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	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	Structure and activity of ChiX: a peptidoglycan hydrolase required for chitinase secretion by Serratia marcescens. Biochemical Journal, 2018, 475, 415-428.	3.7	15
10	Open and compressed conformations of Francisella tularensis ClpP. Proteins: Structure, Function and Bioinformatics, 2017, 85, 188-194.	2.6	7
11	An Improved Model of the Trypanosoma brucei CTP Synthetase Glutaminase Domainâ€“Acivicin Complex. ChemMedChem, 2017, 12, 577-579.	3.2	9
12	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
13	EssC: domain structures inform on the elusive translocation channel in the TypeÂVII secretion system. Biochemical Journal, 2016, 473, 1941-1952.	3.7	48
14	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
15	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
16	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
17	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
18	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

#	Article	IF	Citations
19	How the structure of the large subunit controls function in an oxygen-tolerant [NiFe]-hydrogenase. Biochemical Journal, 2014, 458, 449-458.	3.7	34
20	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
21	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
22	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
23	Structure-Based Design and Synthesis of Antiparasitic Pyrrolopyrimidines Targeting Pteridine Reductase 1. Journal of Medicinal Chemistry, 2014, 57, 6479-6494.	6.4	37
24	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
25	Assessment of Pseudomonas aeruginosa N5,N10-Methylenetetrahydrofolate Dehydrogenase - Cyclohydrolase as a Potential Antibacterial Drug Target. PLoS ONE, 2012, 7, e35973.	2.5	18
26	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
27	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
28	Structure-based Ligand Design and the Promise Held for Antiprotozoan Drug Discovery. Journal of Biological Chemistry, 2009, 284, 11749-11753.	3.4	43
29	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
30	The Non-mevalonate Pathway of Isoprenoid Precursor Biosynthesis. Journal of Biological Chemistry, 2007, 282, 21573-21577.	3.4	316
31	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