Barry Robson

List of Publications by Citations

74 papers	2,475 citations	22 h-index	49 g-index
80 ext. papers	2,685 ext. citations	10 avg, IF	5.06 L-index

#	Paper	IF	Citations
74	GOR method for predicting protein secondary structure from amino acid sequence. *Methods in Enzymology*, **1996**, 266, 540-53	1.7	854
73	An algorithm for secondary structure determination in proteins based on sequence similarity. *FEBS Letters*, **1986**, 205, 303-8	3.8	212
72	Data mining and clinical data repositories: Insights from a 667,000 patient data set. *Computers in Biology and Medicine*, **2006**, 36, 1351-77	7	124
71	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	4.2	89
70	What is a conservative substitution?. *Journal of Molecular Evolution*, **1983**, 19, 171-175	3.1	81
69	Refined models for computer simulation of protein folding. Applications to the study of conserved secondary structure and flexible hinge points during the folding of pancreatic trypsin inhibitor. *Journal of Molecular Biology*, **1979**, 132, 19-51	6.5	68
68	Analysis of the code relating sequence to secondary structure in proteins. *Nature*, **1970**, 227, 62-3	50.4	68
67	Analysis of code relating sequences to conformation in globular prtoeins. Theory and application of expected information. *Biochemical Journal*, **1974**, 141, 853-67	3.8	61
66	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, 1578-86	3.2	52
65	PRO-LIGAND: an approach to de novo molecular design. 3. A genetic algorithm for structure refinement. *Journal of Computer-Aided Molecular Design*, **1995**, 9, 139-48	4.2	51
64	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	8.3	50
63	Structural properties of signal peptides and their membrane insertion. *Biochimie*, **1980**, 62, 231-9	4.6	47
62	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, 869-82	3.8	39
61	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	3.8	31
60	PRO_LIGAND: an approach to de novo molecular design. 4. Application to the design of peptides. *Journal of Computer-Aided Molecular Design*, **1995**, 9, 213-25	4.2	29
59	Protein structure prediction. *Nature*, **1993**, 361, 506	50.4	28
58	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, 883-97	3.8	28

57	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		25
56	Suggestions for a Web based universal exchange and inference language for medicine. *Computers in Biology and Medicine*, **2013**, 43, 2297-310	7	24
55	Protein folding and heterogeneity inside globular proteins. *Nature*, **1978**, 272, 558-60	50.4	24
54	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	7	23
53	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	7	23
52	The dragon on the gold: myths and realities for data mining in biomedicine and biotechnology using digital and molecular libraries. *Journal of Proteome Research*, **2004**, 3, 1113-9	5.6	21
51	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	2.3	21
50	Hyperbolic Dirac Nets for medical decision support. Theory, methods, and comparison with Bayes Nets. *Computers in Biology and Medicine*, **2014**, 51, 183-97	7	20
49	Clinical and pharmacogenomic data mining: 3. Zeta theory as a general tactic for clinical bioinformatics. *Journal of Proteome Research*, **2005**, 4, 445-55	5.6	19
48	The new physician as unwitting quantum mechanic: is adapting Dirac's inference system best practice for personalized medicine, genomics, and proteomics?. *Journal of Proteome Research*, **2007**, 6, 3114-26	5.6	18
47	Reduced variable molecular dynamics. *Journal of Computational Chemistry*, **1995**, 16, 1271-1290	3.5	18
46	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	7	17
45	Computer-aided design and physiological testing of a luteinising hormone-releasing hormone analogue for adjuvant-free immunocastration. *FEBS Letters*, **1987**, 214, 65-70	3.8	16
44	Ab initio SCF-MO calculations on the architectural unit of peptides and protiens. *Journal of the Chemical Society, Faraday Transactions 2*, **1978**, 74, 1311		15
43	Split-complex numbers and Dirac bra-kets. *Communications in Information and Systems*, **2014**, 14, 135-159	0.8	15
42	POPPER, a simple programming language for probabilistic semantic inference in medicine. *Computers in Biology and Medicine*, **2015**, 56, 107-23	7	14
41	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	7	14
40	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, 427-41	4.2	12

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, 930-48	5.6	12
38	Clinical and pharmacogenomic data mining: 1. Generalized theory of expected information and application to the development of tools. *Journal of Proteome Research*, **2003**, 2, 283-302	5.6	12
37	Doppelgänger proteins as drug leads. *Nature Biotechnology*, **1996**, 14, 892-3	44.5	12
36	Studies in the assessment of folding quality for protein modeling and structure prediction. *Journal of Proteome Research*, **2002**, 1, 115-33	5.6	11
35	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, 219-25	3.8	11
34	Modelling of alpha-lactalbumin from the known structure of hen egg white lysozyme using molecular dynamics. *Journal of Computer-Aided Molecular Design*, **1987**, 1, 17-22	4.2	11
33	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	7	10
32	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, 3922-47	5.6	10
31	Bidirectional General Graphs for inference. Principles and implications for medicine. *Computers in Biology and Medicine*, **2019**, 108, 382-399	7	9
30	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	7	9
29	Protein folding revisited. *Progress in Molecular Biology and Translational Science*, **2008**, 84, 161-202	4	9
28	**2009**,		9
27	Clinical and pharmacogenomic data mining: 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	5.6	8
26	The design of biologically active polypeptides. *Critical Reviews in Biochemistry*, **1983**, 14, 273-96		7
25	Designing biologically active polypeptides. *Trends in Biochemical Sciences*, **1980**, 5, 240-244	10.3	7
24	Protein folding. *Trends in Biochemical Sciences*, **1976**, 1, 49-50	10.3	7
23	Studies of the role of a smart web for precision medicine supported by biobanking. *Personalized Medicine*, **2016**, 13, 361-380	2.2	6
22	The prediction of molecular conformation. *Biochemical Society Transactions*, **1982**, 10, 297-8	5.1	6

21	Considerations for a Universal Exchange Language for healthcare **2011**,		5
20	Genomic messaging system language including command extensions for clinical data categories. *Journal of Proteome Research*, **2005**, 4, 275-99	5.6	5
19	Artificial enzymes. *Biochemical Society Transactions*, **1987**, 15, 1191-3	5.1	5
18	Towards intelligent Internet-roaming agents for mining and inference from medical data. *Studies in Health Technology and Informatics*, **2009**, 149, 157-77	0.5	4
17	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
16	Simplified models of protein folding exploiting the Lagrange radius of gyration of the hydrophobic component. *Parallel Computing*, **2000**, 26, 977-998	1	3
15	Calculation of the conformation of glycosphingolipids: GM1- and GM2-gangliosides. *Biochemical Society Transactions*, **1986**, 14, 707-707	5.1	3
14	Conformational study of neurotensin and some of its analogues. *Biochemical Society Transactions*, **1986**, 14, 1259-1260	5.1	3
13	Towards New Tools for Pharmacoepidemiology. *Advances in Pharmacoepidemiology & Drug Safety*, **2012**, 01,		3
12	Towards Automated Reasoning for Drug Discovery and Pharmaceutical Business Intelligence. *Journal of Pharmaceutical Technology & Drug Research*, **2012**, 1, 3		3
11	De novo protein folding on computers. Benefits and challenges.. *Computers in Biology and Medicine*, **2022**, 143, 105292	7	2
10	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	7	2
9	Links between quantum physics and thought. *Studies in Health Technology and Informatics*, **2009**, 149, 236-48	0.5	2
8	Conformational energy calculations on the glycan chain of peptidoglycan. *Biochemical Society Transactions*, **1986**, 14, 629-630	5.1	1
7	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*, **2021**, 140, 105116	7	1
6	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*, **2021**, 141, 105118	7	1
5	Reduced variable molecular dynamics **1997**, 122-149		1
4	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	7	1

3	Conformational energy calculations on muramyl dipeptide. *Biochemical Society Transactions*, **1986**, 14, 630-631	5.1
2	Ribonuclease still under attack. *Nature*, **1980**, 283, 622	50.4
1	Computer languages in pharmaceutical design **1997**, 494-562	