Ross King

List of Publications by Year
in descending order

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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	Testing the reproducibility and robustness of the cancer biology literature by robot. Journal of the Royal Society Interface, 2022, 19, 20210821.	3.4	2
2	A simple spatial extension to the extended connectivity interaction features for binding affinity prediction. Royal Society Open Science, 2022, 9, 211745.	2.4	2
3	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
4	Predicting rice phenotypes with meta and multi-target learning. Machine Learning, 2020, 109, 2195-2212.	5.4	3
5	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
6	Plasmodium dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. Scientific Reports, 2018, 8, 1038.	3.3	31
7	Computing exponentially faster: implementing a non-deterministic universal Turing machine using DNA. Journal of the Royal Society Interface, 2017, 14, 20160990.	3.4	30
8	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
9	The Use of Weighted Graphs for Large-Scale Genome Analysis. PLoS ONE, 2014, 9, e89618.	2.5	4
10	Merits of random forests emerge in evaluation of chemometric classifiers by external validation. Analytica Chimica Acta, 2013, 801, 22-33.	5.4	34
11	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. Open Biology, 2013, 3, 120158.	3.6	32
12	On the formalization and reuse of scientific research. Journal of the Royal Society Interface, 2011, 8, 1440-1448.	3.4	15
13	Functional Expression of Parasite Drug Targets and Their Human Orthologs in Yeast. PLoS Neglected Tropical Diseases, 2011, 5, e1320.	3.0	29
14	Towards Robot Scientists for autonomous scientific discovery. Automated Experimentation, 2010, 2, 1.	2.0	101
15	Enhancement of Plant Metabolite Fingerprinting by Machine Learning Â. Plant Physiology, 2010, 153, 1506-1520.	4.8	24
16	The Automation of Science. Science, 2009, 324, 85-89.	12.6	458
17	Finding Motifs in Protein Secondary Structure for Use in Function Prediction. Journal of Computational Biology, 2006, 13, 719-731.	1.6	14
18	An ontology of scientific experiments. Journal of the Royal Society Interface, 2006, 3, 795-803.	3.4	147

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19	Quantitative pharmacophore models with inductive logic programming. Machine Learning, 2006, 64, 65-90.	5.4	12
20	Are the current ontologies in biology good ontologies?. Nature Biotechnology, 2005, 23, 1095-1098.	17.5	66
21	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
22	Functional genomic hypothesis generation and experimentation by a robot scientist. Nature, 2004, 427, 247-252.	27.8	481
23	Intelligent software for laboratory automation. Trends in Biotechnology, 2004, 22, 440-445.	9.3	15
24	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
25	Modeling quantitative structureâ€“property relationships in calculated reaction pathways using a new 3D quantum topological representation. Analytica Chimica Acta, 2001, 446, 3-13.	5.4	15
26	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
27	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
28	STATLOG: COMPARISON OF CLASSIFICATION ALGORITHMS ON LARGE REAL-WORLD PROBLEMS. Applied Artificial Intelligence, 1995, 9, 289-333.	3.2	234
29	Relating chemical activity to structure: An examination of ILP successes. New Generation Computing, 1995, 13, 411-433.	3.3	65
30	COMPARISON OF ARTIFICIAL INTELLIGENCE METHODS FOR MODELING PHARMACEUTICAL QSARS. Applied Artificial Intelligence, 1995, 9, 213-233.	3.2	30
31	New approaches to QSAR: Neural networks and machine learning. Journal of Computer - Aided Molecular Design, 1993, 1, 279-290.	1.0	26
32	Machine learning approach for the prediction of protein secondary structure. Journal of Molecular Biology, 1990, 216, 441-457.	4.2	100