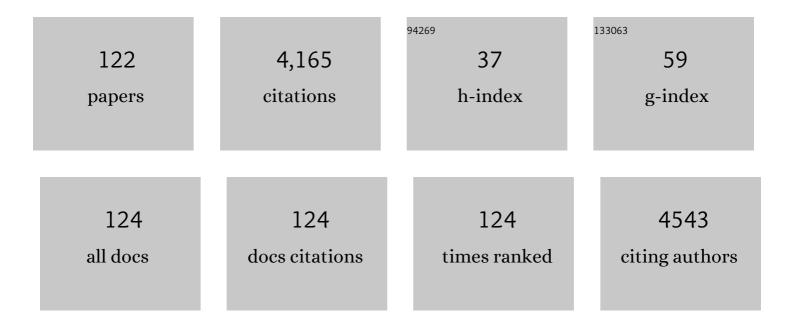
## Shinn-Ying Ho

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3306237/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Tracking the amino acid changes of spike proteins across diverse host species of severe acute respiratory syndrome coronavirus 2. IScience, 2022, 25, 103560.	1.9	5
2	MicroRNA signature for estimating the survival time in patients with bladder urothelial carcinoma. Scientific Reports, 2022, 12, 4141.	1.6	10
3	SPIKES: Identification of physicochemical properties of spike proteins across diverse host species of SARS-CoV-2. STAR Protocols, 2022, 3, 101460.	0.5	1
4	Identification and Characterization of Species-Specific Severe Acute Respiratory Syndrome Coronavirus 2 Physicochemical Properties. Journal of Proteome Research, 2021, 20, 2942-2952.	1.8	4
5	Identification of the miRNA signature associated with survival in patients with ovarian cancer. Aging, 2021, 13, 12660-12690.	1.4	13
6	Predicting the Risk Genes of Autism Spectrum Disorders. Frontiers in Genetics, 2021, 12, 665469.	1.1	8
7	Evolutionary Learning-Derived Clinical-Radiomic Models for Predicting Early Recurrence of Hepatocellular Carcinoma after Resection. Liver Cancer, 2021, 10, 572-582.	4.2	21
8	Endoscopic Images by a Single-Shot Multibox Detector for the Identification of Early Cancerous Lesions in the Esophagus: A Pilot Study. Cancers, 2021, 13, 321.	1.7	29
9	Brachytherapy Approach Using 177Lu Conjugated Gold Nanostars and Evaluation of Biodistribution, Tumor Retention, Dosimetry and Therapeutic Efficacy in Head and Neck Tumor Model. Pharmaceutics, 2021, 13, 1903.	2.0	6
10	Clinical treatment and medication in decreasing the development of major depression caused by spinal fracture. Journal of International Medical Research, 2020, 48, 030006052097288.	0.4	0
11	Novel miRNA signature for predicting the stage of hepatocellular carcinoma. Scientific Reports, 2020, 10, 14452.	1.6	40
12	GREMA: modelling of emulated gene regulatory networks with confidence levels based on evolutionary intelligence to cope with the underdetermined problem. Bioinformatics, 2020, 36, 3833-3840.	1.8	15
13	Heterophilic antibodies influence immunometric assay: a case report and reviews. Immunologic Research, 2020, 68, 104-106.	1.3	2
14	Landscape of Mitochondria Genome and Clinical Outcomes in Stage 1 Lung Adenocarcinoma. Cancers, 2020, 12, 755.	1.7	11
15	Enterotype-based Analysis of Gut Microbiota along the Conventional Adenoma-Carcinoma Colorectal Cancer Pathway. Scientific Reports, 2019, 9, 10923.	1.6	46
16	Identification and characterization of the IncRNA signature associated with overall survival in patients with neuroblastoma. Scientific Reports, 2019, 9, 5125.	1.6	24
17	The Impact of Emergency Interventions and Patient Characteristics on the Risk of Heart Failure in Patients with Nontraumatic OHCA. Emergency Medicine International, 2019, 2019, 1-10.	0.3	7
18	PredCRP: predicting and analysing the regulatory roles of CRP from its binding sites in Escherichia coli. Scientific Reports, 2018, 8, 951.	1.6	41

#	Article	IF	CITATIONS
19	Recognition-based character segmentation for multi-level writing style. International Journal on Document Analysis and Recognition, 2018, 21, 21-39.	2.7	7
20	Prediction of Metastasis in Head and Neck Cancer from Computed Tomography Images. , 2018, , .		3
21	Identifying a miRNA signature for predicting the stage of breast cancer. Scientific Reports, 2018, 8, 16138.	1.6	92
22	High-risk, Expression-Based Prognostic Long Noncoding RNA Signature in Neuroblastoma. JNCI Cancer Spectrum, 2018, 2, pky015.	1.4	17
23	ESA-UbiSite: accurate prediction of human ubiquitination sites by identifying a set of effective negatives. Bioinformatics, 2017, 33, 661-668.	1.8	37
24	Tourette Syndrome as an Independent Risk Factor for Subsequent Sleep Disorders in Children: A Nationwide Population-Based Case–Control Study. Sleep, 2017, 40, .	0.6	31
25	Recognition of handwritten Lanna Dhamma characters using a set of optimally designed moment features. International Journal on Document Analysis and Recognition, 2017, 20, 259-274.	2.7	7
26	Identifying the miRNA signature associated with survival time in patients with lung adenocarcinoma using miRNA expression profiles. Scientific Reports, 2017, 7, 7507.	1.6	60
27	Increased risks of tic disorders in children with epilepsy: A nation-wide population-based case–control study in Taiwan. Research in Developmental Disabilities, 2016, 51-52, 173-180.	1.2	9
28	A hydrophobic spine stabilizes a surface-exposed α-helix according to analysis of the solvent-accessible surface area. BMC Bioinformatics, 2016, 17, 503.	1.2	6
29	SCMBYK: prediction and characterization of bacterial tyrosine-kinases based on propensity scores of dipeptides. BMC Bioinformatics, 2016, 17, 514.	1.2	10
30	Estimating survival time of patients with glioblastoma multiforme and characterization of the identified microRNA signatures. BMC Genomics, 2016, 17, 1022.	1.2	36
31	Increased risk of epilepsy in children with Tourette syndrome: A population-based case-control study. Research in Developmental Disabilities, 2016, 51-52, 181-187.	1.2	11
32	Co-expression analysis identifies long noncoding RNA <i>SNHG1</i> as a novel predictor for event-free survival in neuroblastoma. Oncotarget, 2016, 7, 58022-58037.	0.8	59
33	SCMMTP: identifying and characterizing membrane transport proteins using propensity scores of dipeptides. BMC Genomics, 2015, 16, S6.	1.2	22
34	Prediction of linear B-cell epitopes of hepatitis C virus for vaccine development. BMC Medical Genomics, 2015, 8, S3.	0.7	9
35	Increased risk of glomerulonephritis and chronic kidneyÂdisease in relation to the severity of psoriasis, concomitant medication, and comorbidity: a nationwide population-based cohort study. British Journal of Dermatology, 2015, 173, 146-154.	1.4	87
36	Association between Gastroenterological Malignancy and Diabetes Mellitus and Anti-Diabetic Therapy: A Nationwide, Population-Based Cohort Study. PLoS ONE, 2015, 10, e0125421.	1.1	40

#	Article	IF	CITATIONS
37	Increased Risk of Chronic Kidney Disease in Rheumatoid Arthritis Associated with Cardiovascular Complications $\hat{a} \in A$ National Population-Based Cohort Study. PLoS ONE, 2015, 10, e0136508.	1.1	83
38	Predicting Neuroinflammation in Morphine Tolerance for Tolerance Therapy from Immunostaining Images of Rat Spinal Cord. PLoS ONE, 2015, 10, e0139806.	1.1	7
39	Angiotensin Receptor Blockers Decrease the Risk of Major Adverse Cardiovascular Events in Patients with End-Stage Renal Disease on Maintenance Dialysis: A Nationwide Matched-Cohort Study. PLoS ONE, 2015, 10, e0140633.	1.1	16
40	Is Zolpidem Associated with Increased Risk of Fractures in the Elderly with Sleep Disorders? A Nationwide Case Cross-Over Study in Taiwan. PLoS ONE, 2015, 10, e0146030.	1.1	26
41	GeNOSA: inferring and experimentally supporting quantitative gene regulatory networks in prokaryotes. Bioinformatics, 2015, 31, 2151-2158.	1.8	10
42	Characterizing informative sequence descriptors and predicting binding affinities of heterodimeric protein complexes. BMC Bioinformatics, 2015, 16, S14.	1.2	15
43	Is schizophrenia associated with an increased risk of chronic kidney disease? A nationwide matched-cohort study. BMJ Open, 2015, 5, e006777-e006777.	0.8	40
44	SCMPSP: Prediction and characterization of photosynthetic proteins based on a scoring card method. BMC Bioinformatics, 2015, 16, S8.	1.2	19
45	Discovery of prognostic biomarkers for predicting lung cancer metastasis using microarray and survival data. BMC Bioinformatics, 2015, 16, 54.	1.2	21
46	Increased Risk of Major Depression in the Three Years following a Femoral Neck Fracture–A National Population-Based Follow-Up Study. PLoS ONE, 2014, 9, e89867.	1.1	55
47	Rule-Based Knowledge Acquisition Method for Promoter Prediction in Human andDrosophilaSpecies. Scientific World Journal, The, 2014, 2014, 1-14.	0.8	2
48	Statistical analysis and classification of EEG-based attention network task using optimized feature selection. , 2014, , .		0
49	Increased risk of major depression subsequent to a first-attack and non-infection caused urticaria in adolescence: a nationwide population-based study. BMC Pediatrics, 2014, 14, 181.	0.7	13
50	Bronchial asthma is associated with increased risk of chronic kidney disease. BMC Pulmonary Medicine, 2014, 14, 80.	0.8	42
51	SCMHBP: prediction and analysis of heme binding proteins using propensity scores of dipeptides. BMC Bioinformatics, 2014, 15, S4.	1.2	26
52	HCS-Neurons: identifying phenotypic changes in multi-neuron images upon drug treatments of high-content screening. BMC Bioinformatics, 2013, 14, S12.	1.2	16
53	Predicting protein crystallization using a simple scoring card method. , 2013, , .		3
54	Designing predictors of halophilic and non-halophilic proteins using support vector machines. , 2013, ,		1

#	Article	IF	CITATIONS
55	EEG-based motion sickness classification system with genetic feature selection. , 2013, , .		14
56	Identification and Analysis of Single- and Multiple-Region Mitotic Protein Complexes by Grouping Gene Ontology Terms. Applied Mechanics and Materials, 2013, 421, 277-285.	0.2	0
57	Predicting and Analyzing Lipid-Binding Proteins Using an Efficient Physicochemical Property Mining Method. Applied Mechanics and Materials, 2013, 421, 313-318.	0.2	1
58	Prediction and Analysis of Antibody Amyloidogenesis from Sequences. PLoS ONE, 2013, 8, e53235.	1.1	23
59	SCMCRYS: Predicting Protein Crystallization Using an Ensemble Scoring Card Method with Estimating Propensity Scores of P-Collocated Amino Acid Pairs. PLoS ONE, 2013, 8, e72368.	1.1	74
60	FRKAS: Knowledge Acquisition Using a Fuzzy Rule Base Approach to Insight of DNA-Binding Domains/Proteins. Protein and Peptide Letters, 2013, 20, 299-308.	0.4	0
61	An Efficient Sampling Method for Television Ratings and its Application to Taiwan Cable TV Channels. Journal of Applied Sciences, 2013, 13, 2602-2605.	0.1	Ο
62	Motion sickness estimation system. , 2012, , .		9
63	Prediction and analysis of protein solubility using a novel scoring card method with dipeptide composition. BMC Bioinformatics, 2012, 13, S3.	1.2	52
64	Protein-Protein Interaction Site Predictions with Three-Dimensional Probability Distributions of Interacting Atoms on Protein Surfaces. PLoS ONE, 2012, 7, e37706.	1.1	25
65	Predicting non-classical secretory proteins by using Gene Ontology terms and physicochemical properties. , 2011, , .		0
66	NeurphologyJ: An automatic neuronal morphology quantification method and its application in pharmacological discovery. BMC Bioinformatics, 2011, 12, 230.	1.2	113
67	POPISK: T-cell reactivity prediction using support vector machines and string kernels. BMC Bioinformatics, 2011, 12, 446.	1.2	79
68	Predicting and analyzing DNA-binding domains using a systematic approach to identifying a set of informative physicochemical and biochemical properties. BMC Bioinformatics, 2011, 12, S47.	1.2	42
69	Prediction of non-classical secreted proteins using informative physicochemical properties. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 263-270.	2.2	10
70	Improving protein secondary structure prediction based on short subsequences with local structure similarity. BMC Genomics, 2010, 11, S4.	1.2	29
71	sRNAMap: genomic maps for small non-coding RNAs, their regulators and their targets in microbial genomes. Nucleic Acids Research, 2009, 37, D150-D154.	6.5	81
72	Protein subcellular localization prediction of eukaryotes using a knowledge-based approach. BMC Bioinformatics, 2009, 10, S8.	1.2	35

#	Article	IF	CITATIONS
73	Predicting protein subnuclear localization using GO-amino-acid composition features. BioSystems, 2009, 98, 73-79.	0.9	34
74	Computational identification of ubiquitylation sites from protein sequences. BMC Bioinformatics, 2008, 9, 310.	1.2	163
75	ProLoc-GO: Utilizing informative Gene Ontology terms for sequence-based prediction of protein subcellular localization. BMC Bioinformatics, 2008, 9, 80.	1.2	101
76	A Novel Intelligent Multiobjective Simulated Annealing Algorithm for Designing Robust PID Controllers. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2008, 38, 319-330.	3.4	45
77	OPSO: Orthogonal Particle Swarm Optimization and Its Application to Task Assignment Problems. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2008, 38, 288-298.	3.4	183
78	ProLoc-rGO: Using rule-based knowledge with Gene Ontology terms for prediction of protein subnuclear localization. , 2008, , .		2
79	POPI: predicting immunogenicity of MHC class I binding peptides by mining informative physicochemical properties. Bioinformatics, 2007, 23, 942-949.	1.8	96
80	Boosting Evolutionary Support Vector Machine for Designing Tumor Classifiers from Microarray Data. , 2007, , .		0
81	An Intelligent Two-Stage Evolutionary Algorithm for Dynamic Pathway Identification From Gene Expression Profiles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 648-704.	1.9	50
82	SODOCK: Swarm optimization for highly flexible protein–ligand docking. Journal of Computational Chemistry, 2007, 28, 612-623.	1.5	120
83	Selecting a minimal number of relevant genes from microarray data to design accurate tissue classifiers. BioSystems, 2007, 90, 78-86.	0.9	31
84	Design of accurate predictors for DNA-binding sites in proteins using hybrid SVM–PSSM method. BioSystems, 2007, 90, 234-241.	0.9	43
85	ProLoc: Prediction of protein subnuclear localization using SVM with automatic selection from physicochemical composition features. BioSystems, 2007, 90, 573-581.	0.9	64
86	Prediction of protein mutant stability using classification and regression tool. Biophysical Chemistry, 2007, 125, 462-470.	1.5	28
87	Accurate prediction of enzyme subfamily class using an adaptive fuzzy k-nearest neighbor method. BioSystems, 2007, 90, 405-413.	0.9	48
88	iPTREE-STAB: interpretable decision tree based method for predicting protein stability changes upon mutations. Bioinformatics, 2007, 23, 1292-1293.	1.8	145
89	Sequence analysis and rule development of predicting protein stability change upon mutation using decision tree model. Journal of Molecular Modeling, 2007, 13, 879-890.	0.8	29
90	Interpretable gene expression classifier with an accurate and compact fuzzy rule base for microarray data analysis. BioSystems, 2006, 85, 165-176.	0.9	48

#	Article	IF	CITATIONS
91	Knowledge acquisition and development of accurate rules for predicting protein stability changes. Computational Biology and Chemistry, 2006, 30, 408-415.	1.1	18
92	Optimizing fuzzy neural networks for tuning PID controllers using an orthogonal simulated annealing algorithm OSA. IEEE Transactions on Fuzzy Systems, 2006, 14, 421-434.	6.5	63
93	Design of nearest neighbor classifiers: multi-objective approach. International Journal of Approximate Reasoning, 2005, 40, 3-22.	1.9	32
94	A novel approach to production planning of flexible manufacturing systems using an efficient multi-objective genetic algorithm. International Journal of Machine Tools and Manufacture, 2005, 45, 949-957.	6.2	58
95	Accurate estimation of surface roughness from texture features of the surface image using an adaptive neuro-fuzzy inference system. Precision Engineering, 2005, 29, 95-100.	1.8	65
96	Designing structure-specified mixed H/sub 2//H/sub /spl infin// optimal controllers using an intelligent genetic algorithm IGA. IEEE Transactions on Control Systems Technology, 2005, 13, 1119-1124.	3.2	38
97	A Novel Orthogonal Simulated Annealing Algorithm for Optimization of Electromagnetic Problems. IEEE Transactions on Magnetics, 2004, 40, 1791-1795.	1.2	14
98	An orthogonal simulated annealing algorithm for large floorplanning problems. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2004, 12, 874-877.	2.1	30
99	Intelligent Evolutionary Algorithms for Large Parameter Optimization Problems. IEEE Transactions on Evolutionary Computation, 2004, 8, 522-541.	7.5	219
100	OSA: Orthogonal Simulated Annealing Algorithm and Its Application to Designing Mixed <tex>\$rm H_2 /rm H_infty\$</tex> Optimal Controllers. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2004, 34, 588-600.	3.4	50
101	Inheritable Genetic Algorithm for Biobjective 0/1 Combinatorial Optimization Problems and its Applications. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 609-620.	5.5	72
102	Design of Accurate Classifiers With a Compact Fuzzy-Rule Base Using an Evolutionary Scatter Partition of Feature Space. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 1031-1044.	5.5	61
103	Design and Analysis of an Efficient Evolutionary Image Segmentation Algorithm. Journal of Signal Processing Systems, 2003, 35, 29-42.	1.0	18
104	Mesh optimization for surface approximation using an efficient coarse-to-fine evolutionary algorithm. Pattern Recognition, 2003, 36, 1065-1081.	5.1	17
105	Genetic algorithm with intelligent crossover for colour quantization. Imaging Science Journal, 2003, 51, 151-162.	0.2	1
106	Design of an optimal nearest neighbor classifier using an intelligent genetic algorithm. Pattern Recognition Letters, 2002, 23, 1495-1503.	2.6	70
107	Accurate modeling and prediction of surface roughness by computer vision in turning operations using an adaptive neuro-fuzzy inference system. International Journal of Machine Tools and Manufacture, 2002, 42, 1441-1446.	6.2	111
108	Facial modeling from an uncalibrated face image using a coarse-to-fine genetic algorithm. Pattern Recognition, 2001, 34, 1015-1031.	5.1	28

#	Article	IF	CITATIONS
109	An efficient evolutionary algorithm for accurate polygonal approximation. Pattern Recognition, 2001, 34, 2305-2317.	5.1	59
110	A GA-based systematic reasoning approach for solving traveling salesman problems using an orthogonal array crossover. , 2000, , .		2
111	Efficient image segmentation using a generic and non-parametric approach. , 2000, , .		Ο
112	An analytic solution for the pose determination of human faces from a monocular image. Pattern Recognition Letters, 1998, 19, 1045-1054.	2.6	29
113	Measuring 3-D location and shape parameters of cylinders by a spatial encoding technique. IEEE Transactions on Automation Science and Engineering, 1994, 10, 632-647.	2.4	9
114	Incremental model building of polyhedral objects using structured light. Pattern Recognition, 1993, 26, 33-46.	5.1	10
115	An effective search approach to camera parameter estimation using an arbitrary planar calibration object. Pattern Recognition, 1993, 26, 655-666.	5.1	3
116	Computer vision for robust 3D aircraft recognition with fast library search. Pattern Recognition, 1991, 24, 375-390.	5.1	33
117	Designing an efficient fuzzy classifier using an intelligent genetic algorithm. , 0, , .		3
118	Mesh optimization for surface approximation using an efficient coarse-to-fine evolutionary algorithm. , 0, , .		3
119	Design of high performance fuzzy controllers using flexible parameterized membership functions and intelligent genetic algorithms. , 0, , .		1
120	Flexible protein-ligand docking using particle swarm optimization. , 0, , .		1
121	Predicting Television Ratings and Its Application to Taiwan Cable TV Channels. , 0, , .		0
122	Design of an optimal nearest neighbor classifier using an intelligent genetic algorithm. , 0, , .		4