Robert W Harrison

List of Publications by Year
in descending order

158 papers	4,689 citations	81900 39 h-index	114465 63 g-index
163 all docs	163 docs citations	163 times ranked	3617 citing authors

#	Article	IF	Citations
1	Novel bis-Tetrahydrofuranylurethane-Containing Nonpeptidic Protease Inhibitor (PI) UIC-94017 (TMC114) with Potent Activity against Multi-PI-Resistant Human Immunodeficiency Virus In Vitro. Antimicrobial Agents and Chemotherapy, 2003, 47, 3123-3129.	3.2	355
2	Model Structure of Decorin and Implications for Collagen Fibrillogenesis. Journal of Biological Chemistry, 1996, 271, 31767-31770.	3.4	302
3	High Resolution Crystal Structures of HIV-1 Protease with a Potent Non-peptide Inhibitor (UIC-94017) Active Against Multi-drug-resistant Clinical Strains. Journal of Molecular Biology, 2004, 338, 341-352.	4.2	205
4	Ultra-high Resolution Crystal Structure of HIV-1 Protease Mutant Reveals Two Binding Sites for Clinical Inhibitor TMC114. Journal of Molecular Biology, 2006, 363, 161-173.	4.2	136
5	Effectiveness of Nonpeptide Clinical Inhibitor TMC-114 on HIV-1 Protease with Highly Drug Resistant Mutations D30N, I50V, and L90M. Journal of Medicinal Chemistry, 2006, 49, 1379-1387.	6.4	132
6	Structural implications of drug-resistant mutants of HIV-1 protease: High-resolution crystal structures of the mutant protease/substrate analogue complexes. Proteins: Structure, Function and Bioinformatics, 2001, 43, 455-464.	2.6	125
7	Amprenavir complexes with HIVâ€1 protease and its drugâ€resistant mutants altering hydrophobic clusters. FEBS Journal, 2010, 277, 3699-3714.	4.7	116
8	Structural and kinetic analysis of drug resistant mutants of HIV-1 protease. FEBS Journal, 1999, 263, 238-244.	0.2	115
9	Atomic resolution crystal structures of HIV-1 protease and mutants V82A and I84V with saquinavir. Proteins: Structure, Function and Bioinformatics, 2007, 67, 232-242.	2.6	84
10	Effect of Flap Mutations on Structure of HIV-1 Protease and Inhibition by Saquinavir and Darunavir. Journal of Molecular Biology, 2008, 381, 102-115.	4.2	81
11	Stiffness and energy conservation in molecular dynamics: An improved integrator. Journal of Computational Chemistry, 1993, 14, 1112-1122.	3.3	80
12	Improved<tex>$hboxK$</tex>-Means Clustering Algorithm for Exploring Local Protein Sequence Motifs Representing Common Structural Property. IEEE Transactions on Nanobioscience, 2005, 4, 255-265.	3.3	80
13	Hydration Water and Bulk Water in Proteins Have Distinct Properties in Radial Distributions Calculated from 105 Atomic Resolution Crystal Structures. Journal of Physical Chemistry B, 2008, 112, 12073-12080.	2.6	79
14	Improved Protein Secondary Structure Prediction Using Support Vector Machine With a New Encoding Scheme and an Advanced Tertiary Classifier. IEEE Transactions on Nanobioscience, 2004, 3, 265-271.	3.3	78
15	Structural model of human glucokinase in complex with glucose and ATP: implications for the mutants that cause hypo- and hyperglycemia. Diabetes, 1999, 48, 1698-1705.	0.6	71
16	Crystal structures of HIV protease V82A and L90M mutants reveal changes in the indinavir-binding site. FEBS Journal, 2004, 271, 1516-1524.	0.2	71
17	Molecular basis for substrate recognition and drug resistance from 1.1 to 1.6 A resolution crystal structures of HIV-1 protease mutants with substrate analogs. FEBS Journal, 2005, 272, 5265-5277.	4.7	71
18	Kinetic, Stability, and Structural Changes in High-resolution Crystal Structures of HIV-1 Protease with Drug-resistant Mutations L24I, I50V, and G73S. Journal of Molecular Biology, 2005, 354, 789-800.	4.2	68

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19	Identification of Amino Acids in HIV-1 and Avian Sarcoma Virus Integrase Subsites Required for Specific Recognition of the Long Terminal Repeat Ends. Journal of Biological Chemistry, 2006, 281, 4173-4182.	3.4	66
20	Effect of sequence polymorphism and drug resistance on two HIV-1 Gag processing sites. FEBS Journal, 2002, 269, 4114-4120.	0.2	64
21	The influence of temperature on lysozyme crystals. Structure and dynamics of protein and water. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 98-109.	2.5	59
22	Comparison of the substrate specificity of the human T-cell leukemia virus and human immunodeficiency virus proteinases. FEBS Journal, 2000, 267, 6287-6295.	0.2	59
23	Type-2 fuzzy logic-based classifier fusion for support vector machines. Applied Soft Computing Journal, 2008, 8, 1222-1231.	7.2	58
24	Covalent Reaction Intermediate Revealed in Crystal Structure of the Geobacillus stearothermophilus Carboxylesterase Est30. Journal of Molecular Biology, 2004, 342, 551-561.	4.2	54
25	Analysis of six protein structures predicted by comparative modeling techniques. Proteins: Structure, Function and Bioinformatics, 1995, 23, 463-471.	2.6	52
26	ATP-Binding Site of Human Brain Hexokinase As Studied by Molecular Modeling and Site-Directed Mutagenesisâ€. Biochemistry, 1996, 35, 13157-13164.	2.5	52
27	Machine learning methods accurately predict host specificity of coronaviruses based on spike sequences alone. Biochemical and Biophysical Research Communications, 2020, 533, 553-558.	2.1	52
28	Human Î²-Cell Glucokinase. Journal of Biological Chemistry, 1995, 270, 9939-9946.	3.4	51
29	Drug-Resistant HIV-1 Proteases Identify Enzyme Residues Important for Substrate Selection and Catalytic Rate. Biochemistry, 1998, 37, 13835-13845.	2.5	51
30	Human Immunodeficiency Virus, Type 1 Protease Substrate Specificity Is Limited by Interactions between Substrate Amino Acids Bound in Adjacent Enzyme Subsites. Journal of Biological Chemistry, 1996, 271, 4709-4717.	3.4	49
31	SLC30A3 (ZnT3) Oligomerization by Dityrosine Bonds Regulates Its Subcellular Localization and Metal Transport Capacity. PLoS ONE, 2009, 4, e5896.	2.5	49
32	Mechanism of Drug Resistance Revealed by the Crystal Structure of the Unliganded HIV-1 Protease with F53L Mutation. Journal of Molecular Biology, 2006, 358, 1191-1199.	4.2	48
33	Combining mutations in HIV-1 protease to understand mechanisms of resistance. Proteins: Structure, Function and Bioinformatics, 2002, 48, 107-116.	2.6	46
34	HIV Protease: Historical Perspective and Current Research. Viruses, 2021, 13, 839.	3.3	45
35	Rule Generation for Protein Secondary Structure Prediction With Support Vector Machines and Decision Tree. IEEE Transactions on Nanobioscience, 2006, 5, 46-53.	3.3	43
36	Clustering support vector machines for protein local structure prediction. Expert Systems With Applications, 2007, 32, 518-526.	7.6	43

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37	Molecular dynamics simulations of HIV-1 protease with peptide substrate. Protein Engineering, Design and Selection, 1994, 7, 1353-1363.	2.1	41
38	Structural Basis for Specificity of Retroviral Proteasesâ€. Biochemistry, 1998, 37, 4518-4526.	2.5	41
39	Potent New Antiviral Compound Shows Similar Inhibition and Structural Interactions with Drug Resistant Mutants and Wild Type HIV-1 Proteaseâ€. Journal of Medicinal Chemistry, 2007, 50, 4509-4515.	6.4	40
40	Crystallographic Analysis of Human Immunodeficiency Virus 1 Protease with an Analog of the Conserved CA-p2 Substrate. Interactions with Frequently Occurring Glutamic Acid Residue at P2' Position of Substrates. FEBS Journal, 1997, 249, 523-530.	0.2	39
41	Structural Studies of a Rationally Selected Multi-Drug Resistant HIV-1 Protease Reveal Synergistic Effect of Distal Mutations on Flap Dynamics. PLoS ONE, 2016, 11, e0168616.	2.5	39
42	Analysis of comparative modeling predictions for CASP2 targets 1, 3, 9, and 17. Proteins: Structure, Function and Bioinformatics, 1997, 29, 68-73.	2.6	38
43	Critical differences in HIVâ€1 and HIVâ€2 protease specificity for clinical inhibitors. Protein Science, 2012, 21, 339-350.	7.6	38
44	Crystal structure of MTCP-1: Implications for role of TCL-1 and MTCP-1 in T cell malignancies. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 3413-3418.	7.1	34
45	Transmembrane segments prediction and understanding using support vector machine and decision tree. Expert Systems With Applications, 2006, 30, 64-72.	7.6	34
46	Molecular dynamics simulations of 14 HIV protease mutants in complexes with indinavir. Journal of Molecular Modeling, 2004, 10, 373-381.	1.8	33
47	Structural basis for executioner caspase recognition of P5 position in substrates. Apoptosis: an International Journal on Programmed Cell Death, 2008, 13, 1291-1302.	4.9	33
48	cAMP-dependent Protein Kinase Phosphorylation Produces Interdomain Movement in SUR2B Leading to Activation of the Vascular KATP Channel. Journal of Biological Chemistry, 2008, 283, 7523-7530.	3.4	33
49	Molecular mechanics calculations on HIV-1 protease with peptide substrates correlate with experimental data. Protein Engineering, Design and Selection, 1996, 9, 679-690.	2.1	32
50	The Fourier-Green's function and the rapid evaluation of molecular potentials. Protein Engineering, Design and Selection, 1994, 7, 359-369.	2.1	31
51	Molecular mechanics analysis of drug-resistant mutants of HIV protease. Protein Engineering, Design and Selection, 1999, 12, 469-474.	2.1	31
52	Defining the DNA Substrate Binding Sites on HIV-1 Integrase. Journal of Molecular Biology, 2009, 385, 568-579.	4.2	28
53	AMMP-Vis. , 2005, , .		27
54	Prediction of HIV drug resistance from genotype with encoded three-dimensional protein structure. BMC Genomics, 2014, 15, S1.	2.8	27

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55	Novel P2 Tris-tetrahydrofuran Group in Antiviral Compound 1 (GRL-0519) Fills the S2 Binding Pocket of Selected Mutants of HIV-1 Protease. Journal of Medicinal Chemistry, 2013, 56, 1074-1083.	6.4	26
56	Structures of Darunavir-Resistant HIV-1 Protease Mutant Reveal Atypical Binding of Darunavir to Wide Open Flaps. ACS Chemical Biology, 2014, 9, 1351-1358.	3.4	26
57	The L76V Drug Resistance Mutation Decreases the Dimer Stability and Rate of Autoprocessing of HIV-1 Protease by Reducing Internal Hydrophobic Contacts. Biochemistry, 2011, 50, 4786-4795.	2.5	25
58	Molecular mechanics calculations on rous sarcoma virus protease with peptide substrates. Protein Science, 1997, 6, 2365-2374.	7.6	24
59	Sparse Representation for HIV-1 Protease Drug Resistance Prediction. , 2013, 2013, 342-349.		23
60	MetNetAligner: a web service tool for metabolic network alignments. Bioinformatics, 2009, 25, 1989-1990.	4.1	22
61	Caspase-3 binds diverse P4 residues in peptides as revealed by crystallography and structural modeling. Apoptosis: an International Journal on Programmed Cell Death, 2009, 14, 741-752.	4.9	22
62	Vps33b pathogenic mutations preferentially affect VIPAS39/SPE-39-positive endosomes. Human Molecular Genetics, 2013, 22, 5215-5228.	2.9	22
63	Conformational variation of an extreme drug resistant mutant of HIV protease. Journal of Molecular Graphics and Modelling, 2015, 62, 87-96.	2.4	22
64	Automated prediction of HIV drug resistance from genotype data. BMC Bioinformatics, 2016, 17, 278.	2.6	22
65	Analysis of protein structures reveals regions of rare backbone conformation at functional sites. Proteins: Structure, Function and Bioinformatics, 2003, 53, 872-879.	2.6	21
66	Practical fuzzy decision trees. , 2009, , .		21
67	Binding of Clinical Inhibitors to a Model Precursor of a Rationally Selected Multidrug Resistant HIV-1 Protease Is Significantly Weaker Than That to the Released Mature Enzyme. Biochemistry, 2016, 55, 2390-2400.	2.5	21
68	Granular Decision Tree and Evolutionary Neural SVM for Protein Secondary Structure Prediction. International Journal of Computational Intelligence Systems, 2009, 2, 343-352.	2.7	20
69	Activity of Tethered Human Immunodeficiency Virus 1 Protease Containing Mutations in the Flap Region of One Subunit. FEBS Journal, 1997, 244, 235-241.	0.2	19
70	Drug Resistance Mutation L76V Alters Nonpolar Interactions at the Flapâ€“Core Interface of HIV-1 Protease. ACS Omega, 2018, 3, 12132-12140.	3.5	19
71	Improved Parameters for Generating Partial Charges: Correlation with Observed Dipole Moments. Journal of Molecular Modeling, 1999, 5, 143-152.	1.8	18
72	FIK Model: Novel Efficient Granular Computing Model for Protein Sequence Motifs and Structure Information Discovery. , 2006, , .		18

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73	To Be or Not to Be: Predicting Soluble SecAs as Membrane Proteins. IEEE Transactions on Nanobioscience, 2007, 6, 168-179.	3.3	18
74	Distributed Decentralized Domain Name Service. , 2016, , .		18
75	Structural studies of antiviral inhibitor with HIV-1 protease bearing drug resistant substitutions of V32I, I47V and V82I. Biochemical and Biophysical Research Communications, 2019, 514, 974-978.	2.1	18
76	Bovine leukemia virus protease: comparison with human T-lymphotropic virus and human immunodeficiency virus proteases. Journal of General Virology, 2007, 88, 2052-2063.	2.9	17
77	Analysis of drug resistance in HIV protease. BMC Bioinformatics, 2018, 19, 362.	2.6	16
78	Highly Drug-Resistant HIV-1 Protease Mutant PRS17 Shows Enhanced Binding to Substrate Analogues. ACS Omega, 2019, 4, 8707-8719.	3.5	16
79	A selfâ€assembling neural network for modeling polymers. Journal of Mathematical Chemistry, 1999, 26, 125-137.	1.5	14
80	Structure Based Drug Design for HIV Protease: From Molecular Modeling to Cheminformatics. Current Topics in Medicinal Chemistry, 2007, 7, 1030-1038.	2.1	13
81	Capturing the Reaction Pathway in Near-Atomic-Resolution Crystal Structures of HIV-1 Protease. Biochemistry, 2012, 51, 7726-7732.	2.5	13
82	Potent Antiviral HIV-1 Protease Inhibitor GRL-02031 Adapts to the Structures of Drug Resistant Mutants with Its P1â€²-Pyrrolidinone Ring. Journal of Medicinal Chemistry, 2012, 55, 3387-3397.	6.4	13
83	Identifying representative drug resistant mutants of HIV. BMC Bioinformatics, 2015, 16, S1.	2.6	13
84	Structure of Monellin Refined to 2.3 Ã... Resolution in the Orthorhombic Crystal Form. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 713-719.	2.5	12
85	Molecular Basis for Differential Nucleotide Binding of the Nucleotide-Binding Domain of ABC-Transporter CvaB. Biochemistry, 2006, 45, 14473-14480.	2.5	12
86	Watermarking with wavelets: Simplicity leads to robustness. , 2008, , .		12
87	Tackling the problem of HIV drug resistance. Postepy Biochemii, 2016, 62, 273-279.	0.2	12
88	Model complexes of tumor necrosis factor-Î± with receptors Rl and R2. Protein Engineering, Design and Selection, 1995, 8, 1233-1241.	2.1	11
89	Charge centers and formation of the protein folding core. Proteins: Structure, Function and Bioinformatics, 2001, 43, 353-364.	2.6	11
90	Parallel protein secondary structure prediction schemes using Pthread and OpenMP over hyper-threading technology. Journal of Supercomputing, 2007, 41, 1-16.	3.6	11

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91	Encoding protein structure with functions on graphs. , 2011, , .		11
92	Crystal Structures of Tcl1 Family Oncoproteins and Their Conserved Surface Features. Scientific World Journal, The, 2002, 2, 1876-1884.	2.1	10
93	Evolution of drug resistance in HIV protease. BMC Bioinformatics, 2020, 21, 497.	2.6	10
94	The Effect of Wavelet Families on Watermarking. Journal of Computers, 2009, 4, .	0.4	10
95	Nucleotide-Dependent Dimerization of the C-Terminal Domain of the ABC Transporter CvaB in Colicin V Secretion. Journal of Bacteriology, 2006, 188, 2383-2391.	2.2	9
96	Fast Alignments of Metabolic Networks. , 2008, , .		9
97	Novel efficient granular computing models for protein sequence motifs and structure information discovery. International Journal of Computational Biology and Drug Design, 2009, 2, 168.	0.3	9
98	Decoding HIV resistance: from genotype to therapy. Future Medicinal Chemistry, 2017, 9, 1529-1538.	2.3	9
99	Highly drugâ€resistant HIVâ€1 protease reveals decreased intraâ€subunit interactions due to clusters of mutations. FEBS Journal, 2020, 287, 3235-3254.	4.7	9
100	Close pairs of carboxylates: a possibility of multicenter hydrogen bonds in proteins. Protein Engineering, Design and Selection, 2003, 16, 201-207.	2.1	8
101	Efficient Super Granular SVM Feature Elimination (Super GSVM-FE) model for protein sequence motif information extraction. International Journal of Functional Informatics and Personalised Medicine, 2008, 1, 8.	0.4	8
102	Integrating quantum and molecular mechanics. Journal of Computational Chemistry, 1999, 20, 1618-1633.	3.3	7
103	Super Granular Shrink-SVM Feature Elimination (Super GS-SVM-FE) Model for Protein Sequence Motif Information Extraction. , 2007, , .		7
104	Reaction Intermediates Discovered in Crystal Structures of Enzymes. Advances in Protein Chemistry and Structural Biology, 2012, 87, 57-86.	2.3	7
105	Models of HIV-1 protease with peptides representing its natural substrates. Computational and Theoretical Chemistry, 1998, 423, 1-12.	1.5	6
106	Characterization of a Naphthalene Derivative Inhibitor of Retroviral Integrases. AIDS Research and Human Retroviruses, 2004, 20, 135-144.	1.1	6
107	Homomorphisms of Multisource Trees into Networks with Applications to Metabolic Pathways. , 2007, , .		6
108	Rule set reduction in fuzzy decision trees. , 2009, , .		6

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109	Improving the diffraction quality of MTCP-1 crystals by post-crystallization soaking. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 5-7.	2.5	5
110	Effects of different post-crystallization soaking conditions on the diffraction of Mtcp1 crystals. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 763-765.	2.5	5
111	Structure of murine Tcl1 at 2.5â€…Ã… resolution and implications for the TCL oncogene family. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1545-1551.	2.5	5
112	A model architecture for Big Data applications using relational databases. , 2014, , .		5
113	FDT 2.0: Improving scalability of the fuzzy decision tree induction tool - integrating database storage. , 2014, 2014, 187-190.		5
114	Prediction and Classification of Real and Pseudo MicroRNA Precursors via Data Fuzzification and Fuzzy Decision Trees. Lecture Notes in Computer Science, 2009, , 323-334.	1.3	5
115	Antiviral agent based on the non-structural protein targeting the maturation process of HIV-1: expression and susceptibility of chimeric Vpr as a substrate for cleavage by HIV-1 protease. Protein Engineering, Design and Selection, 2000, 13, 431-436.	2.1	4
116	Identifying essential features for the classification of real and pseudo microRNAs precursors using fuzzy decision trees. , 2010, , .		4
117	High Performance Attack Estimation in Large-Scale Network Flows. , 2018, , .		4
118	Protein Folding: Search for Basic Physical Models. Scientific World Journal, The, 2003, 3, 623-635.	2.1	3
119	Multi-SVM Fuzzy Classification and Fusion Method and Applications in Bioinformatics. Journal of Computational and Theoretical Nanoscience, 2005, 2, 534-542.	0.4	3
120	Web based molecular visualization using procedural shaders in X3D. , 2005, , .		3
121	Clustering Support Vector Machines and Its Application to Local Protein Tertiary Structure Prediction. Lecture Notes in Computer Science, 2006, , 710-717.	1.3	3
122	AMMP-EXTN: Managing User Privacy and Cooperation Demand in a Collaborative Molecule Modeling Virtual System. , 2007, , .		3
123	A rule-based approach for RNA pseudoknot prediction. International Journal of Data Mining and Bioinformatics, 2008, 2, 78.	0.1	3
124	Recognizing Protein Secondary Structures with Neural Networks. , 2017, , .		3
125	Continuous restricted Boltzmann machines. Wireless Networks, 2018, , 1.	3.0	3
126	Molecular Mechanics Calculations on Protein-Ligand Complexes. , 2002, , 115-127.		3

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127	Understanding Protein Structure Prediction Using SVM_DT. Lecture Notes in Computer Science, 2005, , 203-212.	1.3	3
128	Identification of Protein Folding Cores Using Charge Center Model of Protein Structure. Scientific World Journal, The, 2002, 2, 84-86.	2.1	2
129	A Novel Deterministic-Stochastic Crossover Method for Simulating Biochemical Networks. , 2009, , .		2
130	FDT 1.0: An improved fuzzy decision tree induction tool. , 2010, , .		2
131	Protein model assessment using extented fuzzy decision tree with spatial neighborhood features. , 2012, , .		2
132	Fuzzy Restricted Boltzmann Machines. Advances in Intelligent Systems and Computing, 2018, , 392-398.	0.6	2
133	Molecular mechanics calculations on protein-ligand complexes. Journal of Computer - Aided Molecular Design, 1998, 9/11, 115-127.	1.0	1
134	Crystal Structure of Murine Tcl1 Oncoprotein and Conserved Surface Features of the Molecules of the Tcl1 Family. Scientific World Journal, The, 2002, 2, 119-120.	2.1	1
135	Simulation of oscillatory dynamics of blood testosterone levels using the crossover method. , 2010, , .		1
136	A Continuous-Time, Discrete-State Method for Simulating the Dynamics of Biochemical Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 335-341.	3.0	1
137	Understandable learning machine system design for Transmembrane or Embedded Membrane segments prediction. International Journal of Data Mining and Bioinformatics, 2011, 5, 38.	0.1	1
138	HIV drug resistance prediction using multiple regression. , 2013, , .		1
139	A novel approach to determine docking locations using fuzzy logic and shape determination. , 2014, , .		1
140	A Distributed Greedy Heuristic for Computing Voronoi Tessellations with Applications Towards Peer-to-Peer Networks. , 2015, , .		1
141	DISCOVERY OF LOCAL PROTEIN SEQUENCE MOTIFS USING IMPROVED K-MEANS CLUSTERING TECHNIQUE. , 2005, , .		1
142	Protein secondary structure prediction using different encoding schemes and neural network architectures. , 2004, 5433, 74.		0
143	Protein secondary structure prediction using support vector machine with advanced encoding schemes. , 2004, , .		0
144	Alternative target functions for protein structure prediction with neural networks. , 2004, 5433, 100.		0

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145	A New Seed Selection Algorithm that Maximizes Local Structural Similarity in Proteins. , 2006, 2006, 5822-5.		0
146	A Feature Selection Algorithm Based on Graph Theory and Random Forests for Protein Secondary Structure Prediction. , 2007, , 590-600.		0
147	Efficient Algorithms for Structural Recall in Databases. , 2007, , 439-463.		0
148	Understanding the Prediction of Transmembrane Proteins by Support Vector Machine using Association Rule Mining. , 2007, , .		0
149	Current Methods for Protein Secondary-Structure Prediction Based on Support Vector Machines. , 0, , 1-26.		0
150	Protein model assessment via machine learning techniques. International Journal of Functional Informatics and Personalised Medicine, 2010, 3, 215.	0.4	0
151	Enhanced Encoding with Improved Fuzzy Decision Tree Testing Using CASP Templates. IEEE Computational Intelligence Magazine, 2012, 7, 55-60.	3.2	0
152	A deterministic-stochastic crossover algorithm for simulation of complex biochemical systems. , 2013, , .		0
153	Optimization of relational database usage involving Big Data a model architecture for Big Data applications. , 2014, , .		0
154	Identifying representative drug resistant mutants of HIV reverse transcriptase. , 2014, , .		0
155	Guest Editorsâ€™ Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 576-577.	3.0	0
156	Web-Based Intelligence for IDS. Lecture Notes in Computer Science, 2019, , 307-316.	1.3	0
157	Accuracy and Generalization of Deep Learning Applied to Large Scale Attacks. , 2021, , .		0
158	Statistical Estimate for the Size of the Protein Structural Vocabulary. , 2007, , 530-538.		0