

Iain M Wallace

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

29,254
citations

430442

18
h-index

476904

29
g-index

32
all docs

32
docs citations

32
times ranked

48503
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of a small molecule RFXP3/4 agonist that increases food intake in rats upon acute central administration. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019, 29, 991-994.	1.0	19
2	CHEMGENIE: integration of chemogenomics data for applications in chemical biology. <i>Drug Discovery Today</i> , 2018, 23, 151-160.	3.2	13
3	Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles. <i>ACS Central Science</i> , 2016, 2, 687-701.	5.3	68
4	Dark chemical matter as a promising starting point for drug lead discovery. <i>Nature Chemical Biology</i> , 2015, 11, 958-966.	3.9	110
5	Application of Titration-Based Screening for the Rapid Pilot Testing of High-Throughput Assays. <i>Journal of Biomolecular Screening</i> , 2014, 19, 651-660.	2.6	11
6	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217
7	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39
8	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1375-1387.	0.8	5
9	Target Prediction for an Open Access Set of Compounds Active against <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1003253.	1.5	51
10	A phenotypic screening platform to identify small molecule modulators of <i>Chlamydomonas reinhardtii</i> growth, motility and photosynthesis. <i>Genome Biology</i> , 2012, 13, R105.	13.9	15
11	Displaying Chemical Information on a Biological Network Using Cytoscape. <i>Methods in Molecular Biology</i> , 2011, 781, 363-376.	0.4	7
12	Dafadine inhibits DAF-9 to promote dauer formation and longevity of <i>Caenorhabditis elegans</i> . <i>Nature Chemical Biology</i> , 2011, 7, 891-893.	3.9	27
13	Design, Synthesis and Characterization of a Highly Effective Inhibitor for Analog-Sensitive (as) Kinases. <i>PLoS ONE</i> , 2011, 6, e20789.	1.1	7
14	Compound Prioritization Methods Increase Rates of Chemical Probe Discovery in Model Organisms. <i>Chemistry and Biology</i> , 2011, 18, 1273-1283.	6.2	41
15	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	6.0	1,937
16	A predictive model for drug bioaccumulation and bioactivity in <i>Caenorhabditis elegans</i> . <i>Nature Chemical Biology</i> , 2010, 6, 549-557.	3.9	164
17	Highly-multiplexed barcode sequencing: an efficient method for parallel analysis of pooled samples. <i>Nucleic Acids Research</i> , 2010, 38, e142-e142.	6.5	184
18	Fast embedding methods for clustering tens of thousands of sequences. <i>Computational Biology and Chemistry</i> , 2008, 32, 282-286.	1.1	4

#	ARTICLE	IF	CITATIONS
19	An integrated platform of genomic assays reveals small-molecule bioactivities. <i>Nature Chemical Biology</i> , 2008, 4, 498-506.	3.9	178
20	The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods. <i>Nucleic Acids Research</i> , 2007, 35, W645-W648.	6.5	209
21	Evolution of specificity and diversity. , 2007, , 225-235.		1
22	Clustal W and Clustal X version 2.0. <i>Bioinformatics</i> , 2007, 23, 2947-2948.	1.8	25,174
23	Supervised multivariate analysis of sequence groups to identify specificity determining residues. <i>BMC Bioinformatics</i> , 2007, 8, 135.	1.2	24
24	M-Coffee: combining multiple sequence alignment methods with T-Coffee. <i>Nucleic Acids Research</i> , 2006, 34, 1692-1699.	6.5	533
25	Analysis and comparison of benchmarks for multiple sequence alignment. <i>In Silico Biology</i> , 2006, 6, 321-39.	0.4	46
26	Multiple sequence alignments. <i>Current Opinion in Structural Biology</i> , 2005, 15, 261-266.	2.6	94
27	Mind the gaps: Progress in progressive alignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10411-10412.	3.3	19
28	Evaluation of iterative alignment algorithms for multiple alignment. <i>Bioinformatics</i> , 2005, 21, 1408-1414.	1.8	52