

Ethan A Merritt

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60
papers

7,962
citations

33
h-index

60
g-index

60
ext. papers

8,444
ext. citations

6.1
avg, IF

6.02
L-index

#	Paper	IF	Citations
60	Methionyl-tRNA synthetase inhibitor has potent in vivo activity in a novel Giardia lamblia luciferase murine infection model. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 1218-1227	5.1	5
59	Nek8445, a protein kinase required for microtubule regulation and cytokinesis in. <i>Molecular Biology of the Cell</i> , 2020 , 31, 1611-1622	3.5	14
58	A Combined Approach Reveals a Regulatory Mechanism Coupling Src4 Kinase Activity, Localization, and Phosphotransferase-Independent Functions. <i>Molecular Cell</i> , 2019 , 74, 393-408.e20	17.6	20
57	Toxoplasma Calcium-Dependent Protein Kinase 1 Inhibitors: Probing Activity and Resistance Using Cellular Thermal Shift Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	11
56	7 H-Pyrrolo[2,3- d]pyrimidin-4-amine-Based Inhibitors of Calcium-Dependent Protein Kinase 1 Have Distinct Inhibitory and Oral Pharmacokinetic Characteristics Compared with 1 H-Pyrazolo[3,4- d]pyrimidin-4-amine-Based Inhibitors. <i>ACS Infectious Diseases</i> , 2018 , 4, 516-522	5.5	5
55	Screening of the Pathogen Box for inhibitors with dual efficacy against Giardia lamblia and Cryptosporidium parvum. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006673	4.8	23
54	Extended-spectrum antiprotozoal bumped kinase inhibitors: A review. <i>Experimental Parasitology</i> , 2017 , 180, 71-83	2.1	39
53	Development of an Orally Available and Central Nervous System (CNS) Penetrant Toxoplasma gondii Calcium-Dependent Protein Kinase 1 (TgCDPK1) Inhibitor with Minimal Human Ether-a-go-go-Related Gene (hERG) Activity for the Treatment of Toxoplasmosis. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 6531-46	8.3	68
52	Identification and Validation of Small-Gatekeeper Kinases as Drug Targets in Giardia lamblia. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0005107	4.8	13
51	SAR Studies of 5-Aminopyrazole-4-carboxamide Analogues as Potent and Selective Inhibitors of CDPK1. <i>ACS Medicinal Chemistry Letters</i> , 2015 , 6, 1184-1189	4.3	27
50	Potent and selective inhibitors of CDPK1 from and based on a 5-aminopyrazole-4-carboxamide scaffold. <i>ACS Medicinal Chemistry Letters</i> , 2014 , 5, 40-44	4.3	42
49	Development of potent and selective Plasmodium falciparum calcium-dependent protein kinase 4 (PfCDPK4) inhibitors that block the transmission of malaria to mosquitoes. <i>European Journal of Medicinal Chemistry</i> , 2014 , 74, 562-73	6.8	44
48	The gatekeeper residue and beyond: homologous calcium-dependent protein kinases as drug development targets for veterinarian Apicomplexa parasites. <i>Parasitology</i> , 2014 , 141, 1499-1509	2.7	40
47	Neospora caninum calcium-dependent protein kinase 1 is an effective drug target for neosporosis therapy. <i>PLoS ONE</i> , 2014 , 9, e92929	3.7	48
46	Calcium-Dependent Protein Kinases of Apicomplexan Parasites as Drug Targets 2013 , 293-316		1
45	To B or not to B: a question of resolution?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 468-77		47
44	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen Giardia lamblia. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 1194-200		8

43	Multiple determinants for selective inhibition of apicomplexan calcium-dependent protein kinase CDPK1. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 2803-10	8.3	56
42	Benzoylbenzimidazole-based selective inhibitors targeting <i>Cryptosporidium parvum</i> and <i>Toxoplasma gondii</i> calcium-dependent protein kinase-1. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012 , 22, 5264-7	2.9	38
41	Development of <i>Toxoplasma gondii</i> calcium-dependent protein kinase 1 (TgCDPK1) inhibitors with potent anti-toxoplasma activity. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 2416-26	8.3	88
40	Transmission of malaria to mosquitoes blocked by bumped kinase inhibitors. <i>Journal of Clinical Investigation</i> , 2012 , 122, 2301-5	15.9	81
39	Structure of <i>Leishmania major</i> methionyl-tRNA synthetase in complex with intermediate products methionyladenylate and pyrophosphate. <i>Biochimie</i> , 2011 , 93, 570-82	4.6	36
38	The double-length tyrosyl-tRNA synthetase from the eukaryote <i>Leishmania major</i> forms an intrinsically asymmetric pseudo-dimer. <i>Journal of Molecular Biology</i> , 2011 , 409, 159-76	6.5	30
37	Structure determination of glycogen synthase kinase-3 from <i>Leishmania major</i> and comparative inhibitor structure-activity relationships with <i>Trypanosoma brucei</i> GSK-3. <i>Molecular and Biochemical Parasitology</i> , 2011 , 176, 98-108	1.9	32
36	Crystal structures of three protozoan homologs of tryptophanyl-tRNA synthetase. <i>Molecular and Biochemical Parasitology</i> , 2011 , 177, 20-8	1.9	13
35	Some B(eq) are more equivalent than others. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011 , 67, 512-6		9
34	Discovery of Potent and Selective Inhibitors of Calcium-Dependent Protein Kinase 1 (CDPK1) from <i>C. parvum</i> and <i>T. gondii</i> . <i>ACS Medicinal Chemistry Letters</i> , 2010 , 1, 331-335	4.3	110
33	The crystal structure and activity of a putative trypanosomal nucleoside phosphorylase reveal it to be a homodimeric uridine phosphorylase. <i>Journal of Molecular Biology</i> , 2010 , 396, 1244-59	6.5	14
32	Crystal structures of trypanosomal histidyl-tRNA synthetase illuminate differences between eukaryotic and prokaryotic homologs. <i>Journal of Molecular Biology</i> , 2010 , 397, 481-94	6.5	32
31	<i>Toxoplasma gondii</i> calcium-dependent protein kinase 1 is a target for selective kinase inhibitors. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 602-7	17.6	144
30	Crystal structure of the aspartyl-tRNA synthetase from <i>Entamoeba histolytica</i> . <i>Molecular and Biochemical Parasitology</i> , 2010 , 169, 95-100	1.9	13
29	Atomic resolution studies of carbonic anhydrase II. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 616-27		35
28	Validation of crystallographic models containing TLS or other descriptions of anisotropy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 889-900		45
27	<i>Toxoplasma gondii</i> cathepsin L is the primary target of the invasion-inhibitory compound morpholinurea-leucyl-homophenyl-vinyl sulfone phenyl. <i>Journal of Biological Chemistry</i> , 2009 , 284, 26839-40	5.4	48
26	Structures of substrate- and inhibitor-bound adenosine deaminase from a human malaria parasite show a dramatic conformational change and shed light on drug selectivity. <i>Journal of Molecular Biology</i> , 2008 , 381, 975-88	6.5	28

25	Structure of a Trypanosoma brucei alpha/beta-hydrolase fold protein with unknown function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 474-8		4
24	HingeMaster: normal mode hinge prediction approach and integration of complementary predictors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 299-319	4.2	35
23	Optimal description of a protein structure in terms of multiple groups undergoing TLS motion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 439-50		1077
22	TLSMDweb server for the generation of multi-group TLS models. <i>Journal of Applied Crystallography</i> , 2006 , 39, 109-111	3.8	606
21	Structural biology and structure-based inhibitor design of cholera toxin and heat-labile enterotoxin. <i>International Journal of Medical Microbiology</i> , 2004 , 294, 217-23	3.7	31
20	Anchor-based design of improved cholera toxin and E. coli heat-labile enterotoxin receptor binding antagonists that display multiple binding modes. <i>Chemistry and Biology</i> , 2002 , 9, 215-24		39
19	Characterization and crystal structure of a high-affinity pentavalent receptor-binding inhibitor for cholera toxin and E. coli heat-labile enterotoxin. <i>Journal of the American Chemical Society</i> , 2002 , 124, 8818-24	16.4	122
18	Solution and crystallographic studies of branched multivalent ligands that inhibit the receptor-binding of cholera toxin. <i>Journal of the American Chemical Society</i> , 2002 , 124, 12991-8	16.4	114
17	Exploration of the GM1 receptor-binding site of heat-labile enterotoxin and cholera toxin by phenyl-ring-containing galactose derivatives. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 201-12		29
16	Structure of m-carboxyphenyl-alpha-D-galactopyranoside complexed to heat-labile enterotoxin at 1.3 Å resolution: surprising variations in ligand-binding modes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 795-804		8
15	AB(5) toxins: structures and inhibitor design. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 680-6	8.1	111
14	Expanding the model: anisotropic displacement parameters in protein structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1109-17		106
13	Structure-based discovery of a pore-binding ligand: towards assembly inhibitors for cholera and related AB5 toxins. <i>Journal of Molecular Biology</i> , 1999 , 285, 1169-78	6.5	10
12	The 1.25 Å resolution refinement of the cholera toxin B-pentamer: evidence of peptide backbone strain at the receptor-binding site. <i>Journal of Molecular Biology</i> , 1998 , 282, 1043-59	6.5	148
11	Raster3D: photorealistic molecular graphics. <i>Methods in Enzymology</i> , 1997 , 277, 505-24	1.7	3125
10	Structural foundation for the design of receptor antagonists targeting Escherichia coli heat-labile enterotoxin. <i>Structure</i> , 1997 , 5, 1485-99	5.2	56
9	Structural studies of receptor binding by cholera toxin mutants. <i>Protein Science</i> , 1997 , 6, 1516-28	6.3	89
8	E. Coli Heat Labile Enterotoxin and Cholera Toxin B-Pentamer Crystallographic Studies of Biological Activity. <i>Molecular Biology Intelligence Unit</i> , 1996 , 147-172		2

7	Structural diversity in a conserved cholera toxin epitope involved in ganglioside binding. <i>Protein Science</i> , 1995 , 4, 841-8	6.3	8
6	The Arg7Lys mutant of heat-labile enterotoxin exhibits great flexibility of active site loop 47-56 of the A subunit. <i>Biochemistry</i> , 1995 , 34, 10996-1004	3.2	31
5	AB5 toxins. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 165-71	8.1	251
4	Surprising leads for a cholera toxin receptor-binding antagonist: crystallographic studies of CTB mutants. <i>Structure</i> , 1995 , 3, 561-70	5.2	25
3	Crystal structure of cholera toxin B-pentamer bound to receptor GM1 pentasaccharide. <i>Protein Science</i> , 1994 , 3, 166-75	6.3	462
2	Protein crystallography and infectious diseases. <i>Protein Science</i> , 1994 , 3, 1670-86	6.3	46
1	Galactose-binding site in Escherichia coli heat-labile enterotoxin (LT) and cholera toxin (CT). <i>Molecular Microbiology</i> , 1994 , 13, 745-53	4.1	120