Kirsten R Wolthers

List of Publications by Year
in descending order

31 papers	974 citations	777949 13 h-index	536525 29 g-index
32 all docs	32 docs citations	32 times ranked	1485 citing authors

#	Article	IF	Citations
1	Steady-state and pre-steady state kinetic analysis of ornithine 4,5-aminomutase. Methods in Enzymology, 2022, , 173-195.	0.4	0
2	Sequence Divergence in the Arginase Domain of Ornithine Decarboxylase/Arginase in <i>Fusobacteriacea</i> Leads to Loss of Function in Oral Associated Species. Biochemistry, 2022, 61, 1378-1391.	1.2	2
3	A Fold Type II PLP-Dependent Enzyme from <i>Fusobacterium nucleatum</i> Functions as a Serine Synthase and Cysteine Synthase. Biochemistry, 2021, 60, 524-536.	1.2	5
4	S224 Presents a Catalytic Trade-off in PLP-Dependentl-Lanthionine Synthase fromFusobacterium nucleatum. Biochemistry, 2020, 59, 4250-4261.	1.2	2
5	Structural and Kinetic Insight into the Biosynthesis of H₂S and <scp>l</scp>-Lanthionine from <scp>l</scp>-Cysteine by a Pyridoxal <scp>l</scp>-Phosphate-Dependent Enzyme from <i>Fusobacterium nucleatum</i>. Biochemistry, 2019, 58, 3592-3603.	1.2	11
6	Structural insight into the high reduction potentials observed for <i>Fusobacterium nucleatum</i> flavodoxin. Protein Science, 2019, 28, 1460-1472.	3.1	3
7	Kinetic characterization of acetone monooxygenase from Gordonia sp. strain TY-5. AMB Express, 2018, 8, 181.	1.4	13
8	Active site arginine controls the stereochemistry of hydride transfer in cyclohexanone monooxygenase. Archives of Biochemistry and Biophysics, 2018, 659, 47-56.	1.4	6
9	Active site variants provide insight into the nature of conformational changes that accompany the cyclohexanone monooxygenase catalytic cycle. Archives of Biochemistry and Biophysics, 2018, 654, 85-96.	1.4	4
10	Optimal electrostatic interactions between substrate and protein are essential for radical chemistry in ornithine 4,5-aminomutase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1077-1084.	1.1	4
11	Role of active site loop in coenzyme binding and flavin reduction in cytochrome P450 reductase. Archives of Biochemistry and Biophysics, 2016, 606, 111-119.	1.4	3
12	Microfluidics Integrated Biosensors: A Leading Technology towards Lab-on-a-Chip and Sensing Applications. Sensors, 2015, 15, 30011-30031.	2.1	385
13	Kinetic analysis of electron flux in cytochrome P450 reductases reveals differences in rate-determining steps in plant and mammalian enzymes. Archives of Biochemistry and Biophysics, 2015, 584, 107-115.	1.4	12
14	Proximal FAD histidine residue influences interflavin electron transfer in cytochrome P450 reductase and methionine synthase reductase. Archives of Biochemistry and Biophysics, 2014, 547, 18-26.	1.4	3
15	Isotope Effects for Deuterium Transfer and Mutagenesis of Tyr187 Provide Insight into Controlled Radical Chemistry in Adenosylcobalamin-Dependent Ornithine 4,5-Aminomutase. Biochemistry, 2014, 53, 5432-5443.	1.2	4
16	Mitochondrial transcription factor A (Tfam) is a pro-inflammatory extracellular signaling molecule recognized by brain microglia. Molecular and Cellular Neurosciences, 2014, 60, 88-96.	1.0	57
17	Kinetic analysis of cytochrome P450 reductase from<i>Artemisia annua</i>reveals accelerated rates of NADPH-dependent flavin reduction. FEBS Journal, 2013, 280, 6627-6642.	2.2	14
18	Mutagenesis of a Conserved Glutamate Reveals the Contribution of Electrostatic Energy to Adenosylcobalamin Coâ€“C Bond Homolysis in Ornithine 4,5-Aminomutase and Methylmalonyl-CoA Mutase. Biochemistry, 2013, 52, 878-888.	1.2	18

#	Article	IF	Citations
19	Aromatic substitution of the <scp>FAD</scp>â€shielding tryptophan reveals its differential role in regulating electron flux in methionine synthase reductase and cytochromeÂ<scp>P</scp>450 reductase. FEBS Journal, 2013, 280, 1460-1474.	2.2	7
20	Role of histidine 225 in adenosylcobalamin-dependent ornithine 4,5-aminomutase. Bioorganic Chemistry, 2012, 40, 39-47.	2.0	12
21	Tryptophan 697 Modulates Hydride and Interflavin Electron Transfer in Human Methionine Synthase Reductase. Biochemistry, 2011, 50, 11131-11142.	1.2	13
22	ELDOR Spectroscopy Reveals that Energy Landscapes in Human Methionine Synthase Reductase are Extensively Remodelled Following Ligand and Partner Protein Binding. ChemBioChem, 2011, 12, 863-867.	1.3	13
23	Large-scale Domain Dynamics and Adenosylcobalamin Reorientation Orchestrate Radical Catalysis in Ornithine 4,5-Aminomutase. Journal of Biological Chemistry, 2010, 285, 13942-13950.	1.6	48
24	Cobalamin uptake and reactivation occurs through specific protein interactions in the methionine synthaseâ€"methionine synthase reductase complex. FEBS Journal, 2009, 276, 1942-1951.	2.2	34
25	Mechanism of Radical-based Catalysis in the Reaction Catalyzed by Adenosylcobalamin-dependent Ornithine 4,5-Aminomutase. Journal of Biological Chemistry, 2008, 283, 34615-34625.	1.6	33
26	Mechanism of Coenzyme Binding to Human Methionine Synthase Reductase Revealed through the Crystal Structure of the FNR-like Module and Isothermal Titration Calorimetry,. Biochemistry, 2007, 46, 11833-11844.	1.2	39
27	Protein Interactions in the Human Methionine Synthaseâˆ'Methionine Synthase Reductase Complex and Implications for the Mechanism of Enzyme Reactivationâ€. Biochemistry, 2007, 46, 6696-6709.	1.2	41
28	Crystal structure and solution characterization of the activation domain of human methionine synthase. FEBS Journal, 2007, 274, 738-750.	2.2	16
29	Electron Transfer in Human Methionine Synthase Reductase Studied by Stopped-Flow Spectrophotometry. Biochemistry, 2004, 43, 490-500.	1.2	31
30	Molecular Dissection of Human Methionine Synthase Reductase:â€‰ Determination of the Flavin Redox Potentials in Full-Length Enzyme and Isolated Flavin-Binding Domains. Biochemistry, 2003, 42, 3911-3920.	1.2	54
31	Identification and in Vitro Biological Activities of Hop Proanthocyanidins:Â Inhibition of nNOS Activity and Scavenging of Reactive Nitrogen Species. Journal of Agricultural and Food Chemistry, 2002, 50, 3435-3443.	2.4	87