Barry Robson

List of Publications by Year
in descending order

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77	3,007	257357	168321
papers	citations	24 h-index	53 g-index

80	80	80	2525
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	[32] GOR method for predicting protein secondary structure from amino acid sequence. Methods in Enzymology, 1996, 266, 540-553.	0.4	1,034
2	An algorithm for secondary structure determination in proteins based on sequence similarity. FEBS Letters, 1986, 205, 303-308.	1.3	274
3	Data mining and clinical data repositories: Insights from a 667,000 patient data set. Computers in Biology and Medicine, 2006, 36, 1351-1377.	3.9	150
4	PRO_LIGAND: An approach to de novo molecular design. 1. Application to the design of organic molecules. Journal of Computer-Aided Molecular Design, 1995, 9, 13-32.	1.3	118
5	What is a conservative substitution?. Journal of Molecular Evolution, 1983, 19, 171-175.	0.8	105
6	Analysis of the Code Relating Sequence to Secondary Structure in Proteins. Nature, 1970, 227, 62-63.	13.7	76
7	Analysis of the code relating sequence to conformation in globular proteins. Theory and application of expected information. Biochemical Journal, 1974, 141, 853-867.	1.7	75
8	Refined models for computer simulation of protein folding. Journal of Molecular Biology, 1979, 132, 19-51.	2.0	72
9	Influence of the local amino acid sequence upon the zones of the torsional angles .phi. and .psi. adopted by residues in proteins. Biochemistry, 1991, 30, 1578-1586.	1.2	57
10	PRO_LIGAND: An Approach to de Novo Molecular Design. 2. Design of Novel Molecules from Molecular Field Analysis (MFA) Models and Pharmacophores. Journal of Medicinal Chemistry, 1994, 37, 3994-4002.	2.9	56
11	PRO_LIGAND: An approach to de novo molecular design. 3. A genetic algorithm for structure refinement. Journal of Computer-Aided Molecular Design, 1995, 9, 139-148.	1.3	56
12	Structural properties of signal peptides and their membrane insertion. Biochimie, 1980, 62, 231-239.	1.3	52
13	Analysis of the code relating sequence to conformation in globular proteins. Development of a stereochemical alphabet on the basis of intra-residue information. Biochemical Journal, 1974, 141, 869-882.	1.7	42
14	Protein structure prediction. Nature, 1993, 361, 506-506.	13.7	39
15	Analysis of the code relating sequence to conformation in globular proteins. An informational analysis of the role of the residue in determining the conformation of its neighbours in the primary sequence. Biochemical Journal, 1974, 141, 883-897.	1.7	34
16	Analysis of the code relating sequence to conformation in globular proteins. The distribution of residue pairs in turns and kinks in the backbone chain. Biochemical Journal, 1974, 141, 899-904.	1.7	34
17	PRO_LIGAND: An approach to de novo molecular design. 4. Application to the design of peptides. Journal of Computer-Aided Molecular Design, 1995, 9, 213-225.	1.3	31
18	Data-mining to build a knowledge representation store for clinical decision support. Studies on curation and validation based on machine performance in multiple choice medical licensing examinations. Computers in Biology and Medicine, 2016, 73, 71-93.	3.9	31

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19	Implementation of a web based universal exchange and inference language for medicine: Sparse data, probabilities and inference in data mining of clinical data repositories. Computers in Biology and Medicine, 2015, 66, 82-102.	3.9	29
20	Expert system for protein engineering: its application in the study of chloramphenicol acetyltransferase and avian pancreatic polypeptide. Journal of Molecular Graphics, 1987, 5, 8-17.	1.7	28
21	The Dragon on the Gold:Â Myths and Realities for Data Mining in Biomedicine and Biotechnology Using Digital and Molecular Libraries. Journal of Proteome Research, 2004, 3, 1113-1119.	1.8	28
22	Suggestions for a Web based universal exchange and inference language for medicine. Computers in Biology and Medicine, 2013, 43, 2297-2310.	3.9	28
23	Clinical and Pharmacogenomic Data Mining:Â 3. Zeta Theory As a General Tactic for Clinical Bioinformatics. Journal of Proteome Research, 2005, 4, 445-455.	1.8	26
24	Protein folding and heterogeneity inside globular proteins. Nature, 1978, 272, 558-560.	13.7	25
25	Hyperbolic Dirac Nets for medical decision support. Theory, methods, and comparison with Bayes Nets. Computers in Biology and Medicine, 2014, 51, 183-197.	3.9	23
26	The New Physician as Unwitting Quantum Mechanic:â€‰ Is Adapting Dirac's Inference System Best Practice for Personalized Medicine, Genomics, and Proteomics?. Journal of Proteome Research, 2007, 6, 3114-3126.	1.8	22
27	Conformational behaviour of the architectural units of peptides and proteins. Assessment of current understanding by ab initio quantum mechanical methods and refinement of the dipeptide energy surface. Journal of Theoretical Biology, 1979, 76, 83-98.	0.8	21
28	Studies in using a universal exchange and inference language for evidence based medicine. Semi-automated learning and reasoning for PICO methodology, systematic review, and environmental epidemiology. Computers in Biology and Medicine, 2016, 79, 299-323.	3.9	21
29	Reduced variable molecular dynamics. Journal of Computational Chemistry, 1995, 16, 1271-1290.	1.5	20
30	Split-complex numbers and Dirac <i>bra-kets</i>. Communications in Information and Systems, 2014, 14, 135-159.	0.3	20
31	Protein Folding Revisited. Progress in Molecular Biology and Translational Science, 2008, 84, 161-202.	0.9	19
32	Drug discovery using very large numbers of patents. General strategy with extensive use of match and edit operations. Journal of Computer-Aided Molecular Design, 2011, 25, 427-441.	1.3	19
33	Suggestions for a web based universal exchange and inference language for medicine. Continuity of patient care with PCAST disaggregation. Computers in Biology and Medicine, 2015, 56, 51-66.	3.9	18
34	Ab initio SCF-MO calculations on the architectural unit of peptides and protiens. Journal of the Chemical Society, Faraday Transactions 2, 1978, 74, 1311.	1.1	17
35	Computer-aided design and physiological testing of a luteinising hormone-releasing hormone analogue for â€˜adjuvant-freeâ€™ immunocastration. FEBS Letters, 1987, 214, 65-70.	1.3	17
36	Clinical and Pharmacogenomic Data Mining:Â 1. Generalized Theory of Expected Information and Application to the Development of Tools. Journal of Proteome Research, 2003, 2, 283-302.	1.8	17

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37	POPPER, a simple programming language for probabilistic semantic inference in medicine. Computers in Biology and Medicine, 2015, 56, 107-123.	3.9	16
38	Studies on rationales for an expert system approach to the interpretation of protein sequence data Preliminary analysis of the human epidermal growth factor receptor. FEBS Letters, 1987, 214, 219-225.	1.3	15
39	Genomic Messaging System and DNA Mark-Up Language for Information-Based Personalized Medicine with Clinical and Proteome Research Applications. Journal of Proteome Research, 2004, 3, 930-948.	1.8	14
40	Clinical and Pharmacogenomic Data Mining: 4. The FANO Program and Command Set as an Example of Tools for Biomedical Discovery and Evidence Based Medicine. Journal of Proteome Research, 2008, 7, 3922-3947.	1.8	14
41	Modelling of Î±-lactalbumin from the known structure of hen egg white lysozyme using molecular dynamics. Journal of Computer-Aided Molecular Design, 1987, 1, 17-22.	1.3	12
42	DoppelgÃnger proteins as drug leads. Nature Biotechnology, 1996, 14, 892-893.	9.4	12
43	Studies in the Assessment of Folding Quality for Protein Modeling and Structure Prediction. Journal of Proteome Research, 2002, 1, 115-133.	1.8	12
44	Clinical and Pharmacogenomic Data Mining:Â 2. A Simple Method for the Combination of Information from Associations and Multivariances to Facilitate Analysis, Decision, and Design in Clinical Research and Practice. Journal of Proteome Research, 2004, 3, 697-711.	1.8	12
45	Bidirectional General Graphs for inference. Principles and implications for medicine. Computers in Biology and Medicine, 2019, 108, 382-399.	3.9	12
46	Extension of the Quantum Universal Exchange Language to precision medicine and drug lead discovery. Preliminary example studies using the mitochondrial genome. Computers in Biology and Medicine, 2020, 117, 103621.	3.9	11
47	Studies in the use of data mining, prediction algorithms, and a universal exchange and inference language in the analysis of socioeconomic health data. Computers in Biology and Medicine, 2019, 112, 103369.	3.9	9
48	Studies of the role of a smart web for precision medicine supported by biobanking. Personalized Medicine, 2016, 13, 361-380.	0.8	8
49	Protein folding. Trends in Biochemical Sciences, 1976, 1, 49-50.	3.7	7
50	Designing biologically active polypeptides. Trends in Biochemical Sciences, 1980, 5, 240-244.	3.7	7
51	The Design of Biologically Active Polypeptides. Critical Reviews in Biochemistry, 1983, 14, 273-296.	7.5	7
52	Genomic Messaging System Language Including Command Extensions for Clinical Data Categories. Journal of Proteome Research, 2005, 4, 275-299.	1.8	7
53	Testing machine learning techniques for general application by using protein secondary structure prediction. A brief survey with studies of pitfalls and benefits using a simple progressive learning approach. Computers in Biology and Medicine, 2021, 138, 104883.	3.9	7
54	Folding proteins along the dotted lines. Nature, 1975, 254, 386-387.	13.7	6

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55	The prediction of molecular conformation. Biochemical Society Transactions, 1982, 10, 297-298.	1.6	6
56	Mining real-world high dimensional structured data in medicine and its use in decision support. Some different perspectives on unknowns, interdependency, and distinguishability. Computers in Biology and Medicine, 2022, 141, 105118.	3.9	6
57	De novo protein folding on computers. Benefits and challenges. Computers in Biology and Medicine, 2022, 143, 105292.	3.9	6
58	Artificial enzymes. Biochemical Society Transactions, 1987, 15, 1191-1193.	1.6	5
59	Considerations for a Universal Exchange Language for healthcare. , 2011, , .		5
60	Missing link in folding of trypsin inhibitor. Nature, 1974, 250, 707-708.	13.7	4
61	Conformational study of neurotensin and some of its analogues. Biochemical Society Transactions, 1986, 14, 1259-1260.	1.6	4
62	Simplified models of protein folding exploiting the Lagrange radius of gyration of the hydrophobic component. Parallel Computing, 2000, 26, 977-998.	1.3	4
63	Towards Automated Reasoning for Drug Discovery and Pharmaceutical Business Intelligence. Journal of Pharmaceutical Technology & Drug Research, 2012, 1, 3.	1.0	4
64	Computers and preventative diagnosis. A survey with bioinformatics examples of mitochondrial small open reading frame peptides as portents of a new generation of powerful biomarkers. Computers in Biology and Medicine, 2022, 140, 105116.	3.9	4
65	Towards intelligent Internet-roaming agents for mining and inference from medical data. Studies in Health Technology and Informatics, 2009, 149, 157-77.	0.2	4
66	The age of Aquarius?. Nature, 1978, 272, 206-207.	13.7	3
67	Calculation of the conformation of glycosphingolipids: GM1- and GM2-gangliosides. Biochemical Society Transactions, 1986, 14, 707-707.	1.6	3
68	Interesting things for computer systems to do: Keeping and data mining millions of patient records, guiding patients and physicians, and passing medical licensing exams. , 2015, , .		3
69	Towards New Tools for Pharmacoepidemiology. Advances in Pharmacoepidemiology & Drug Safety, 2012, 01, .	0.1	3
70	Links between quantum physics and thought. Studies in Health Technology and Informatics, 2009, 149, 236-48.	0.2	2
71	Conformational energy calculations on the glycan chain of peptidoglycan. Biochemical Society Transactions, 1986, 14, 629-630.	1.6	1
72	Reduced variable molecular dynamics. , 1997, , 122-149.		1

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73	Principles of Quantum Mechanics for Artificial Intelligence in medicine. Discussion with reference to the Quantum Universal Exchange Language (Q-UEL). Computers in Biology and Medicine, 2022, 143, 105323.	3.9	1
74	Ribonuclease still under attack. Nature, 1980, 283, 622-622.	13.7	0
75	Conformational energy calculations on muramyl dipeptide. Biochemical Society Transactions, 1986, 14, 630-631.	1.6	0
76	The Concept of Novel Compositions of Matter: A Theoretical Analysis. Intellectual Property Rights Open Access, 2014, 2, .	0.1	0
77	Computer languages in pharmaceutical design. , 1997, , 494-562.		0