Ross King

List of Publications by Year
in descending order

32 papers	2,810 citations	331670 21 h-index	414414 32 g-index
32 all docs	32 docs citations	32 times ranked	2830 citing authors

#	Article	IF	Citations
1	Functional genomic hypothesis generation and experimentation by a robot scientist. Nature, 2004, 427, 247-252.	27.8	481
2	The Automation of Science. Science, 2009, 324, 85-89.	12.6	458
3	Hierarchical metabolomics demonstrates substantial compositional similarity between genetically modified and conventional potato crops. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14458-14462.	7.1	367
4	STATLOG: COMPARISON OF CLASSIFICATION ALGORITHMS ON LARGE REAL-WORLD PROBLEMS. Applied Artificial Intelligence, 1995, 9, 289-333.	3.2	234
5	Structure-activity relationships derived by machine learning: the use of atoms and their bond connectivities to predict mutagenicity by inductive logic programming.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 438-442.	7.1	211
6	An ontology of scientific experiments. Journal of the Royal Society Interface, 2006, 3, 795-803.	3.4	147
7	Towards Robot Scientists for autonomous scientific discovery. Automated Experimentation, 2010, 2, 1.	2.0	101
8	Machine learning approach for the prediction of protein secondary structure. Journal of Molecular Biology, 1990, 216, 441-457.	4.2	100
9	Cheaper faster drug development validated by the repositioning of drugs against neglected tropical diseases. Journal of the Royal Society Interface, 2015, 12, 20141289.	3.4	97
10	On the optimization of classes for the assignment of unidentified reading frames in functional genomics programmes: the need for machine learning. Trends in Biotechnology, 2000, 18, 93-98.	9.3	78
11	Are the current ontologies in biology good ontologies?. Nature Biotechnology, 2005, 23, 1095-1098.	17.5	66
12	Relating chemical activity to structure: An examination of ILP successes. New Generation Computing, 1995, 13, 411-433.	3.3	65
13	New Approach to Pharmacophore Mapping and QSAR Analysis Using Inductive Logic Programming. Application to Thermolysin Inhibitors and Glycogen Phosphorylase b Inhibitors. Journal of Medicinal Chemistry, 2002, 45, 399-409.	6.4	57
14	Merits of random forests emerge in evaluation of chemometric classifiers by external validation. Analytica Chimica Acta, 2013, 801, 22-33.	5.4	34
15	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. Open Biology, 2013, 3, 120158.	3.6	32
16	Plasmodium dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. Scientific Reports, 2018, 8, 1038.	3.3	31
17	COMPARISON OF ARTIFICIAL INTELLIGENCE METHODS FOR MODELING PHARMACEUTICAL QSARS. Applied Artificial Intelligence, 1995, 9, 213-233.	3.2	30
18	Computing exponentially faster: implementing a non-deterministic universal Turing machine using DNA. Journal of the Royal Society Interface, 2017, 14, 20160990.	3.4	30

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19	Functional Expression of Parasite Drug Targets and Their Human Orthologs in Yeast. PLoS Neglected Tropical Diseases, 2011, 5, e1320.	3.0	29
20	New approaches to QSAR: Neural networks and machine learning. Journal of Computer - Aided Molecular Design, 1993, 1, 279-290.	1.0	26
21	Enhancement of Plant Metabolite Fingerprinting by Machine Learning Â. Plant Physiology, 2010, 153, 1506-1520.	4.8	24
22	Closed-loop cycles of experiment design, execution, and learning accelerate systems biology model development in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18142-18147.	7.1	19
23	Modeling quantitative structure–property relationships in calculated reaction pathways using a new 3D quantum topological representation. Analytica Chimica Acta, 2001, 446, 3-13.	5.4	15
24	Intelligent software for laboratory automation. Trends in Biotechnology, 2004, 22, 440-445.	9.3	15
25	On the formalization and reuse of scientific research. Journal of the Royal Society Interface, 2011, 8, 1440-1448.	3.4	15
26	Finding Motifs in Protein Secondary Structure for Use in Function Prediction. Journal of Computational Biology, 2006, 13, 719-731.	1.6	14
27	Quantitative pharmacophore models with inductive logic programming. Machine Learning, 2006, 64, 65-90.	5.4	12
28	Transformational machine learning: Learning how to learn from many related scientific problems. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
29	The Use of Weighted Graphs for Large-Scale Genome Analysis. PLoS ONE, 2014, 9, e89618.	2.5	4
30	Predicting rice phenotypes with meta and multi-target learning. Machine Learning, 2020, 109, 2195-2212.	5.4	3
31	Testing the reproducibility and robustness of the cancer biology literature by robot. Journal of the Royal Society Interface, 2022, 19, 20210821.	3.4	2
32	A simple spatial extension to the extended connectivity interaction features for binding affinity prediction. Royal Society Open Science, 2022, 9, 211745.	2.4	2