Penchit Chitnumsub

List of Publications by Year
in descending order

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39 papers	1,692 citations	361413 20 h-index	315739 38 g-index
39 all docs	39 docs citations	39 times ranked	1837 citing authors

#	Article	IF	Citations
1	Mechanism-guided tunnel engineering to increase the efficiency of a flavin-dependent halogenase. Nature Catalysis, 2022, 5, 534-544.	34.4	46
2	Structural dynamics and in silico design of pyrazolopyran-based inhibitors against Plasmodium serine hydroxymethyltransferases. Journal of Molecular Liquids, 2022, 362, 119737.	4.9	2
3	Enhancement of catalytic performance of a metagenome-derived thermophilic oligosaccharide-specific xylanase by binding module removal and random mutagenesis. Journal of Bioscience and Bioengineering, 2021, 131, 13-19.	2.2	13
4	Dissecting the low catalytic capability of flavin-dependent halogenases. Journal of Biological Chemistry, 2021, 296, 100068.	3.4	26
5	Structural insights into a flavin-dependent dehalogenase HadA explain catalysis and substrate inhibition via quadruple Ï€-stacking. Journal of Biological Chemistry, 2021, 297, 100952.	3.4	6
6	Catalytic and structural insights into a stereospecific and thermostable Class II aldolase HpaI from Acinetobacter baumannii. Journal of Biological Chemistry, 2021, 297, 101280.	3.4	6
7	The structure of PlasmodiumÂfalciparum hydroxymethyldihydropterin pyrophosphokinaseâ€dihydropteroate synthase reveals the basis of sulfa resistance. FEBS Journal, 2020, 287, 3273-3297.	4.7	24
8	Real-time detection of changes in yeast plasma membrane potential using genetically encoded voltage indicator proteins. FEMS Yeast Research, 2020, 20, .	2.3	0
9	A flap motif in human serine hydroxymethyltransferase is important for structural stabilization, ligand binding, and control of product release. Journal of Biological Chemistry, 2019, 294, 10490-10502.	3.4	11
10	Identification of a Hotspot Residue for Improving the Thermostability of a Flavinâ€Dependent Monooxygenase. ChemBioChem, 2019, 20, 3020-3031.	2.6	27
11	Crystal structure of Plasmodium falciparum adenosine deaminase reveals a novel binding pocket for inosine. Archives of Biochemistry and Biophysics, 2019, 667, 6-13.	3.0	4
12	Potent Inhibitors of Plasmodial Serine Hydroxymethyltransferase (SHMT) Featuring a Spirocyclic Scaffold. ChemMedChem, 2018, 13, 931-943.	3.2	21
13	Hybrid Inhibitors of Malarial Dihydrofolate Reductase with Dual Binding Modes That Can Forestall Resistance. ACS Medicinal Chemistry Letters, 2018, 9, 1235-1240.	2.8	19
14	Antimalarial Inhibitors Targeting Serine Hydroxymethyltransferase (SHMT) with in Vivo Efficacy and Analysis of their Binding Mode Based on X-ray Cocrystal Structures. Journal of Medicinal Chemistry, 2017, 60, 4840-4860.	6.4	40
15	Conformational Aspects in the Design of Inhibitors for Serine Hydroxymethyltransferase (SHMT): Biphenyl, Aryl Sulfonamide, and Aryl Sulfone Motifs. Chemistry - A European Journal, 2017, 23, 14345-14357.	3.3	20
16	Structure-based protein engineering for thermostable and alkaliphilic enhancement of endo-Î²-1,4-xylanase for applications in pulp bleaching. Journal of Biotechnology, 2017, 259, 95-102.	3.8	27
17	Human and Plasmodium serine hydroxymethyltransferases differ in rate-limiting steps and pH-dependent substrate inhibition behavior. Archives of Biochemistry and Biophysics, 2017, 630, 91-100.	3.0	13
18	Role of Plasmodium vivax Dihydropteroate Synthase Polymorphisms in Sulfa Drug Resistance. Antimicrobial Agents and Chemotherapy, 2016, 60, 4453-4463.	3.2	24

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19	Inhibitors of Plasmodial Serine Hydroxymethyltransferase (SHMT): Cocrystal Structures of Pyrazolopyrans with Potent Blood- and Liver-Stage Activities. Journal of Medicinal Chemistry, 2015, 58, 3117-3130.	6.4	46
20	Kinetic Mechanism and the Rate-limiting Step of Plasmodium vivax Serine Hydroxymethyltransferase. Journal of Biological Chemistry, 2015, 290, 8656-8665.	3.4	10
21	Structures ofPlasmodium vivaxserine hydroxymethyltransferase: implications for ligand-binding specificity and functional control. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3177-3186.	2.5	23
22	The structure ofPlasmodium falciparumserine hydroxymethyltransferase reveals a novel redox switch that regulates its activities. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1517-1527.	2.5	22
23	Malarial dihydrofolate reductase as a paradigm for drug development against a resistance-compromised target. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16823-16828.	7.1	237
24	Combined Spatial Limitation around Residues 16 and 108 of Plasmodium falciparum Dihydrofolate Reductase Explains Resistance to Cycloguanil. Antimicrobial Agents and Chemotherapy, 2012, 56, 3928-3935.	3.2	27
25	Trypanosomal Dihydrofolate Reductase Reveals Natural Antifolate Resistance. ACS Chemical Biology, 2011, 6, 905-911.	3.4	42
26	Formation of catalytically active cross-species heterodimers of thymidylate synthase from Plasmodium falciparum and Plasmodium vivax. Molecular Biology Reports, 2011, 38, 1029-1037.	2.3	5
27	Preclinical Evaluation of the Antifolate QN254, 5-Chloro-Nâ€²6â€²-(2,5-Dimethoxy-Benzyl)-Quinazoline-2,4,6-Triamine, as an Antimalarial Drug Candidate. Antimicrobial Agents and Chemotherapy, 2010, 54, 2603-2610.	3.2	25
28	Crystallization and preliminary crystallographic studies of dihydrofolate reductase-thymidylate synthase fromTrypanosoma cruzi, the Chagas disease pathogen. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1175-1178.	0.7	8
29	Exploiting Structural Analysis, in Silico Screening, and Serendipity To Identify Novel Inhibitors of Drug-Resistant Falciparum Malaria. ACS Chemical Biology, 2009, 4, 29-40.	3.4	54
30	The role of tryptophan-48 in catalysis and binding of inhibitors of Plasmodium falciparum dihydrofolate reductase. International Journal for Parasitology, 2007, 37, 787-793.	3.1	9
31	Folate metabolism as a source of molecular targets for antimalarials. Future Microbiology, 2006, 1, 113-125.	2.0	44
32	Subunit complementation of thymidylate synthase in Plasmodium falciparum bifunctional dihydrofolate reductase-thymidylate synthase. Molecular and Biochemical Parasitology, 2005, 139, 83-90.	1.1	9
33	Crystal structure of dihydrofolate reductase from Plasmodium vivax: Pyrimethamine displacement linked with mutation-induced resistance. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13046-13051.	7.1	86
34	Characterization, crystallization and preliminary X-ray analysis of bifunctional dihydrofolate reductaseâ€“thymidylate synthase fromPlasmodium falciparum. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 780-783.	2.5	47
35	Insights into antifolate resistance from malarial DHFR-TS structures. Nature Structural and Molecular Biology, 2003, 10, 357-365.	8.2	343
36	Pyrimethamine analogs as strong inhibitors of double and quadruple mutants of dihydrofolate reductase in human malaria parasites. Organic and Biomolecular Chemistry, 2003, 1, 960-964.	2.8	54

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37	Three-dimensional structure of M. tuberculosis dihydrofolate reductase reveals opportunities for the design of novel tuberculosis drugs. Journal of Molecular Biology, 2000, 295, 307-323.	4.2	187
38	The nucleation of monomeric parallel Î²-sheet-like structures and their self-assembly in aqueous solution. Bioorganic and Medicinal Chemistry, 1999, 7, 39-59.	3.0	77
39	Improved Synthesis of the Boc and Fmoc Derivatives of 4-(2â€˜-Aminoethyl)-6-dibenzofuranpropionic Acid:â€‰An Unnatural Amino Acid That Nucleates Î²-Sheet Folding. Journal of Organic Chemistry, 1997, 62, 2259-2262.	3.2	8