

Blaine H M Mooers

List of Publications by Year in descending order

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48
papers

1,663
citations

304743

22
h-index

302126

39
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49
all docs

49
docs citations

49
times ranked

1837
citing authors

#	ARTICLE	IF	CITATIONS
1	Coupling of acceptor-substituted diazo compounds and tertiary thioamides: synthesis of enamino carbonyl compounds and their pharmacological evaluation. <i>RSC Advances</i> , 2022, 12, 19431-19444.	3.6	1
2	Structural basis of acquired resistance to selpercatinib and pralsetinib mediated by non-gatekeeper RET mutations. <i>Annals of Oncology</i> , 2021, 32, 261-268.	1.2	143
3	Templates for writing <sc>PyMOL</sc> scripts. <i>Protein Science</i> , 2021, 30, 262-269.	7.6	29
4	Modernizing computing by structural biologists with Jupyter and Colab. , 2021, , .		0
5	A PyMOL Snippet Library for Jupyter to Boost Researcher Productivity. <i>Computing in Science and Engineering</i> , 2021, 23, 47-53.	1.2	2
6	The L730V/I RET roof mutations display different activities toward pralsetinib and selpercatinib. <i>Npj Precision Oncology</i> , 2021, 5, 48.	5.4	30
7	Simulations of Promising Indolizidineâ€” ± 6 - \hat{I}^2 Nicotinic Acetylcholine Receptor Complexes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7934.	4.1	1
8	Engineering Crystal Packing in RNA Structures I: Past and Future Strategies for Engineering RNA Packing in Crystals. <i>Crystals</i> , 2021, 11, 952.	2.2	7
9	Precision therapy for RET-altered cancers with RET inhibitors. <i>Trends in Cancer</i> , 2021, 7, 1074-1088.	7.4	87
10	Shortcuts for faster image creation in PyMOL. <i>Protein Science</i> , 2020, 29, 268-276.	7.6	87
11	SRSF1 regulates exosome microRNA enrichment in human cancer cells. <i>Cell Communication and Signaling</i> , 2020, 18, 130.	6.5	23
12	RET kinase alterations in targeted cancer therapy. , 2020, 3, 472-481.		7
13	Structural basis of resistance of mutant RET protein-tyrosine kinase to its inhibitors nintedanib and vandetanib. <i>Journal of Biological Chemistry</i> , 2019, 294, 10428-10437.	3.4	43
14	Protein features for assembly of the RNA editing helicase 2 subcomplex (REH2C) in Trypanosome holo-editosomes. <i>PLoS ONE</i> , 2019, 14, e0211525.	2.5	4
15	Cover Image, Volume 9, Issue 6. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1517.	6.4	0
16	Dynamic RNA holoâ€”editosomes with subcomplex variants: Insights into the control of trypanosome editing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1502.	6.4	24
17	Drug resistance profiles of mutations in the RET kinase domain. <i>British Journal of Pharmacology</i> , 2018, 175, 3504-3515.	5.4	61
18	Control Mechanisms of the Holo-Editosome in Trypanosomes. <i>Nucleic Acids and Molecular Biology</i> , 2018, , 125-144.	0.2	3

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19	REH2C Helicase and GRBC Subcomplexes May Base Pair through mRNA and Small Guide RNA in Kinetoplastid Editosomes. <i>Journal of Biological Chemistry</i> , 2016, 291, 5753-5764.	3.4	22
20	Simplifying and enhancing the use of PyMOL with horizontal scripts. <i>Protein Science</i> , 2016, 25, 1873-1882.	7.6	35
21	Direct-methods structure determination of a trypanosome RNA-editing substrate fragment with translational pseudosymmetry. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 477-487.	2.3	5
22	DEAH-RHA helicaseâ€Znf cofactor systems in kinetoplastid RNA editing and evolutionarily distant RNA processes. <i>RNA & Disease (Houston, Tex)</i> , 2016, 3, .	1.0	3
23	Structures and Energetics of Four Adjacent GÂ-U Pairs That Stabilize an RNA Helix. <i>Journal of Physical Chemistry B</i> , 2015, 119, 13252-13261.	2.6	17
24	Human Î³-Glutamyl Transpeptidase 1. <i>Journal of Biological Chemistry</i> , 2015, 290, 17576-17586.	3.4	53
25	Fusion RNAs in Crystallographic Studies of Double-Stranded RNA from Trypanosome RNA Editing. <i>Methods in Molecular Biology</i> , 2015, 1240, 191-216.	0.9	1
26	Native Variants of the MRB1 Complex Exhibit Specialized Functions in Kinetoplastid RNA Editing. <i>PLoS ONE</i> , 2015, 10, e0123441.	2.5	19
27	Structural Studies of a Double-Stranded RNA from Trypanosome RNA Editing by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2015, 1240, 165-189.	0.9	2
28	Novel insights into eukaryotic Î³-glutamyltranspeptidase 1 from the crystal structure of the glutamate-bound human enzyme.. <i>Journal of Biological Chemistry</i> , 2014, 289, 11569.	3.4	0
29	After Embedding in Membranes Antiapoptotic Bcl-XL Protein Binds Both Bcl-2 Homology Region 3 and Helix 1 of Proapoptotic Bax Protein to Inhibit Apoptotic Mitochondrial Permeabilization. <i>Journal of Biological Chemistry</i> , 2014, 289, 11873-11896.	3.4	61
30	Glycosylation of Skp1 Affects Its Conformation and Promotes Binding to a Model F-Box Protein. <i>Biochemistry</i> , 2014, 53, 1657-1669.	2.5	42
31	Native mitochondrial RNA-binding complexes in kinetoplastid RNA editing differ in guide RNA composition. <i>Rna</i> , 2014, 20, 1142-1152.	3.5	31
32	Novel Insights into Eukaryotic Î³-Glutamyltranspeptidase 1 from the Crystal Structure of the Glutamate-bound Human Enzyme. <i>Journal of Biological Chemistry</i> , 2013, 288, 31902-31913.	3.4	66
33	Crystal structure of a new benzoic acid inhibitor of influenza neuraminidase bound with a new tilt induced by overpacking subsite C6. <i>BMC Structural Biology</i> , 2012, 12, 7.	2.3	11
34	The crystal structure of an oligo(U):pre-mRNA duplex from a trypanosome RNA editing substrate. <i>Rna</i> , 2011, 17, 1870-1883.	3.5	23
35	Evaluation at atomic resolution of the role of strain in destabilizing the temperatureâ€sensitive T4 lysozyme mutant Arg 96 â† His. <i>Protein Science</i> , 2009, 18, 863-870.	7.6	12
36	Contributions of all 20 amino acids at site 96 to the stability and structure of T4 lysozyme. <i>Protein Science</i> , 2009, 18, 871-880.	7.6	23

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37	Crystallographic studies of DNA and RNA. <i>Methods</i> , 2009, 47, 168-176.	3.8	34
38	Extension to 2268 atoms of direct methods in the determination of the unknown structure of bacteriophage P22 lysozyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 165-176.	2.5	22
39	The structural basis of myotonic dystrophy from the crystal structure of CUG repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16626-16631.	7.1	161
40	Use of an ion-binding site to bypass the 1000-atom limit to structure determination by direct methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1726-1737.	2.5	9
41	Relocation or Duplication of the Helix A Sequence of T4 Lysozyme Causes Only Modest Changes in Structure but Can Increase or Decrease the Rate of Folding. <i>Biochemistry</i> , 2004, 43, 1296-1301.	2.5	13
42	Repacking the Core of T4 Lysozyme by Automated Design. <i>Journal of Molecular Biology</i> , 2003, 332, 741-756.	4.2	54
43	Multiple methionine substitutions are tolerated in T4 lysozyme and have coupled effects on folding and stability. <i>Biophysical Chemistry</i> , 2002, 100, 325-340.	2.8	16
44	The crystal structures of psoralen cross-linked DNAs: drug-dependent formation of Holliday junctions. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2001, 308, 15-26.	4.2	48
45	The Holliday junction in an inverted repeat DNA sequence: Sequence effects on the structure of four-way junctions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3971-3976.	7.1	232
46	The structures and relative stabilities of d(G $\hat{\cdot}$ G) reverse Hoogsteen, d(G $\hat{\cdot}$ T) reverse wobble, and d(G $\hat{\cdot}$ C) reverse Watson-Crick base-pairs in DNA crystals. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1997, 269, 796-810.	4.2	17
47	Z-DNA crystallography. <i>Journal of Molecular Biology</i> , 1997, 44, 65-90.		34
48	Alternating and Non-alternating dG-dC Hexanucleotides Crystallize as Canonical A-DNA. <i>Journal of Molecular Biology</i> , 1995, 249, 772-784.	4.2	45