William Nigel Hunter

List of Publications by Year
in descending order

31 papers	894 citations	623734 14 h-index	477307 29 g-index
31 all docs	31 docs citations	31 times ranked	1583 citing authors

#	Article	IF	Citations
1	The Non-mevalonate Pathway of Isoprenoid Precursor Biosynthesis. Journal of Biological Chemistry, 2007, 282, 21573-21577.	3.4	316
2	Leishmania Trypanothione Synthetase-Amidase Structure Reveals a Basis for Regulation of Conflicting Synthetic and Hydrolytic Activities. Journal of Biological Chemistry, 2008, 283, 17672-17680.	3.4	86
3	Recombinant Human PPAR-Î²/Î´ Ligand-binding Domain is Locked in an Activated Conformation by Endogenous Fatty Acids. Journal of Molecular Biology, 2006, 356, 1005-1013.	4.2	79
4	EssC: domain structures inform on the elusive translocation channel in the TypeÂVII secretion system. Biochemical Journal, 2016, 473, 1941-1952.	3.7	48
5	Structure-based Ligand Design and the Promise Held for Antiprotozoan Drug Discovery. Journal of Biological Chemistry, 2009, 284, 11749-11753.	3.4	43
6	Structure-Based Design and Synthesis of Antiparasitic Pyrrolopyrimidines Targeting Pteridine Reductase 1. Journal of Medicinal Chemistry, 2014, 57, 6479-6494.	6.4	37
7	How the structure of the large subunit controls function in an oxygen-tolerant [NiFe]-hydrogenase. Biochemical Journal, 2014, 458, 449-458.	3.7	34
8	Crystal structures of IspF from Plasmodium falciparum and Burkholderia cenocepacia: comparisons inform antimicrobial drug target assessment. BMC Structural Biology, 2014, 14, 1.	2.3	34
9	Membrane interactions and selfâ€association of components of the Ess/Type <scp>VII</scp> secretion system of Staphylococcus aureus. FEBS Letters, 2016, 590, 349-357.	2.8	27
10	Exploiting the 2-Amino-1,3,4-thiadiazole Scaffold To Inhibit Trypanosoma brucei Pteridine Reductase in Support of Early-Stage Drug Discovery. ACS Omega, 2017, 2, 5666-5683.	3.5	24
11	Isoprenoid Precursor Biosynthesis Offers Potential Targets for Drug Discovery Against Diseases Caused by Apicomplexan Parasites. Current Topics in Medicinal Chemistry, 2011, 11, 2048-2059.	2.1	18
12	Assessment of Pseudomonas aeruginosa N5,N10-Methylenetetrahydrofolate Dehydrogenase - Cyclohydrolase as a Potential Antibacterial Drug Target. PLoS ONE, 2012, 7, e35973.	2.5	18
13	Structure ofStaphylococcus aureusadenylosuccinate lyase (PurB) and assessment of its potential as a target for structure-based inhibitor discovery. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 881-888.	2.5	17
14	Structure and activity of ChiX: a peptidoglycan hydrolase required for chitinase secretion by Serratia marcescens. Biochemical Journal, 2018, 475, 415-428.	3.7	15
15	AcinetobacterÂbaumannii <scp>F</scp>ol<scp>D</scp> ligand complexesÂâ€“Âpotent inhibitors of folate metabolism and a reâ€evaluation of the structure of <scp>LY</scp>374571. FEBS Journal, 2012, 279, 4350-4360.	4.7	14
16	Characterization of 2,4-Diamino-6-oxo-1,6-dihydropyrimidin-5-yl Ureido Based Inhibitors of Trypanosoma brucei FolD and Testing for Antiparasitic Activity. Journal of Medicinal Chemistry, 2015, 58, 7938-7948.	6.4	12
17	Structures of bacterial kynurenine formamidase reveal a crowded binuclear zinc catalytic site primed to generate a potent nucleophile. Biochemical Journal, 2014, 462, 581-589.	3.7	9
18	An Improved Model of the Trypanosoma brucei CTP Synthetase Glutaminase Domainâ€“Acivicin Complex. ChemMedChem, 2017, 12, 577-579.	3.2	9

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19	High-resolution structure of the M14-type cytosolic carboxypeptidase fromBurkholderia cenocepaciarefined exploitingPDB_REDOstrategies. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 279-289.	2.5	8
20	Engineering a surrogate human heteromeric Î±/Î² glycine receptor orthosteric site exploiting the structural homology and stability of acetylcholine-binding protein. IUCrJ, 2019, 6, 1014-1023.	2.2	8
21	Open and compressed conformations of Francisella tularensis ClpP. Proteins: Structure, Function and Bioinformatics, 2017, 85, 188-194.	2.6	7
22	Crystal structure of the C-terminal domain of tubulin-binding cofactor C from Leishmania major. Molecular and Biochemical Parasitology, 2015, 201, 26-30.	1.1	5
23	Amino acid substitutions in the human homomeric Î²3 GABAA receptor that enable activation by GABA. Journal of Biological Chemistry, 2019, 294, 2375-2385.	3.4	5
24	Structures ofPseudomonas aeruginosaÎ²-ketoacyl-(acyl-carrier-protein) synthase II (FabF) and a C164Q mutant provide templates for antibacterial drug discovery and identify a buried potassium ion and a ligand-binding site that is an artefact of the crystal form. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1020-1026.	0.8	4
25	The structure of tubulin-binding cofactor A fromLeishmania majorinfers a mode of association during the early stages of microtubule assembly. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 539-546.	0.8	4
26	BurkholderiaÂpseudomallei d â€alanineâ€•d â€alanine ligase; detailed characterisation and assessment of a potential antibiotic drug target. FEBS Journal, 2019, 286, 4509-4524.	4.7	4
27	An assessment of three human methylenetetrahydrofolate dehydrogenase/cyclohydrolaseâ€“ligand complexes following further refinement. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 148-152.	0.8	3
28	A Structural Rationale for N â€Methylbicuculline Acting as a Promiscuous Competitive Antagonist of Inhibitory Pentameric Ligandâ€Gated Ion Channels. ChemBioChem, 2020, 21, 1526-1533.	2.6	3
29	The structure of lipopolysaccharide transport protein B (LptB) from Burkholderia pseudomallei. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 227-232.	0.8	1
30	The thermodynamic profile and molecular interactions of a C(9)-cytisine derivative-binding acetylcholine-binding protein from Aplysia californica. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 74-80.	0.8	1
31	Interactions between 2â€²-fluoro-(carbamoylpyridinyl)deschloroepibatidine analogues and acetylcholine-binding protein inform on potent antagonist activity against nicotinic receptors. Acta Crystallographica Section D: Structural Biology, 2022, 78, 353-362.	2.3	1