

Jadwiga Bienkowska

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

895
citations

933447

10
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

1207
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemotherapy induces dynamic immune responses in breast cancers that impact treatment outcome. Nature Communications, 2020, 11, 6175.	12.8	92
2	PINCER: improved CRISPR/Cas9 screening by efficient cleavage at conserved residues. Nucleic Acids Research, 2020, 48, 9462-9477.	14.5	6
3	Discovering What Dimensionality Reduction Really Tells Us About RNA-Seq Data. Journal of Computational Biology, 2015, 22, 715-728.	1.6	9
4	Lymphotoxin-LIGHT Pathway Regulates the Interferon Signature in Rheumatoid Arthritis. PLoS ONE, 2014, 9, e112545.	2.5	40
5	Optimization of a high-throughput whole blood expression profiling methodology and its application to assess the pharmacodynamics of interferon (IFN) beta-1a or polyethylene glycol-conjugated IFN beta-1a in healthy clinical trial subjects. BMC Research Notes, 2013, 6, 8.	1.4	12
6	A computational framework for boosting confidence in high-throughput protein-protein interaction datasets. Genome Biology, 2012, 13, R76.	9.6	44
7	iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. Journal of Molecular Biology, 2011, 405, 1295-1310.	4.2	56
8	LTHREADER: Prediction of extracellular ligand-receptor interactions in cytokines using localized threading. Protein Science, 2008, 17, 279-292.	7.6	8
9	Experimental comparison and cross-validation of Affymetrix HT plate and cartridge array gene expression platforms. Genomics, 2008, 92, 359-365.	2.9	3
10	Optimal contact map alignment of protein-protein interfaces. Bioinformatics, 2008, 24, 2324-2328.	4.1	24
11	LTHREADER: PREDICTION OF LIGAND-RECEPTOR INTERACTIONS USING LOCALIZED THREADING. , 2006, , .		0
12	Threading algorithms. , 2005, , .		2
13	List of contributors* *Authors' names are followed by the starting page number(s) of their contribution(s).. New Comprehensive Biochemistry, 1998, 32, xi-xiii.	0.1	0
14	Analysis and algorithms for protein sequence-structure alignment. New Comprehensive Biochemistry, 1998, 32, 227-283.	0.1	16
15	Current Limitations to Protein Threading Approaches. Journal of Computational Biology, 1997, 4, 217-225.	1.6	40
16	Biology's new Rosetta stone. Nature, 1997, 385, 29-30.	27.8	56
17	Crystal structure of the zeta isoform of the 14-3-3 protein. Nature, 1995, 376, 191-194.	27.8	487