

# Jinn-Moon Yang

## List of Publications by Citations

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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	GEMDOCK: a generic evolutionary method for molecular docking. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 55, 288-304	4.2	380
131	iGEMDOCK: a graphical environment of enhancing GEMDOCK using pharmacological interactions and post-screening analysis. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 1, S33	3.6	221
130	Consensus scoring criteria for improving enrichment in virtual screening. <i>Journal of Chemical Information and Modeling</i> , <b>2005</b> , 45, 1134-46	6.1	182
129	The cAMP receptor-like protein CLP is a novel c-di-GMP receptor linking cell-cell signaling to virulence gene expression in <i>Xanthomonas campestris</i> . <i>Journal of Molecular Biology</i> , <b>2010</b> , 396, 646-62	6.5	150
128	(PS)2: protein structure prediction server. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W152-7	20.1	110
127	(PS)2-v2: template-based protein structure prediction server. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 366	3.6	85
126	Aurintricarboxylic acid inhibits influenza virus neuraminidase. <i>Antiviral Research</i> , <b>2009</b> , 81, 123-31	10.8	85
125	Protein structure database search and evolutionary classification. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 3646-59	5.1	83
124	Steric recognition of T-cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. <i>Immunology</i> , <b>2012</b> , 136, 459-459	7.8	78
123	An evolutionary algorithm for large traveling salesman problems. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , <b>2004</b> , 34, 1718-29		78
122	Crystal structure of a secondary vitamin D3 binding site of milk beta-lactoglobulin. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 71, 1197-210	4.2	76
121	A pharmacophore-based evolutionary approach for screening selective estrogen receptor modulators. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 205-20	4.2	74
120	Combinatorial computational approaches to identify tetracycline derivatives as flavivirus inhibitors. <i>PLoS ONE</i> , <b>2007</b> , 2, e428	3.7	72
119	PhosphoPOINT: a comprehensive human kinase interactome and phospho-protein database. <i>Bioinformatics</i> , <b>2008</b> , 24, i14-20	7.2	69
118	KDM4B as a target for prostate cancer: structural analysis and selective inhibition by a novel inhibitor. <i>Journal of Medicinal Chemistry</i> , <b>2014</b> , 57, 5975-85	8.3	68
117	Kappa-alpha plot derived structural alphabet and BLOSUM-like substitution matrix for rapid search of protein structure database. <i>Genome Biology</i> , <b>2007</b> , 8, R31	18.3	61
116	Relationship between protein structures and disulfide-bonding patterns. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53, 1-5	4.2	49

115	Applying family competition to evolution strategies for constrained optimization. <i>Lecture Notes in Computer Science</i> , <b>1997</b> , 201-211	0.9	47
114	Crowning proteins: modulating the protein surface properties using crown ethers. <i>Angewandte Chemie - International Edition</i> , <b>2014</b> , 53, 13054-8	16.4	41
113	Development and evaluation of a generic evolutionary method for protein-ligand docking. <i>Journal of Computational Chemistry</i> , <b>2004</b> , 25, 843-57	3.5	40
112	3D-partner: a web server to infer interacting partners and binding models. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W561-7	20.1	37
111	Flexible ligand docking using a robust evolutionary algorithm. <i>Journal of Computational Chemistry</i> , <b>2000</b> , 21, 988-998	3.5	37
110	DNA mimic proteins: functions, structures, and bioinformatic analysis. <i>Biochemistry</i> , <b>2014</b> , 53, 2865-74	3.2	32
109	SiMMap: a web server for inferring site-moiety map to recognize interaction preferences between protein pockets and compound moieties. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W424-30	20.1	32
108	PACComplex: a web server to infer peptide antigen families and binding models from TCR-pMHC complexes. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W254-60	20.1	31
107	Co-evolution positions and rules for antigenic variants of human influenza A/H3N2 viruses. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 1, S41	3.6	30
106	Staphylococcus aureus protein SAUGI acts as a uracil-DNA glycosylase inhibitor. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 1354-64	20.1	29
105	Synthesis of acylguanidine zanamivir derivatives as neuraminidase inhibitors and the evaluation of their bio-activities. <i>Organic and Biomolecular Chemistry</i> , <b>2013</b> , 11, 3943-8	3.9	28
104	Changed epitopes drive the antigenic drift for influenza A (H3N2) viruses. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 1, S31	3.6	28
103	A Robust Evolutionary Algorithm for Training Neural Networks. <i>Neural Computing and Applications</i> , <b>2001</b> , 10, 214-230	4.8	28
102	PPISearch: a web server for searching homologous protein-protein interactions across multiple species. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W369-75	20.1	27
101	Membrane protein-regulated networks across human cancers. <i>Nature Communications</i> , <b>2019</b> , 10, 3131	17.4	26
100	Novel Class IIa-Selective Histone Deacetylase Inhibitors Discovered Using an in Silico Virtual Screening Approach. <i>Scientific Reports</i> , <b>2017</b> , 7, 3228	4.9	26
99	Module organization and variance in protein-protein interaction networks. <i>Scientific Reports</i> , <b>2015</b> , 5, 9386	4.9	25
98	Rational Design for Crystallization of $\beta$ -Lactoglobulin and Vitamin D3 Complex: Revealing a Secondary Binding Site. <i>Crystal Growth and Design</i> , <b>2008</b> , 8, 4268-4276	3.5	25

97	Uncovering Flexible Active Site Conformations of SARS-CoV-2 3CL Proteases through Protease Pharmacophore Clusters and COVID-19 Drug Repurposing. <i>ACS Nano</i> , <b>2021</b> , 15, 857-872	16.7	24
96	Design and synthesis of 1,2,3-triazole-containing N-acyl zanamivir analogs as potent neuraminidase inhibitors. <i>European Journal of Medicinal Chemistry</i> , <b>2016</b> , 123, 397-406	6.8	23
95	Fine-grained protein fold assignment by support vector machines using generalized npeptide coding schemes and jury voting from multiple-parameter sets. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 50, 531-6	4.2	22
94	KIDFamMap: a database of kinase-inhibitor-disease family maps for kinase inhibitor selectivity and binding mechanisms. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D430-40	20.1	21
93	Structures of Helicobacter pylori shikimate kinase reveal a selective inhibitor-induced-fit mechanism. <i>PLoS ONE</i> , <b>2012</b> , 7, e33481	3.7	21
92	The inhibitory effects of PGG and EGCG against the SARS-CoV-2 3C-like protease. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 591, 130-130	3.4	21
91	Antigenic sites of H1N1 influenza virus hemagglutinin revealed by natural isolates and inhibition assays. <i>Vaccine</i> , <b>2012</b> , 30, 6327-37	4.1	19
90	Core site-moiety maps reveal inhibitors and binding mechanisms of orthologous proteins by screening compound libraries. <i>PLoS ONE</i> , <b>2012</b> , 7, e32142	3.7	19
89	3D-interologs: an evolution database of physical protein- protein interactions across multiple genomes. <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 3, S7	4.5	19
88	An evolutionary algorithm for the synthesis of multilayer coatings at oblique light incidence. <i>Journal of Lightwave Technology</i> , <b>2001</b> , 19, 559-570	4	19
87	GEM: a Gaussian Evolutionary Method for predicting protein side-chain conformations. <i>Protein Science</i> , <b>2002</b> , 11, 1897-907	6.3	18
86	Novel Lactulose and Melibiose Targeting Autophagy to Reduce PolyQ Aggregation in Cell Models of Spinocerebellar Ataxia 3. <i>CNS and Neurological Disorders - Drug Targets</i> , <b>2016</b> , 15, 351-9	2.6	18
85	Pathway-based screening strategy for multitarget inhibitors of diverse proteins in metabolic pathways. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003127	5	17
84	7-Chloro-6-piperidin-1-yl-quinoline-5,8-dione (PT-262), a novel ROCK inhibitor blocks cytoskeleton function and cell migration. <i>Biochemical Pharmacology</i> , <b>2011</b> , 81, 856-65	6	17
83	Structural simulation and protein engineering to convert an endo-chitosanase to an exo-chitosanase. <i>Protein Engineering, Design and Selection</i> , <b>2008</b> , 21, 561-6	1.9	17
82	Some issues of designing genetic algorithms for traveling salesman problems. <i>Soft Computing</i> , <b>2004</b> , 8, 689-697	3.5	17
81	fastSCOP: a fast web server for recognizing protein structural domains and SCOP superfamilies. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W438-43	20.1	15
80	The potential of lactulose and melibiose, two novel trehalase-indigestible and autophagy-inducing disaccharides, for polyQ-mediated neurodegenerative disease treatment. <i>NeuroToxicology</i> , <b>2015</b> , 48, 120-30	4.4	14

79	Nicotinic Acetylcholine Receptor Subtype Alpha-9 Mediates Triple-Negative Breast Cancers Based on a Spontaneous Pulmonary Metastasis Mouse Model. <i>Frontiers in Cellular Neuroscience</i> , <b>2017</b> , 11, 336	6.1	14
78	5-Demethyltangeretin is more potent than tangeretin in inhibiting dimethylbenz(a)anthracene (DMBA)/12-O-tetradecanoylphorbol-13-acetate (TPA)-induced skin tumorigenesis. <i>Journal of Functional Foods</i> , <b>2014</b> , 11, 528-537	5.1	14
77	Repurposing existing drugs: identification of SARS-CoV-2 3C-like protease inhibitors. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , <b>2021</b> , 36, 147-153	5.6	14
76	CRISPR/Cas9 Genome Editing of Epidermal Growth Factor Receptor Sufficiently Abolished Oncogenicity in Anaplastic Thyroid Cancer. <i>Disease Markers</i> , <b>2018</b> , 2018, 3835783	3.2	13
75	An evolutionary approach for gene expression patterns. <i>IEEE Transactions on Information Technology in Biomedicine</i> , <b>2004</b> , 8, 69-78		13
74	Heterogeneous Selection Genetic Algorithms For Traveling Salesman Problems. <i>Engineering Optimization</i> , <b>2003</b> , 35, 297-311	2	13
73	Omics-based Investigation of Diet-induced Obesity Synergized with HBx, Src, and p53 Mutation Accelerating Hepatocarcinogenesis in Zebrafish Model. <i>Cancers</i> , <b>2019</b> , 11,	6.6	13
72	Efficient evolutionary algorithm for the thin-film synthesis of inhomogeneous optical coatings. <i>Applied Optics</i> , <b>2001</b> , 40, 3256-67	1.7	12
71	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). <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 8019-29	8.3	11
70	Roles of amino acids in the Escherichia coli octaprenyl diphosphate synthase active site probed by structure-guided site-directed mutagenesis. <i>Biochemistry</i> , <b>2012</b> , 51, 3412-9	3.2	11
69	A family competition evolutionary algorithm for automated docking of flexible ligands to proteins. <i>IEEE Transactions on Information Technology in Biomedicine</i> , <b>2000</b> , 4, 225-37		11
68	Identification of neuraminidase inhibitors against dual H274Y/I222R mutant strains. <i>Scientific Reports</i> , <b>2017</b> , 7, 12336	4.9	10
67	Parallel screening of wild-type and drug-resistant targets for anti-resistance neuraminidase inhibitors. <i>PLoS ONE</i> , <b>2013</b> , 8, e56704	3.7	10
66	PCFamily: a web server for searching homologous protein complexes. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W516-22	20.1	10
65	MoNetFamily: a web server to infer homologous modules and module-module interaction networks in vertebrates. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W263-70	20.1	10
64	A genetic algorithm with adaptive mutations and family competition for training neural networks. <i>International Journal of Neural Systems</i> , <b>2000</b> , 10, 333-52	6.2	10
63	Anchor-based classification and type-C inhibitors for tyrosine kinases. <i>Scientific Reports</i> , <b>2015</b> , 5, 10938	4.9	9
62	Pharmacophore anchor models of flaviviral NS3 proteases lead to drug repurposing for DENV infection. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 548	3.6	9

61	Total synthetic protoapigenone WYC02 inhibits cervical cancer cell proliferation and tumour growth through PIK3 signalling pathway. <i>Basic and Clinical Pharmacology and Toxicology</i> , <b>2013</b> , 113, 8-18 <sup>3.1</sup>	9
60	CAPIH: a Web interface for comparative analyses and visualization of host-HIV protein-protein interactions. <i>BMC Microbiology</i> , <b>2009</b> , 9, 164	4.5 9
59	An evolutionary algorithm for synthesizing optical thin-film designs. <i>Lecture Notes in Computer Science</i> , <b>1998</b> , 947-956	0.9 9
58	A combined evolutionary algorithm for real parameters optimization	9
57	Zika Virus NS3 Protease Pharmacophore Anchor Model and Drug Discovery. <i>Scientific Reports</i> , <b>2020</b> , 10, 8929	4.9 8
56	Optical coating designs using the family competition evolutionary algorithm. <i>Evolutionary Computation</i> , <b>2001</b> , 9, 421-43	4.3 8
55	Management of different kinds of head and neck defects with the submental flap for reconstruction. <i>European Archives of Oto-Rhino-Laryngology</i> , <b>2015</b> , 272, 3815-9	3.5 7
54	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2019</b> , 17, 1940005	1 6
53	Moiety-linkage map reveals selective nonbisphosphonate inhibitors of human geranylgeranyl diphosphate synthase. <i>Journal of Chemical Information and Modeling</i> , <b>2013</b> , 53, 2299-311	6.1 6
52	Genome-wide structural modelling of TCR-pMHC interactions. <i>BMC Genomics</i> , <b>2013</b> , 14 Suppl 5, S5	4.5 6
51	Reconstructing genome-wide protein-protein interaction networks using multiple strategies with homologous mapping. <i>PLoS ONE</i> , <b>2015</b> , 10, e0116347	3.7 6
50	Homopharma: a new concept for exploring the molecular binding mechanisms and drug repurposing. <i>BMC Genomics</i> , <b>2014</b> , 15 Suppl 9, S8	4.5 6
49	Solving traveling salesman problems by combining global and local search mechanisms	6
48	DAPID: a 3D-domain annotated protein-protein interaction database. <i>Genome Informatics</i> , <b>2006</b> , 17, 206-15	6
47	Steric recognition of T-cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. <i>Immunology</i> , <b>2012</b> , 136, 139-52	7.8 5
46	An integrated approach with new strategies for QSAR models and lead optimization. <i>BMC Genomics</i> , <b>2017</b> , 18, 104	4.5 4
45	A site-moiety map and virtual screening approach for discovery of novel 5-LOX inhibitors. <i>Scientific Reports</i> , <b>2020</b> , 10, 10510	4.9 4
44	Evaluating Instantaneous Perfusion Responses of Parotid Glands to Gustatory Stimulation Using High-Temporal-Resolution Echo-Planar Diffusion-Weighted Imaging. <i>American Journal of Neuroradiology</i> , <b>2016</b> , 37, 1909-1915	4.4 4

43	Inferring homologous protein-protein interactions through pair position specific scoring matrix. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 2, S11	3.6	4
42	Clinical assessment of diode laser-assisted endoscopic intrasphenoidal vidian neurectomy in the treatment of refractory rhinitis. <i>Lasers in Medical Science</i> , <b>2017</b> , 32, 2097-2104	3.1	3
41	Alternative splicing in human cancer cells is modulated by the amiloride derivative 3,5-diamino-6-chloro-N-(N-(2,6-dichlorobenzoyl)carbamidoyl)pyrazine-2-carboxide. <i>Molecular Oncology</i> , <b>2019</b> , 13, 1744-1762	7.9	3
40	Space-related pharma-motifs for fast search of protein binding motifs and polypharmacological targets. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S21	4.5	3
39	LigSeeSVM: ligand-based virtual screening using support vector machines and data fusion. <i>International Journal of Computational Biology and Drug Design</i> , <b>2011</b> , 4, 274-89	0.4	3
38	GemAffinity: a scoring function for predicting binding affinity and virtual screening. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2012</b> , 6, 27-41	0.5	3
37	TSCC: Two-Stage Combinatorial Clustering for virtual screening using protein-ligand interactions and physicochemical features. <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 4, S26	4.5	3
36	Evolutionary conservation of DNA-contact residues in DNA-binding domains. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 6, S3	3.6	3
35	Modeling the Binding and Inhibition Mechanism of Nucleotides and Sulfotransferase Using Molecular Docking. <i>Journal of the Chinese Chemical Society</i> , <b>2003</b> , 50, 655-663	1.5	3
34	Consensus scoring criteria in structure-based virtual screening		3
33	A robust evolutionary algorithm for global optimization. <i>Engineering Optimization</i> , <b>2002</b> , 34, 405-425	2	3
32	A new evolutionary approach to developing neural autonomous agents		3
31	Convolutional neural network for human cancer types prediction by integrating protein interaction networks and omics data. <i>Scientific Reports</i> , <b>2021</b> , 11, 20691	4.9	3
30	Target Identification Using Homopharma and Network-Based Methods for Predicting Compounds Against Dengue Virus-Infected Cells. <i>Molecules</i> , <b>2020</b> , 25,	4.8	2
29	Vascular anatomy is a determining factor of successful submental flap raising: a retrospective study of 70 clinical cases. <i>PeerJ</i> , <b>2017</b> , 5, e3606	3.1	2
28	ATRIPIPI: AN ATOM-RESIDUE PREFERENCE SCORING FUNCTION FOR PROTEIN-PROTEIN INTERACTIONS. <i>International Journal on Artificial Intelligence Tools</i> , <b>2010</b> , 19, 251-266	0.9	2
27	A robust evolutionary algorithm for optical thin-film designs		2
26	Identification of the PCA29 gene signature as a predictor in prostate cancer. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2019</b> , 17, 1940006	1	1



25	An Integrated Genomic Strategy to Identify CHRNA4 as a Diagnostic/Prognostic Biomarker for Targeted Therapy in Head and Neck Cancer. <i>Cancers</i> , <b>2020</b> , 12,	6.6	1
24	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 13	3.5	1
23	Clinical application of suction-tube-assisted septal submucosal dissection for endoscopic septoplasty. <i>European Archives of Oto-Rhino-Laryngology</i> , <b>2017</b> , 274, 1471-1475	3.5	1
22	Diode laser assisted minimal invasive sphenoidotomy for endoscopic transphenoidal pituitary surgery: our technique and results. <i>Lasers in Surgery and Medicine</i> , <b>2015</b> , 47, 239-42	3.6	1
21	Binding Affinity Analysis of Protein-Ligand Complexes <b>2008</b> ,		1
20	An Evolutionary Approach with Pharmacophore-Based Scoring Functions for Virtual Database Screening. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 481-492	0.9	1
19	Incorporation family competition into Gaussian and Cauchy mutations to training neural networks using an evolutionary algorithm		1
18	An Evolutionary Approach for Molecular Docking. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 2372-2383	0.9	1
17	A Nanodiamond-Based Surface Topography Downregulates the MicroRNA miR6236 to Enhance Neuronal Development and Regeneration. <i>ACS Applied Bio Materials</i> , <b>2021</b> , 4, 890-902	4.1	1
16	Loss of Fis1 impairs proteostasis during skeletal muscle aging in Drosophila. <i>Aging Cell</i> , <b>2021</b> , 20, e13379	3.9	1
15	Boolean function network analysis of time course liver transcriptome data to reveal novel circadian transcriptional regulators in mammals. <i>Journal of the Chinese Medical Association</i> , <b>2019</b> , 82, 872-880	2.8	1
14	Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes <b>2018</b> ,		1
13	Ugonin J Acts as a SARS-CoV-2 3C-like Protease Inhibitor and Exhibits Anti-inflammatory Properties. <i>Frontiers in Pharmacology</i> , <b>2021</b> , 12, 720018	5.6	1
12	An integrated systematic approach for investigating microcurrent electrical nerve stimulation (MENS) efficacy in STZ-induced diabetes mellitus. <i>Life Sciences</i> , <b>2021</b> , 279, 119650	6.8	0
11	Furin and TMPRSS2 Resistant Spike Induces Robust Humoral and Cellular Immunity Against SARS-CoV-2 Lethal Infection.. <i>Frontiers in Immunology</i> , <b>2022</b> , 13, 872047	8.4	0
10	Template-based scoring functions for visualising biological insights of H-2Kb-peptide-TCR complexes. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2013</b> , 8, 326-37	0.5	
9	The Relevance of Protein-Ligand Interaction Profiles in Computer-Aided Novel Compound Design and Applications. <i>Current Bioinformatics</i> , <b>2011</b> , 6, 383-388	4.7	
8	Soft energy function and generic evolutionary method for discriminating native from nonnative protein conformations. <i>Journal of Computational Chemistry</i> , <b>2008</b> , 29, 1364-73	3.5	



- 7 GEMPLS: A New QSAR Method Combining Generic Evolutionary Method and Partial Least Squares. *Lecture Notes in Computer Science*, **2005**, 125-135 0.9
- 6 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
- 5 A Gaussian Evolutionary Method for Predicting Protein-Protein Interaction Sites **2007**, 143-154
- 4 Flexible Ligand Docking Using a Robust Evolutionary Algorithm **2000**, 95-106
- 3 Pharmacophore anchor models of ATAT1 to discover potential inhibitors and lead optimization. *Computational Biology and Chemistry*, **2021**, 93, 107513 3.6
- 2 CoMI: consensus mutual information for tissue-specific gene signatures.. *BMC Bioinformatics*, **2022**, 22, 624 3.6
- 1 Discovery of moiety preference by Shapley value in protein kinase family using random forest models.. *BMC Bioinformatics*, **2022**, 23, 130 3.6