Jinn-Moon Yang

List of Publications by Year in Descending Order

132 papers	3,220 citations	28 h-index	53 g-index
153 ext. papers	3,755 ext. citations	5.8 avg, IF	5.19 L-index

#	Paper	IF	Citations
132	CoMI: consensus mutual information for tissue-specific gene signatures.. *BMC Bioinformatics*, **2022**, 22, 624	3.6	
131	Discovery of moiety preference by Shapley value in protein kinase family using random forest models.. *BMC Bioinformatics*, **2022**, 23, 130	3.6	
130	Furin and TMPRSS2 Resistant Spike Induces Robust Humoral and Cellular Immunity Against SARS-CoV-2 Lethal Infection.. *Frontiers in Immunology*, **2022**, 13, 872047	8.4	0
129	Convolutional neural network for human cancer types prediction by integrating protein interaction networks and omics data. *Scientific Reports*, **2021**, 11, 20691	4.9	3
128	A Nanodiamond-Based Surface Topography Downregulates the MicroRNA miR6236 to Enhance Neuronal Development and Regeneration. *ACS Applied Bio Materials*, **2021**, 4, 890-902	4.1	1
127	Uncovering Flexible Active Site Conformations of SARS-CoV-2 3CL Proteases through Protease Pharmacophore Clusters and COVID-19 Drug Repurposing. *ACS Nano*, **2021**, 15, 857-872	16.7	24
126	Loss of Fis1 impairs proteostasis during skeletal muscle aging in Drosophila. *Aging Cell*, **2021**, 20, e13379	9.9	1
125	The inhibitory effects of PGG and EGCG against the SARS-CoV-2 3C-like protease. *Biochemical and Biophysical Research Communications*, **2021**, 591, 130-130	3.4	21
124	Repurposing existing drugs: identification of SARS-CoV-2 3C-like protease inhibitors. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **2021**, 36, 147-153	5.6	14
123	An integrated systematic approach for investigating microcurrent electrical nerve stimulation (MENS) efficacy in STZ-induced diabetes mellitus. *Life Sciences*, **2021**, 279, 119650	6.8	0
122	Pharmacophore anchor models of ATAT1 to discover potential inhibitors and lead optimization. *Computational Biology and Chemistry*, **2021**, 93, 107513	3.6	
121	Ugonin J Acts as a SARS-CoV-2 3C-like Protease Inhibitor and Exhibits Anti-inflammatory Properties. *Frontiers in Pharmacology*, **2021**, 12, 720018	5.6	1
120	Zika Virus NS3 Protease Pharmacophore Anchor Model and Drug Discovery. *Scientific Reports*, **2020**, 10, 8929	4.9	8
119	An Integrated Genomic Strategy to Identify CHRNB4 as a Diagnostic/Prognostic Biomarker for Targeted Therapy in Head and Neck Cancer. *Cancers*, **2020**, 12,	6.6	1
118	A site-moiety map and virtual screening approach for discovery of novel 5-LOX inhibitors. *Scientific Reports*, **2020**, 10, 10510	4.9	4
117	Target Identification Using Homopharma and Network-Based Methods for Predicting Compounds Against Dengue Virus-Infected Cells. *Molecules*, **2020**, 25,	4.8	2
116	Alternative splicing in human cancer cells is modulated by the amiloride derivative 3,5-diamino-6-chloro-N-(N-(2,6-dichlorobenzoyl)carbamimidoyl)pyrazine-2-carboxide. *Molecular Oncology*, **2019**, 13, 1744-1762	7.9	3

115	Identification of the PCA29 gene signature as a predictor in prostate cancer. *Journal of Bioinformatics and Computational Biology*, **2019**, 17, 1940006	1	1
114	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. *Journal of Bioinformatics and Computational Biology*, **2019**, 17, 1940005	1	6
113	Membrane protein-regulated networks across human cancers. *Nature Communications*, **2019**, 10, 3131	17.4	26
112	Omics-based Investigation of Diet-induced Obesity Synergized with HBx, Src, and p53 Mutation Accelerating Hepatocarcinogenesis in Zebrafish Model. *Cancers*, **2019**, 11,	6.6	13
111	Boolean function network analysis of time course liver transcriptome data to reveal novel circadian transcriptional regulators in mammals. *Journal of the Chinese Medical Association*, **2019**, 82, 872-880	2.8	1
110	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. *BMC Systems Biology*, **2018**, 12, 13	3.5	1
109	CRISPR/Cas9 Genome Editing of Epidermal Growth Factor Receptor Sufficiently Abolished Oncogenicity in Anaplastic Thyroid Cancer. *Disease Markers*, **2018**, 2018, 3835783	3.2	13
108	Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes **2018**,		1
107	An integrated approach with new strategies for QSAR models and lead optimization. *BMC Genomics* , **2017**, 18, 104	4.5	4
106	Identification of neuraminidase inhibitors against dual H274Y/I222R mutant strains. *Scientific Reports*, **2017**, 7, 12336	4.9	10
105	Clinical assessment of diode laser-assisted endoscopic intrasphenoidal vidian neurectomy in the treatment of refractory rhinitis. *Lasers in Medical Science*, **2017**, 32, 2097-2104	3.1	3
104	Pharmacophore anchor models of flaviviral NS3 proteases lead to drug repurposing for DENV infection. *BMC Bioinformatics*, **2017**, 18, 548	3.6	9
103	Vascular anatomy is a determining factor of successful submental flap raising: a retrospective study of 70 clinical cases. *PeerJ*, **2017**, 5, e3606	3.1	2
102	Novel Class IIa-Selective Histone Deacetylase Inhibitors Discovered Using an in Silico Virtual Screening Approach. *Scientific Reports*, **2017**, 7, 3228	4.9	26
101	Clinical application of suction-tube-assisted septal submucosal dissection for endoscopic septoplasty. *European Archives of Oto-Rhino-Laryngology*, **2017**, 274, 1471-1475	3.5	1
100	Nicotinic Acetylcholine Receptor Subtype Alpha-9 Mediates Triple-Negative Breast Cancers Based on a Spontaneous Pulmonary Metastasis Mouse Model. *Frontiers in Cellular Neuroscience*, **2017**, 11, 336	6.1	14
99	Identification of Inhibitors for the DEDDh Family of Exonucleases and a Unique Inhibition Mechanism by Crystal Structure Analysis of CRN-4 Bound with 2-Morpholin-4-ylethanesulfonate (MES). *Journal of Medicinal Chemistry*, **2016**, 59, 8019-29	8.3	11
98	Evaluating Instantaneous Perfusion Responses of Parotid Glands to Gustatory Stimulation Using High-Temporal-Resolution Echo-Planar Diffusion-Weighted Imaging. *American Journal of Neuroradiology*, **2016**, 37, 1909-1915	4.4	4

97	Novel Lactulose and Melibiose Targeting Autophagy to Reduce PolyQ Aggregation in Cell Models of Spinocerebellar Ataxia 3. *CNS and Neurological Disorders - Drug Targets*, **2016**, 15, 351-9	2.6	18
96	Design and synthesis of 1,2,3-triazole-containing N-acyl zanamivir analogs as potent neuraminidase inhibitors. *European Journal of Medicinal Chemistry*, **2016**, 123, 397-406	6.8	23
95	Management of different kinds of head and neck defects with the submental flap for reconstruction. *European Archives of Oto-Rhino-Laryngology*, **2015**, 272, 3815-9	3.5	7
94	Anchor-based classification and type-C inhibitors for tyrosine kinases. *Scientific Reports*, **2015**, 5, 10938	4.9	9
93	The potential of lactulose and melibiose, two novel trehalase-indigestible and autophagy-inducing disaccharides, for polyQ-mediated neurodegenerative disease treatment. *NeuroToxicology*, **2015**, 48, 120-30	4.4	14
92	Module organization and variance in protein-protein interaction networks. *Scientific Reports*, **2015**, 5, 9386	4.9	25
91	Diode laser assisted minimal invasive sphenoidotomy for endoscopic transphenoidal pituitary surgery: our technique and results. *Lasers in Surgery and Medicine*, **2015**, 47, 239-42	3.6	1
90	Reconstructing genome-wide protein-protein interaction networks using multiple strategies with homologous mapping. *PLoS ONE*, **2015**, 10, e0116347	3.7	6
89	DNA mimic proteins: functions, structures, and bioinformatic analysis. *Biochemistry*, **2014**, 53, 2865-74	3.2	32
88	KDM4B as a target for prostate cancer: structural analysis and selective inhibition by a novel inhibitor. *Journal of Medicinal Chemistry*, **2014**, 57, 5975-85	8.3	68
87	Crowning proteins: modulating the protein surface properties using crown ethers. *Angewandte Chemie - International Edition*, **2014**, 53, 13054-8	16.4	41
86	Homopharma: a new concept for exploring the molecular binding mechanisms and drug repurposing. *BMC Genomics*, **2014**, 15 Suppl 9, S8	4.5	6
85	5-Demethyltangeretin is more potent than tangeretin in inhibiting dimethylbenz(a)anthracene (DMBA)/12-O-tetradecanoylphorbol-13-acetate (TPA)-induced skin tumorigenesis. *Journal of Functional Foods*, **2014**, 11, 528-537	5.1	14
84	Staphylococcus aureus protein SAUGI acts as a uracil-DNA glycosylase inhibitor. *Nucleic Acids Research*, **2014**, 42, 1354-64	20.1	29
83	Total synthetic protoapigenone WYC02 inhibits cervical cancer cell proliferation and tumour growth through PIK3 signalling pathway. *Basic and Clinical Pharmacology and Toxicology*, **2013**, 113, 8-18	3.1	9
82	Inferring homologous protein-protein interactions through pair position specific scoring matrix. *BMC Bioinformatics*, **2013**, 14 Suppl 2, S11	3.6	4
81	Moiety-linkage map reveals selective nonbisphosphonate inhibitors of human geranylgeranyl diphosphate synthase. *Journal of Chemical Information and Modeling*, **2013**, 53, 2299-311	6.1	6
80	Genome-wide structural modelling of TCR-pMHC interactions. *BMC Genomics*, **2013**, 14 Suppl 5, S5	4.5	6

79	Synthesis of acylguanidine zanamivir derivatives as neuraminidase inhibitors and the evaluation of their bio-activities. *Organic and Biomolecular Chemistry*, **2013**, 11, 3943-8	3.9	28
78	KIDFamMap: a database of kinase-inhibitor-disease family maps for kinase inhibitor selectivity and binding mechanisms. *Nucleic Acids Research*, **2013**, 41, D430-40	20.1	21
77	Pathway-based screening strategy for multitarget inhibitors of diverse proteins in metabolic pathways. *PLoS Computational Biology*, **2013**, 9, e1003127	5	17
76	Template-based scoring functions for visualising biological insights of H-2Kb-peptide-TCR complexes. *International Journal of Data Mining and Bioinformatics*, **2013**, 8, 326-37	0.5	
75	Parallel screening of wild-type and drug-resistant targets for anti-resistance neuraminidase inhibitors. *PLoS ONE*, **2013**, 8, e56704	3.7	10
74	Steric recognition of T-cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. *Immunology*, **2012**, 136, 139-52	7.8	5
73	Steric recognition of T-cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. *Immunology*, **2012**, 136, 459-459	7.8	78
72	Antigenic sites of H1N1 influenza virus hemagglutinin revealed by natural isolates and inhibition assays. *Vaccine*, **2012**, 30, 6327-37	4.1	19
71	Roles of amino acids in the Escherichia coli octaprenyl diphosphate synthase active site probed by structure-guided site-directed mutagenesis. *Biochemistry*, **2012**, 51, 3412-9	3.2	11
70	Space-related pharma-motifs for fast search of protein binding motifs and polypharmacological targets. *BMC Genomics*, **2012**, 13 Suppl 7, S21	4.5	3
69	Core site-moiety maps reveal inhibitors and binding mechanisms of orthologous proteins by screening compound libraries. *PLoS ONE*, **2012**, 7, e32142	3.7	19
68	MoNetFamily: a web server to infer homologous modules and module-module interaction networks in vertebrates. *Nucleic Acids Research*, **2012**, 40, W263-70	20.1	10
67	GemAffinity: a scoring function for predicting binding affinity and virtual screening. *International Journal of Data Mining and Bioinformatics*, **2012**, 6, 27-41	0.5	3
66	Structures of Helicobacter pylori shikimate kinase reveal a selective inhibitor-induced-fit mechanism. *PLoS ONE*, **2012**, 7, e33481	3.7	21
65	LigSeeSVM: ligand-based virtual screening using support vector machines and data fusion. *International Journal of Computational Biology and Drug Design*, **2011**, 4, 274-89	0.4	3
64	7-Chloro-6-piperidin-1-yl-quinoline-5,8-dione (PT-262), a novel ROCK inhibitor blocks cytoskeleton function and cell migration. *Biochemical Pharmacology*, **2011**, 81, 856-65	6	17
63	Changed epitopes drive the antigenic drift for influenza A (H3N2) viruses. *BMC Bioinformatics*, **2011** , 12 Suppl 1, S31	3.6	28
62	iGEMDOCK: a graphical environment of enhancing GEMDOCK using pharmacological interactions and post-screening analysis. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S33	3.6	221

61	PAComplex: a web server to infer peptide antigen families and binding models from TCR-pMHC complexes. *Nucleic Acids Research*, **2011**, 39, W254-60	20.1	31
60	The Relevance of Protein-Ligand Interaction Profiles in Computer-Aided Novel Compound Design and Applications. *Current Bioinformatics*, **2011**, 6, 383-388	4.7	
59	PCFamily: a web server for searching homologous protein complexes. *Nucleic Acids Research*, **2010**, 38, W516-22	20.1	10
58	SiMMap: a web server for inferring site-moiety map to recognize interaction preferences between protein pockets and compound moieties. *Nucleic Acids Research*, **2010**, 38, W424-30	20.1	32
57	The cAMP receptor-like protein CLP is a novel c-di-GMP receptor linking cell-cell signaling to virulence gene expression in Xanthomonas campestris. *Journal of Molecular Biology*, **2010**, 396, 646-62	6.5	150
56	ATRIPPI: AN ATOM-RESIDUE PREFERENCE SCORING FUNCTION FOR PROTEIN□PROTEIN INTERACTIONS. *International Journal on Artificial Intelligence Tools*, **2010**, 19, 251-266	0.9	2
55	3D-interologs: an evolution database of physical protein- protein interactions across multiple genomes. *BMC Genomics*, **2010**, 11 Suppl 3, S7	4.5	19
54	TSCC: Two-Stage Combinatorial Clustering for virtual screening using protein-ligand interactions and physicochemical features. *BMC Genomics*, **2010**, 11 Suppl 4, S26	4.5	3
53	PPISearch: a web server for searching homologous protein-protein interactions across multiple species. *Nucleic Acids Research*, **2009**, 37, W369-75	20.1	27
52	(PS)2-v2: template-based protein structure prediction server. *BMC Bioinformatics*, **2009**, 10, 366	3.6	85
51	Co-evolution positions and rules for antigenic variants of human influenza A/H3N2 viruses. *BMC Bioinformatics*, **2009**, 10 Suppl 1, S41	3.6	30
50	CAPIH: a Web interface for comparative analyses and visualization of host-HIV protein-protein interactions. *BMC Microbiology*, **2009**, 9, 164	4.5	9
49	Aurintricarboxylic acid inhibits influenza virus neuraminidase. *Antiviral Research*, **2009**, 81, 123-31	10.8	85
48	Evolutionary conservation of DNA-contact residues in DNA-binding domains. *BMC Bioinformatics*, **2008**, 9 Suppl 6, S3	3.6	3
47	Rational Design for Crystallization of □Lactoglobulin and Vitamin D3 Complex: Revealing a Secondary Binding Site□*Crystal Growth and Design*, **2008**, 8, 4268-4276	3.5	25
46	Binding Affinity Analysis of Protein-Ligand Complexes **2008**,		1
45	PhosphoPOINT: a comprehensive human kinase interactome and phospho-protein database. *Bioinformatics*, **2008**, 24, i14-20	7.2	69
44	Structural simulation and protein engineering to convert an endo-chitosanase to an exo-chitosanase. *Protein Engineering, Design and Selection*, **2008**, 21, 561-6	1.9	17

43	Crystal structure of a secondary vitamin D3 binding site of milk beta-lactoglobulin. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1197-210	4.2	76
42	Soft energy function and generic evolutionary method for discriminating native from nonnative protein conformations. *Journal of Computational Chemistry*, **2008**, 29, 1364-73	3.5	
41	3D-partner: a web server to infer interacting partners and binding models. *Nucleic Acids Research*, **2007**, 35, W561-7	20.1	37
40	fastSCOP: a fast web server for recognizing protein structural domains and SCOP superfamilies. *Nucleic Acids Research*, **2007**, 35, W438-43	20.1	15
39	Kappa-alpha plot derived structural alphabet and BLOSUM-like substitution matrix for rapid search of protein structure database. *Genome Biology*, **2007**, 8, R31	18.3	61
38	Combinatorial computational approaches to identify tetracycline derivatives as flavivirus inhibitors. *PLoS ONE*, **2007**, 2, e428	3.7	72
37	A Gaussian Evolutionary Method for Predicting Protein-Protein Interaction Sites **2007**, 143-154		
36	Protein structure database search and evolutionary classification. *Nucleic Acids Research*, **2006**, 34, 3646-59	20.1	83
35	(PS)2: protein structure prediction server. *Nucleic Acids Research*, **2006**, 34, W152-7	20.1	110
34	DAPID: a 3D-domain annotated protein-protein interaction database. *Genome Informatics*, **2006**, 17, 206-15		6
33	Consensus scoring criteria for improving enrichment in virtual screening. *Journal of Chemical Information and Modeling*, **2005**, 45, 1134-46	6.1	182
32	GEMPLS: A New QSAR Method Combining Generic Evolutionary Method and Partial Least Squares. *Lecture Notes in Computer Science*, **2005**, 125-135	0.9	
31	A pharmacophore-based evolutionary approach for screening selective estrogen receptor modulators. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 205-20	4.2	74
30	An evolutionary approach for gene expression patterns. *IEEE Transactions on Information Technology in Biomedicine*, **2004**, 8, 69-78		13
29	Some issues of designing genetic algorithms for traveling salesman problems. *Soft Computing*, **2004**, 8, 689-697	3.5	17
28	GEMDOCK: a generic evolutionary method for molecular docking. *Proteins: Structure, Function and Bioinformatics*, **2004**, 55, 288-304	4.2	380
27	Development and evaluation of a generic evolutionary method for protein-ligand docking. *Journal of Computational Chemistry*, **2004**, 25, 843-57	3.5	40
26	An evolutionary algorithm for large traveling salesman problems. *IEEE Transactions on Systems, Man, and Cybernetics*, **2004**, 34, 1718-29		78

25	Comparative Molecular Binding Energy Analysis of HIV-1 Protease Inhibitors Using Genetic Algorithm-Based Partial Least Squares Method. *Lecture Notes in Computer Science*, **2004**, 385-386	0.9	
24	An Evolutionary Approach with Pharmacophore-Based Scoring Functions for Virtual Database Screening. *Lecture Notes in Computer Science*, **2004**, 481-492	0.9	1
23	Modeling the Binding and Inhibition Mechanism of Nucleotides and Sulfotransferase Using Molecular Docking. *Journal of the Chinese Chemical Society*, **2003**, 50, 655-663	1.5	3
22	Fine-grained protein fold assignment by support vector machines using generalized npeptide coding schemes and jury voting from multiple-parameter sets. *Proteins: Structure, Function and Bioinformatics*, **2003**, 50, 531-6	4.2	22
21	Relationship between protein structures and disulfide-bonding patterns. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 1-5	4.2	49
20	Heterogeneous Selection Genetic Algorithms For Traveling Salesman Problems. *Engineering Optimization*, **2003**, 35, 297-311	2	13
19	An Evolutionary Approach for Molecular Docking. *Lecture Notes in Computer Science*, **2003**, 2372-2383	0.9	1
18	GEM: a Gaussian Evolutionary Method for predicting protein side-chain conformations. *Protein Science*, **2002**, 11, 1897-907	6.3	18
17	A robust evolutionary algorithm for global optimization. *Engineering Optimization*, **2002**, 34, 405-425	2	3
16	A Robust Evolutionary Algorithm for Training Neural Networks. *Neural Computing and Applications*, **2001**, 10, 214-230	4.8	28
15	Optical coating designs using the family competition evolutionary algorithm. *Evolutionary Computation*, **2001**, 9, 421-43	4.3	8
14	Efficient evolutionary algorithm for the thin-film synthesis of inhomogeneous optical coatings. *Applied Optics*, **2001**, 40, 3256-67	1.7	12
13	An evolutionary algorithm for the synthesis of multilayer coatings at oblique light incidence. *Journal of Lightwave Technology*, **2001**, 19, 559-570	4	19
12	Flexible ligand docking using a robust evolutionary algorithm. *Journal of Computational Chemistry*, **2000**, 21, 988-998	3.5	37
11	A family competition evolutionary algorithm for automated docking of flexible ligands to proteins. *IEEE Transactions on Information Technology in Biomedicine*, **2000**, 4, 225-37		11
10	A genetic algorithm with adaptive mutations and family competition for training neural networks. *International Journal of Neural Systems*, **2000**, 10, 333-52	6.2	10
9	Flexible Ligand Docking Using a Robust Evolutionary Algorithm **2000**, 95-106		
8	An evolutionary algorithm for synthesizing optical thin-film designs. *Lecture Notes in Computer Science*, **1998**, 947-956	0.9	9

7	Applying family competition to evolution strategies for constrained optimization. *Lecture Notes in Computer Science*, **1997**, 201-211	0.9	47
6	Consensus scoring criteria in structure-based virtual screening		3
5	Solving traveling salesman problems by combining global and local search mechanisms		6
4	A robust evolutionary algorithm for optical thin-film designs		2
3	A new evolutionary approach to developing neural autonomous agents		3
2	Incorporation family competition into Gaussian and Cauchy mutations to training neural networks using an evolutionary algorithm		1
1	A combined evolutionary algorithm for real parameters optimization		9