

T Joseph Kappock

List of Publications by Citations

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36
papers

1,527
citations

18
h-index

36
g-index

36
ext. papers

1,653
ext. citations

6.6
avg, IF

4.01
L-index

#	Paper	IF	Citations
36	Pterin-Dependent Amino Acid Hydroxylases. <i>Chemical Reviews</i> , 1996 , 96, 2659-2756	68.1	275
35	Diverse carotenoids protect against chemically induced neoplastic transformation. <i>Carcinogenesis</i> , 1991 , 12, 671-8	4.6	235
34	Single-molecule paleoenzymology probes the chemistry of resurrected enzymes. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 592-6	17.6	149
33	Lipases provide a new mechanistic model for polyhydroxybutyrate (PHB) synthases: characterization of the functional residues in <i>Chromatium vinosum</i> PHB synthase. <i>Biochemistry</i> , 2000 , 39, 3927-36	3.2	97
32	A specialized citric acid cycle requiring succinyl-coenzyme A (CoA):acetate CoA-transferase (AarC) confers acetic acid resistance on the acidophile <i>Acetobacter aceti</i> . <i>Journal of Bacteriology</i> , 2008 , 190, 4933-40	3.5	77
31	Modular evolution of the purine biosynthetic pathway. <i>Current Opinion in Chemical Biology</i> , 2000 , 4, 567-37	3.7	69
30	X-ray crystal structure of aminoimidazole ribonucleotide synthetase (PurM), from the <i>Escherichia coli</i> purine biosynthetic pathway at 2.5 Å resolution. <i>Structure</i> , 1999 , 7, 1155-66	5.2	61
29	Spectroscopic Characterization of the Catalytically Competent Ferrous Site of the Resting, Activated, and Substrate-Bound Forms of Phenylalanine Hydroxylase. <i>Journal of the American Chemical Society</i> , 1997 , 119, 1901-1915	16.4	55
28	Three-dimensional structure of N5-carboxyaminoimidazole ribonucleotide synthetase: a member of the ATP grasp protein superfamily. <i>Biochemistry</i> , 1999 , 38, 15480-92	3.2	50
27	X-ray crystal structure of glycinamide ribonucleotide synthetase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1998 , 37, 15647-62	3.2	49
26	Solubilization, cellular uptake, and activity of beta-carotene and other carotenoids as inhibitors of neoplastic transformation in cultured cells. <i>Methods in Enzymology</i> , 1993 , 214, 55-68	1.7	43
25	Crystal structure of <i>Escherichia coli</i> PurE, an unusual mutase in the purine biosynthetic pathway. <i>Structure</i> , 1999 , 7, 1395-406	5.2	41
24	Spectroscopic and kinetic properties of unphosphorylated rat hepatic phenylalanine hydroxylase expressed in <i>Escherichia coli</i> . Comparison of resting and activated states. <i>Journal of Biological Chemistry</i> , 1995 , 270, 30532-44	5.4	41
23	Structure of a NADH-insensitive hexameric citrate synthase that resists acid inactivation. <i>Biochemistry</i> , 2006 , 45, 13487-99	3.2	38
22	Evidence for the direct transfer of the carboxylate of N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) to generate 4-carboxy-5-aminoimidazole ribonucleotide catalyzed by <i>Escherichia coli</i> PurE, an N5-CAIR mutase. <i>Biochemistry</i> , 1999 , 38, 3012-8	3.2	36
21	Biochemical and structural studies of N5-carboxyaminoimidazole ribonucleotide mutase from the acidophilic bacterium <i>Acetobacter aceti</i> . <i>Biochemistry</i> , 2006 , 45, 8193-208	3.2	26
20	Alanine racemase from the acidophile <i>Acetobacter aceti</i> . <i>Protein Expression and Purification</i> , 2007 , 51, 39-48	2	21

19	Acidophilic adaptations in the structure of <i>Acetobacter aceti</i> N5-carboxyaminoimidazole ribonucleotide mutase (PurE). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1753-60		20
18	N5-CAIR mutase: role of a CO2 binding site and substrate movement in catalysis. <i>Biochemistry</i> , 2007 , 46, 2842-55	3.2	18
17	Crystal structures of <i>Acetobacter aceti</i> succinyl-coenzyme A (CoA):acetate CoA-transferase reveal specificity determinants and illustrate the mechanism used by class I CoA-transferases. <i>Biochemistry</i> , 2012 , 51, 8422-34	3.2	17
16	You are lost without a map: Navigating the sea of protein structures. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 258-68	4	16
15	<i>Treponema denticola</i> PurE Is a bacterial AIR carboxylase. <i>Biochemistry</i> , 2011 , 50, 4623-37	3.2	15
14	Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile <i>Acetobacter aceti</i> has a distinctive electrostatic surface and inherent acid stability. <i>Protein Science</i> , 2012 , 21, 686-96	6.3	14
13	Cloning and transcriptional analysis of <i>Crepis alpina</i> fatty acid desaturases affecting the biosynthesis of crepenyic acid. <i>Journal of Experimental Botany</i> , 2007 , 58, 1421-32	7	11
12	Atomic-resolution crystal structure of thioredoxin from the acidophilic bacterium <i>Acetobacter aceti</i> . <i>Protein Science</i> , 2007 , 16, 92-8	6.3	10
11	The partial substrate dethiaacetyl-coenzyme A mimics all critical carbon acid reactions in the condensation half-reaction catalyzed by <i>Thermoplasma acidophilum</i> citrate synthase. <i>Biochemistry</i> , 2009 , 48, 7878-91	3.2	8
10	Function and X-ray crystal structure of <i>Escherichia coli</i> YfdE. <i>PLoS ONE</i> , 2013 , 8, e67901	3.7	8
9	Functional analysis of the acetic acid resistance (aar) gene cluster in <i>Acetobacter aceti</i> strain 1023. <i>Acetic Acid Bacteria</i> , 2013 , 2, 3		7
8	An active site-tail interaction in the structure of hexahistidine-tagged <i>Thermoplasma acidophilum</i> citrate synthase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 1292-9	1.1	6
7	Multiple active site histidine protonation states in <i>Acetobacter aceti</i> N5-carboxyaminoimidazole ribonucleotide mutase detected by REDOR NMR. <i>Biochemistry</i> , 2007 , 46, 9507-12	3.2	4
6	Draft Genome Sequence of <i>Acetobacter aceti</i> Strain 1023, a Vinegar Factory Isolate. <i>Genome Announcements</i> , 2014 , 2,		3
5	Functional Dissection of the Bipartite Active Site of the Class I Coenzyme A (CoA)-Transferase Succinyl-CoA:Acetate CoA-Transferase. <i>Frontiers in Chemistry</i> , 2016 , 4, 23	5	3
4	Metal stopping reagents facilitate discontinuous activity assays of the de novo purine biosynthesis enzyme PurE. <i>Analytical Biochemistry</i> , 2014 , 452, 43-5	3.1	2
3	The purine machine scores a base hit. <i>ACS Chemical Biology</i> , 2008 , 3, 460-2	4.9	1
2	Altered pathway routing in a class of <i>Salmonella enterica</i> serovar Typhimurium mutants defective in aminoimidazole ribonucleotide synthetase. <i>Journal of Bacteriology</i> , 2001 , 183, 2234-40	3.5	1

1 A biosynthetic enzyme worms its way out of a conserved mechanism. *Structure*, **2013**, 21, 1719-20 5.2