

Matthew A Young

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

3,689
citations

361413

20
h-index

552781

26
g-index

28
all docs

28
docs citations

28
times ranked

4348
citing authors

#	ARTICLE	IF	CITATIONS
1	Mg ²⁺ regulation of kinase signaling and immune function. <i>Journal of Experimental Medicine</i> , 2019, 216, 1828-1842.	8.5	37
2	Kinase-Independent Small-Molecule Inhibition of JAK-STAT Signaling. <i>Journal of the American Chemical Society</i> , 2015, 137, 7929-7934.	13.7	29
3	Targeting deubiquitinase activity with a novel small-molecule inhibitor as therapy for B-cell malignancies. <i>Blood</i> , 2015, 125, 3588-3597.	1.4	104
4	Emerging Potential of Therapeutic Targeting of Ubiquitin-Specific Proteases in the Treatment of Cancer. <i>Cancer Research</i> , 2014, 74, 4955-4966.	0.9	159
5	Degrasyn-like symmetrical compounds: Possible therapeutic agents for multiple myeloma (MM-I). <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 1450-1458.	3.0	12
6	Price To Be Paid for Two-Metal Catalysis: Magnesium Ions That Accelerate Chemistry Unavoidably Limit Product Release from a Protein Kinase. <i>Journal of the American Chemical Society</i> , 2012, 134, 15357-15370.	13.7	67
7	Briefly Bound to Activate: Transient Binding of a Second Catalytic Magnesium Activates the Structure and Dynamics of CDK2 Kinase for Catalysis. <i>Structure</i> , 2011, 19, 675-690.	3.3	93
8	Structure of a Thyroid Hormone Receptor DNA-Binding Domain Homodimer Bound to an Inverted Palindrome DNA Response Element. <i>Molecular Endocrinology</i> , 2010, 24, 1650-1664.	3.7	29
9	Improved enrichment strategies for phosphorylated peptides on titanium dioxide using methyl esterification and pH gradient elution. <i>Analytical Biochemistry</i> , 2008, 377, 234-242.	2.4	45
10	Regulation of luteinizing hormone receptor mRNA expression by mevalonate kinase – role of the catalytic center in mRNA recognition. <i>FEBS Journal</i> , 2008, 275, 3397-3407.	4.7	14
11	A Src-Like Inactive Conformation in the Abl Tyrosine Kinase Domain. <i>PLoS Biology</i> , 2006, 4, e144.	5.6	277
12	Structure of the Kinase Domain of an Imatinib-Resistant Abl Mutant in Complex with the Aurora Kinase Inhibitor VX-680. <i>Cancer Research</i> , 2006, 66, 1007-1014.	0.9	282
13	High yield bacterial expression of active c-Abl and c-Src tyrosine kinases. <i>Protein Science</i> , 2005, 14, 3135-3139.	7.6	206
14	Molecular Dynamics Simulations of the 136 Unique Tetranucleotide Sequences of DNA Oligonucleotides. I. Research Design and Results on d(CpG) Steps. <i>Biophysical Journal</i> , 2004, 87, 3799-3813.	0.5	245
15	Assessment of the molecular dynamics structure of DNA in solution based on calculated and observed NMR NOESY volumes and dihedral angles from scalar coupling constants. <i>Biopolymers</i> , 2003, 68, 3-15.	2.4	38
16	Structural Basis for the Autoinhibition of c-Abl Tyrosine Kinase. <i>Cell</i> , 2003, 112, 859-871.	28.9	762
17	Characterization of potent inhibitors of the Bcr-Abl and the c-kit receptor tyrosine kinases. <i>Cancer Research</i> , 2002, 62, 4244-55.	0.9	131
18	Dynamic Coupling between the SH2 and SH3 Domains of c-Src and Hck Underlies Their Inactivation by C-Terminal Tyrosine Phosphorylation. <i>Cell</i> , 2001, 105, 115-126.	28.9	366

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19	Molecular dynamics simulation reveals sequence-intrinsic and protein-induced geometrical features of the OL1 DNA operator. <i>Biopolymers</i> , 2001, 59, 205-225.	2.4	6
20	One nanosecond molecular dynamics simulation of the N-terminal domain of the λ repressor protein. <i>Biopolymers</i> , 2000, 53, 596-605.	2.4	11
21	Molecular dynamics simulation accurately predicts the experimentally-observed distributions of the (C, N, O) protein atoms around water molecules and sodium ions. , 2000, 39, 212-215.		5
22	Molecular dynamics simulation of nucleic acids: Successes, limitations, and promise. <i>Biopolymers</i> , 2000, 56, 232-256.	2.4	307
23	Molecular dynamics simulation of nucleic acids: Successes, limitations, and promise* . , 2000, 56, 232.		3
24	Molecular dynamics simulation of nucleic acids: Successes, limitations, and promise* We would like to dedicate this article to Peter Kollman, a friend, collaborator, mentor, and all around good guy. Peter was very enthusiastic about DNA simulation; he will be sorely missed.. <i>Biopolymers</i> , 2000, 56, 232.	2.4	5
25	Molecular Dynamics Information Extraction. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1999, , 127-147.	0.5	1
26	Conformational Properties of the TATA-Box Binding Sequence of DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 757-765.	3.5	44
27	Intrusion of Counterions into the Spine of Hydration in the Minor Groove of B-DNA: Fractional Occupancy of Electronegative Pockets. <i>Journal of the American Chemical Society</i> , 1997, 119, 59-69.	13.7	379
28	[5] Structure determination and analysis of local bending in an A-tract DNA duplex: Comparison of results from crystallography, nuclear magnetic resonance, and molecular dynamics simulation on d(CGCAAAAATGCG). <i>Methods in Enzymology</i> , 1995, 261, 121-144.	1.0	32