Artem G Evdokimov

List of Publications by Year
in descending order

42	2,356	172457	265206
papers	citations	29 h-index	42 g-index

42	42	42	3479
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural and functional characterization of Mpp75Aa1.1, a putative beta-pore forming protein from Brevibacillus laterosporus active against the western corn rootworm. PLoS ONE, 2021, 16, e0258052.	2.5	5
2	Crystal structure of a Vip3B family insecticidal protein reveals a new fold and a unique tetrameric assembly. Protein Science, 2020, 29, 824-829.	7.6	27
3	Disabled insecticidal proteins: A novel tool to understand differences in insect receptor utilization. Insect Biochemistry and Molecular Biology, 2019, 105, 79-88.	2.7	14
4	Continuous evolution of Bacillus thuringiensis toxins overcomes insect resistance. Nature, 2016, 533, 58-63.	27.8	159
5	Mechanistic insights into the first Lygus-active Î²-pore forming protein. Archives of Biochemistry and Biophysics, 2016, 600, 1-11.	3.0	21
6	The inhibition of human farnesyl pyrophosphate synthase by nitrogen-containing bisphosphonates. Elucidating the role of active site threonine 201 and tyrosine 204 residues using enzyme mutants. Bone, 2015, 81, 478-486.	2.9	45
7	Structure of the fullâ€length insecticidal protein <scp>C</scp>ry1<scp>A</scp>c reveals intriguing details of toxin packaging into in vivo formed crystals. Protein Science, 2014, 23, 1491-1497.	7.6	55
8	Small-molecule phosphodiesterase probes: discovery of potent and selective CNS-penetrable quinazoline inhibitors of PDE1. MedChemComm, 2014, 5, 1290-1296.	3.4	31
9	Discovery of Brain-Penetrant, Irreversible Kynurenine Aminotransferase II Inhibitors for Schizophrenia. ACS Medicinal Chemistry Letters, 2012, 3, 187-192.	2.8	77
10	The Enzymology of alanine aminotransferase (AlaAT) isoforms from Hordeum vulgare and other organisms, and the HvAlaAT crystal structure. Archives of Biochemistry and Biophysics, 2012, 528, 90-101.	3.0	34
11	Structural basis for effectiveness of siderophore-conjugated monocarbams against clinically relevant strains ofPseudomonas aeruginosa. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22002-22007.	7.1	129
12	Multiplex Enzyme Assays and Inhibitor Screening by Mass Spectrometry. Journal of Biomolecular Screening, 2010, 15, 1001-1007.	2.6	17
13	New kinase regulation mechanism found in HipBA: a bacterial persistence switch. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 875-879.	2.5	22
14	Crystal structure of the Yersinia pestis GTPase activator YopE. Protein Science, 2009, 11, 401-408.	7.6	58
15	Farnesyl pyrophosphate synthase enantiospecificity with a chiral risedronate analog, [6,7-dihydro-5H-cyclopenta[c]pyridin-7-yl(hydroxy)methylene]bis(phosphonic acid) (NE-10501): Synthetic, structural, and modeling studies. Bioorganic and Medicinal Chemistry Letters, 2008, 18, 2878-2882.	2.2	10
16	Structural evidence for substrateâ€induced synergism and halfâ€sites reactivity in biotin carboxylase. Protein Science, 2008, 17, 1706-1718.	7.6	67
17	Structural biology approaches to antibacterial drug discovery. Expert Opinion on Drug Discovery, 2007, 2, 1085-1101.	5.0	6
18	Engineering the catalytic domain of human protein tyrosine phosphatase Î² for structure-based drug discovery. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1435-1445.	2.5	23

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19	Serendipitous discovery of novel bacterial methionine aminopeptidase inhibitors. Proteins: Structure, Function and Bioinformatics, 2006, 66, 538-546.	2.6	22
20	Structural basis for the fast maturation of Arthropoda green fluorescent protein. EMBO Reports, 2006, 7, 1006-1012.	4.5	99
21	Design and synthesis of novel N-sulfonyl-2-indole carboxamides as potent PPAR-Î³ binding agents with potential application to the treatment of osteoporosis. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5659-5663.	2.2	46
22	Design and synthesis of substituted pyridine derivatives as HIF-1Î± prolyl hydroxylase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5616-5620.	2.2	37
23	The development of 2-benzimidazole substituted pyrimidine based inhibitors of lymphocyte specific kinase (Lck). Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5973-5977.	2.2	59
24	1,2,3,4-Tetrahydroisoquinolinyl sulfamic acids as phosphatase PTP1B inhibitors. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 1574-1578.	2.2	78
25	Design and synthesis of a series of novel pyrazolopyridines as HIF 1-Î± prolyl hydroxylase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5687-5690.	2.2	70
26	Structure-based design, synthesis, and SAR evaluation of a new series of 8-hydroxyquinolines as HIF-1Î± prolyl hydroxylase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5517-5522.	2.2	56
27	A novel series of imidazo[1,2-a]pyridine derivatives as HIF-1Î± prolyl hydroxylase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 5598-5601.	2.2	61
28	MALDI-TOF MS as a label-free approach to rapid inhibitor screening. Journal of the American Society for Mass Spectrometry, 2006, 17, 815-822.	2.8	58
29	Mechanism of insulin sensitization by BMOV (bis maltolato oxo vanadium); unliganded vanadium (VO4) as the active component. Journal of Inorganic Biochemistry, 2003, 96, 321-330.	3.5	127
30	Similar modes of polypeptide recognition by export chaperones in flagellar biosynthesis and type III secretion. Nature Structural and Molecular Biology, 2003, 10, 789-793.	8.2	96
31	Structural Basis for the Substrate Specificity of Tobacco Etch Virus Protease. Journal of Biological Chemistry, 2002, 277, 50564-50572.	3.4	206
32	Differential effects of short affinity tags on the crystallization ofPyrococcus furiosusmaltodextrin-binding protein. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 392-397.	2.5	85
33	Three-dimensional structure of the type III secretion chaperone SycE fromYersinia pestis. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 398-406.	2.5	45
34	Structural basis for oligosaccharide recognition by Pyrococcus furiosus maltodextrin-binding protein. Journal of Molecular Biology, 2001, 305, 891-904.	4.2	56
35	Unusual molecular architecture of the Yersinia pestis cytotoxin YopM: a leucine-rich repeat protein with the shortest repeating unit 1 1Edited by R. Huber. Journal of Molecular Biology, 2001, 312, 807-821.	4.2	149
36	Structures of furanosides: geometrical analysis of low-temperature X-ray and neutron crystal structures of five crystalline methyl pentofuranosides. Acta Crystallographica Section B: Structural Science, 2001, 57, 213-220.	1.8	21

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37	Structure of the N-terminal domain ofYersinia pestisYopH at 2.0â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 793-799.	2.5	39
38	Overproduction, purification, crystallization and preliminary X-ray diffraction analysis of YopM, an essential virulence factor extruded by the plague bacteriumYersinia pestis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1676-1679.	2.5	8
39	Anti-Human Immunodeficiency Virus Activity of Novel Aminoglycoside-Arginine Conjugates at Early Stages of Infection. AIDS Research and Human Retroviruses, 2000, 16, 627-634.	1.1	36
40	Structures of Furanosides:â€‰ A Study of the Conformational Space of Methyl Î±-d-Lyxofuranoside by Density Functional Methods. Journal of Physical Chemistry A, 2000, 104, 5291-5297.	2.5	13
41	Structures of Furanosides:Â Density Functional Calculations and High-Resolution X-ray and Neutron Diffraction Crystal Structures. Journal of Physical Chemistry A, 1999, 103, 744-753.	2.5	39
42	Arginine-aminoglycoside conjugates that bind to HIV transactivation responsive element RNA in vitro. FEBS Letters, 1999, 445, 73-79.	2.8	50