Wayne F Anderson

List of Publications by Year
in descending order

43 papers	1,359 citations	331670 21 h-index	361022 35 g-index
46 all docs	46 docs citations	46 times ranked	2377 citing authors

#	Article	IF	Citations
1	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. PLoS ONE, 2014, 9, e94816.	2.5	249
2	Identification of novel small molecule inhibitors against NS2B/NS3 serine protease from Zika virus. Antiviral Research, 2017, 139, 49-58.	4.1	113
3	Targeting Human Central Nervous System Protein Kinases: An Isoform Selective p38Î±MAPK Inhibitor That Attenuates Disease Progression in Alzheimerâ€™s Disease Mouse Models. ACS Chemical Neuroscience, 2015, 6, 666-680.	3.5	75
4	The structure of the yrdC gene product from Escherichia coli reveals a new fold and suggests a role in RNA binding. Protein Science, 2000, 9, 2557-2566.	7.6	74
5	Development of Novel In Vivo Chemical Probes to Address CNS Protein Kinase Involvement in Synaptic Dysfunction. PLoS ONE, 2013, 8, e66226.	2.5	58
6	Structure-Based Mutational Studies of Substrate Inhibition of Betaine Aldehyde Dehydrogenase BetB from Staphylococcus aureus. Applied and Environmental Microbiology, 2014, 80, 3992-4002.	3.1	52
7	An acetylatable lysine controls CRP function in E. coli. Molecular Microbiology, 2018, 107, 116-131.	2.5	51
8	New ligation independent cloning vectors for expression of recombinant proteins with a self-cleaving CPD/6xHis-tag. BMC Biotechnology, 2017, 17, 1.	3.3	42
9	Structure of the fibrinogen Î³â€chain integrin binding and factor XIIIa crossâ€linking sites obtained through carrier protein driven crystallization. Protein Science, 1999, 8, 2663-2671.	7.6	39
10	The bacterial Ras/Rap1 site-specific endopeptidase RRSP cleaves Ras through an atypical mechanism to disrupt Ras-ERK signaling. Science Signaling, 2018, 11, .	3.6	39
11	A comparative genomics approach identifies contact-dependent growth inhibition as a virulence determinant. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6811-6821.	7.1	39
12	Structural, Functional, and Inhibition Studies of a Gcn5-related N-Acetyltransferase (GNAT) Superfamily Protein PA4794. Journal of Biological Chemistry, 2013, 288, 30223-30235.	3.4	37
13	Structure of the Essential Mtb FadD32 Enzyme: A Promising Drug Target for Treating Tuberculosis. ACS Infectious Diseases, 2016, 2, 579-591.	3.8	37
14	Listeria monocytogenes InlP interacts with afadin and facilitates basement membrane crossing. PLoS Pathogens, 2018, 14, e1007094.	4.7	35
15	A Novel Phosphatidylinositol 4,5-Bisphosphate Binding Domain Mediates Plasma Membrane Localization of ExoU and Other Patatin-like Phospholipases. Journal of Biological Chemistry, 2015, 290, 2919-2937.	3.4	34
16	Structure to function of an Î±-glucan metabolic pathway that promotes Listeria monocytogenes pathogenesis. Nature Microbiology, 2017, 2, 16202.	13.3	33
17	Structure of the LdcB LD-Carboxypeptidase Reveals the Molecular Basis of Peptidoglycan Recognition. Structure, 2014, 22, 949-960.	3.3	31
18	A Selective and Brain Penetrant p38Î±MAPK Inhibitor Candidate for Neurologic and Neuropsychiatric Disorders That Attenuates Neuroinflammation and Cognitive Dysfunction. Journal of Medicinal Chemistry, 2019, 62, 5298-5311.	6.4	31

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19	A Novel Polyamine Allosteric Site of SpeG from Vibrio cholerae Is Revealed by Its Dodecameric Structure. Journal of Molecular Biology, 2015, 427, 1316-1334.	4.2	24
20	Transferase Versus Hydrolase: The Role of Conformational Flexibility in Reaction Specificity. Structure, 2017, 25, 295-304.	3.3	23
21	Structural and immunological characterization of E. coli derived recombinant CRM197 protein used as carrier in conjugate vaccines. Bioscience Reports, 2018, 38, .	2.4	23
22	Potential for Reduction of Streptogramin A Resistance Revealed by Structural Analysis of Acetyltransferase VatA. Antimicrobial Agents and Chemotherapy, 2014, 58, 7083-7092.	3.2	19
23	Crystal structures of the transpeptidase domain of the Mycobacterium tuberculosis penicillinâ€binding protein PonA1 reveal potential mechanisms of antibiotic resistance. FEBS Journal, 2016, 283, 2206-2218.	4.7	18
24	An Unusual Cation-Binding Site and Distinct Domainâ€“Domain Interactions Distinguish Class II Enolpyruvylshikimate-3-phosphate Synthases. Biochemistry, 2016, 55, 1239-1245.	2.5	18
25	Structural and functional analysis of betaine aldehyde dehydrogenase fromStaphylococcus aureus. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1159-1175.	2.5	16
26	Crystal Structures of the SpoIID Lytic Transglycosylases Essential for Bacterial Sporulation. Journal of Biological Chemistry, 2016, 291, 14915-14926.	3.4	15
27	Structural Basis for DNA Recognition by the Two-Component Response Regulator RcsB. MBio, 2018, 9, .	4.1	15
28	CSGID Solves Structures and Identifies Phenotypes for Five Enzymes in Toxoplasma gondii. Frontiers in Cellular and Infection Microbiology, 2018, 8, 352.	3.9	14
29	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 55-64.	2.3	13
30	Discovery of Selective Inhibitors of the Clostridium difficile Dehydroquinate Dehydratase. PLoS ONE, 2014, 9, e89356.	2.5	12
31	Substrate-Induced Allosteric Change in the Quaternary Structure of the Spermidine N-Acetyltransferase SpeG. Journal of Molecular Biology, 2015, 427, 3538-3553.	4.2	12
32	Loop-to-helix transition in the structure of multidrug regulator AcrR at the entrance of the drug-binding cavity. Journal of Structural Biology, 2016, 194, 18-28.	2.8	12
33	Crystal structure of nonphosphorylated receiver domain of the stress response regulator RcsB from Escherichia coli. Protein Science, 2016, 25, 2216-2224.	7.6	9
34	Structure of the Bacillus anthracis dTDP- l -rhamnose biosynthetic pathway enzyme: dTDP-Î±- d -glucose 4,6-dehydratase, RfbB. Journal of Structural Biology, 2018, 202, 175-181.	2.8	8
35	Analysis of crystalline and solution states of ligand-free spermidineN-acetyltransferase (SpeG) fromEscherichia coli. Acta Crystallographica Section D: Structural Biology, 2019, 75, 545-553.	2.3	8
36	Structure of the Bacillus anthracis dTDP-<scp>L</scp>-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose reductase (RfbD). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 644-650.	0.8	6

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37	Structure of the Bacillus anthracis dTDP-<scp>L</scp>-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose 3,5-epimerase (RfbC). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 664-671.	0.8	6
38	The spermidine acetyltransferase SpeG regulates transcription of the small RNA rprA. PLoS ONE, 2018, 13, e0207563.	2.5	4
39	Sensor Domain of Histidine Kinase VxrA of Vibrio cholerae: Hairpin-Swapped Dimer and Its Conformational Change. Journal of Bacteriology, 2021, 203, .	2.2	4
40	Small angle X-ray scattering data and structure factor fitting for the study of the quaternary structure of the spermidine N-acetyltransferase SpeG. Data in Brief, 2016, 6, 47-52.	1.0	3
41	Structural Genomics Support for Infectious Disease Drug Design. ACS Infectious Diseases, 2015, 1, 127-129.	3.8	2
42	Structure of theBacillus anthracisdTDP-L-rhamnose-biosynthetic enzyme glucose-1-phosphate thymidylyltransferase (RfbA). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 621-628.	0.8	2
43	Fluorescence-based thermal shift data on multidrug regulator AcrR from Salmonella enterica subsp. entrica serovar Typhimurium str. LT2. Data in Brief, 2016, 7, 537-539.	1.0	0