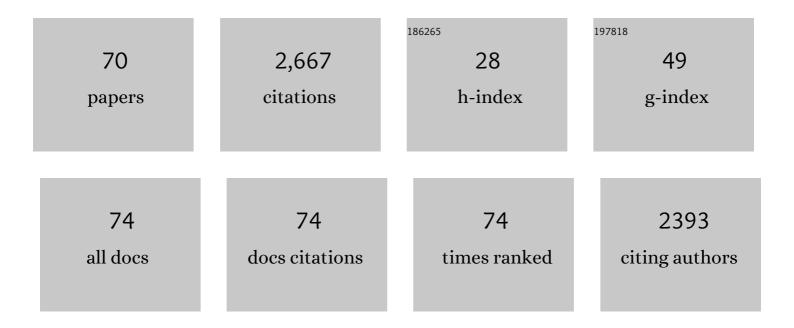
List of Publications by Year in descending order

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KADI FICHED

#	Article	IF	CITATIONS
1	Heterologous production and biophysical characterization of catabolic Nitratireductor pacificus pht-3B reductive dehalogenase. Methods in Enzymology, 2022, 668, 327-347.	1.0	2
2	Structural and biochemical characterization of the prenylated flavin mononucleotide-dependent indole-3-carboxylic acid decarboxylase. Journal of Biological Chemistry, 2022, 298, 101771.	3.4	10
3	Heterologous expression of cobalamin dependent class-III enzymes. Protein Expression and Purification, 2021, 177, 105743.	1.3	6
4	The In Vitro Production of prFMN for Reconstitution of UbiD Enzymes. Methods in Molecular Biology, 2021, 2280, 219-227.	0.9	2
5	Structure and Mechanism of <i>Pseudomonas aeruginosa</i> PA0254/HudA, a prFMN-Dependent Pyrrole-2-carboxylic Acid Decarboxylase Linked to Virulence. ACS Catalysis, 2021, 11, 2865-2878.	11.2	15
6	A Noncanonical Tryptophan Analogue Reveals an Active Site Hydrogen Bond Controlling Ferryl Reactivity in a Heme Peroxidase. Jacs Au, 2021, 1, 913-918.	7.9	8
7	UbiD domain dynamics underpins aromatic decarboxylation. Nature Communications, 2021, 12, 5065.	12.8	14
8	Structural basis of terephthalate recognition by solute binding protein TphC. Nature Communications, 2021, 12, 6244.	12.8	12
9	Ferulic Acid Decarboxylase Controls Oxidative Maturation of the Prenylated Flavin Mononucleotide Cofactor. ACS Chemical Biology, 2020, 15, 2466-2475.	3.4	13
10	Catabolic Reductive Dehalogenase Substrate Complex Structures Underpin Rational Repurposing of Substrate Scope. Microorganisms, 2020, 8, 1344.	3.6	7
11	Rewiring the "Push-Pull―Catalytic Machinery of a Heme Enzyme Using an Expanded Genetic Code. ACS Catalysis, 2020, 10, 2735-2746.	11.2	25
12	Arginine to Lysine Mutations Increase the Aggregation Stability of a Single-Chain Variable Fragment through Unfolded-State Interactions. Biochemistry, 2019, 58, 3413-3421.	2.5	24
13	Enzymatic control of cycloadduct conformation ensures reversible 1,3-dipolar cycloaddition in a prFMN-dependent decarboxylase. Nature Chemistry, 2019, 11, 1049-1057.	13.6	28
14	The UbiX flavin prenyltransferase reaction mechanism resembles class I terpene cyclase chemistry. Nature Communications, 2019, 10, 2357.	12.8	28
15	Unexpected Roles of a Tether Harboring a Tyrosine Gatekeeper Residue in Modular Nitrite Reductase Catalysis. ACS Catalysis, 2019, 9, 6087-6099.	11.2	17
16	Heterologous production, reconstitution and EPR spectroscopic analysis of prFMN dependent enzymes. Methods in Enzymology, 2019, 620, 489-508.	1.0	8
17	Enzymatic Carboxylation of 2-Furoic Acid Yields 2,5-Furandicarboxylic Acid (FDCA). ACS Catalysis, 2019, 9, 2854-2865.	11.2	74
18	NADPH-Driven Organohalide Reduction by a Nonrespiratory Reductive Dehalogenase. Biochemistry, 2018, 57, 3493-3502.	2.5	12

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19	Heterologous Production and Purification of a Functional Chloroform Reductive Dehalogenase. ACS Chemical Biology, 2018, 13, 548-552.	3.4	12
20	The role of conserved residues in Fdc decarboxylase in prenylated flavin mononucleotide oxidative maturation, cofactor isomerization, and catalysis. Journal of Biological Chemistry, 2018, 293, 2272-2287.	3.4	35
21	Oxidative Maturation and Structural Characterization of Prenylated FMN Binding by UbiD, a Decarboxylase Involved in Bacterial Ubiquinone Biosynthesis. Journal of Biological Chemistry, 2017, 292, 4623-4637.	3.4	42
22	Regioselective <i>para</i> â€Carboxylation of Catechols with a Prenylated Flavin Dependent Decarboxylase. Angewandte Chemie - International Edition, 2017, 56, 13893-13897.	13.8	64
23	Regioselektive <i>para</i> â€Carboxylierung von Catecholen mit einer Prenylflavinâ€abhägigen Decarboxylase. Angewandte Chemie, 2017, 129, 14081-14085.	2.0	6
24	Analysis of Heme Iron Coordination in DGCR8: The Heme-Binding Component of the Microprocessor Complex. Biochemistry, 2016, 55, 5073-5083.	2.5	11
25	An oxidative N-demethylase reveals PAS transition from ubiquitous sensor to enzyme. Nature, 2016, 539, 593-597.	27.8	21
26	Structures of the methyltransferase component of <i>Desulfitobacterium hafniense</i> DCB-2 <i>O</i> -demethylase shed light on methyltetrahydrofolate formation. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1900-1908.	2.5	5
27	UbiX is a flavin prenyltransferase required for bacterial ubiquinone biosynthesis. Nature, 2015, 522, 502-506.	27.8	168
28	New cofactor supports α,β-unsaturated acid decarboxylation via 1,3-dipolar cycloaddition. Nature, 2015, 522, 497-501.	27.8	197
29	A microbial platform for renewable propane synthesis based on a fermentative butanol pathway. Biotechnology for Biofuels, 2015, 8, 61.	6.2	53
30	Epoxyqueuosine Reductase Structure Suggests a Mechanism for Cobalamin-dependent tRNA Modification. Journal of Biological Chemistry, 2015, 290, 27572-27581.	3.4	34
31	Glutamate 338 is an electrostatic facilitator of C–Co bond breakage in a dynamic/electrostatic model of catalysis by ornithine aminomutase. FEBS Journal, 2015, 282, 1242-1255.	4.7	1
32	Reductive dehalogenase structure suggests a mechanism for B12-dependent dehalogenation. Nature, 2015, 517, 513-516.	27.8	260
33	Human P450-like oxidation of diverse proton pump inhibitor drugs by â€~gatekeeper' mutants of flavocytochrome P450 BM3. Biochemical Journal, 2014, 460, 247-259.	3.7	31
34	Energy Landscapes and Catalysis in Nitric-oxide Synthase. Journal of Biological Chemistry, 2014, 289, 11725-11738.	3.4	25
35	A Conformational Sampling Model for Radical Catalysis in Pyridoxal Phosphate- and Cobalamin-dependent Enzymes. Journal of Biological Chemistry, 2014, 289, 34161-34174.	3.4	5
36	Structure and Biochemical Properties of the Alkene Producing Cytochrome P450 OleTJE (CYP152L1) from the Jeotgalicoccus sp. 8456 Bacterium. Journal of Biological Chemistry, 2014, 289, 6535-6550.	3.4	153

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37	Another Role for CO with Nitrogenase? CO Stimulates Hydrogen Evolution Catalyzed by Variant <i>Azotobacter vinelandii</i> Mo-Nitrogenases. Biochemistry, 2014, 53, 6151-6160.	2.5	9
38	Electro-enzymatic viologen-mediated substrate reduction using pentaerythritol tetranitrate reductase and a parallel, segmented fluid flow system. Catalysis Science and Technology, 2013, 3, 1505.	4.1	20
39	The copper supply pathway to a <i><scp>S</scp>almonella</i> <scp>C</scp> u, <scp>Z</scp> nâ€superoxide dismutase ( <scp>SodCll</scp> ) involves <scp>P</scp> <sub>1</sub> <scp><sub>B</sub></scp> â€type <scp>ATPase</scp> copper efflux and periplasmic <scp>CueP</scp> . Molecular Microbiology, 2013, 87, 466-477.	2.5	96
40	The transcriptional regulator CprK detects chlorination by combining direct and indirect readout mechanisms. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120323.	4.0	17
41	Structure of the cobalamin-binding protein of a putative <i>O</i> -demethylase from <i>Desulfitobacterium hafniense</i> DCB-2. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1609-1616.	2.5	6
42	Characterization of a novel copper-haem <i>c</i> dissimilatory nitrite reductase from <i>Ralstonia pickettii</i> . Biochemical Journal, 2012, 444, 219-226.	3.7	15
43	Heterologous expression, purification and cofactor reconstitution of the reductive dehalogenase PceA from Dehalobacter restrictus. Protein Expression and Purification, 2012, 85, 224-229.	1.3	28
44	Flavocytochrome P450 BM3 mutant W1046A is a NADH-dependent fatty acid hydroxylase: Implications for the mechanism of electron transfer in the P450 BM3 dimer. Archives of Biochemistry and Biophysics, 2011, 507, 75-85.	3.0	38
45	Glutamate–haem ester bond formation is disfavoured in flavocytochrome P450 BM3: characterization of glutamate substitution mutants at the haem site of P450 BM3. Biochemical Journal, 2010, 427, 455-466.	3.7	13
46	A short, chemoenzymatic route to chiral β-aryl-γ-amino acids using reductases from anaerobic bacteria. Organic and Biomolecular Chemistry, 2010, 8, 533-535.	2.8	33
47	Continuous two-phase flow miniaturised bioreactor for monitoring anaerobic biocatalysis by pentaerythritol tetranitrate reductase. Lab on A Chip, 2010, 10, 1929.	6.0	22
48	Structural basis for VO2+ inhibition of nitrogenase activity (A): 31P and 23Na interactions with the metal at the nucleotide binding site of the nitrogenase Fe protein identified by ENDOR spectroscopy. Journal of Biological Inorganic Chemistry, 2008, 13, 623-635.	2.6	6
49	Structural basis for VO2+-inhibition of nitrogenase activity: (B) pH-sensitive inner-sphere rearrangements in the 1H-environment of the metal coordination site of the nitrogenase Fe–protein identified by ENDOR spectroscopy. Journal of Biological Inorganic Chemistry, 2008, 13, 637-650.	2.6	3
50	Structureâ€Based Insight into the Asymmetric Bioreduction of the CC Double Bond of α,βâ€Unsaturated Nitroalkenes by Pentaerythritol Tetranitrate Reductase. Advanced Synthesis and Catalysis, 2008, 350, 2789-2803.	4.3	84
51	Highly Enantioselective Reduction of β,β-Disubstituted Aromatic Nitroalkenes Catalyzed by <i>Clostridium sporogenes</i> . Journal of Organic Chemistry, 2008, 73, 4295-4298.	3.2	84
52	Conformations generated during turnover of the Azotobacter vinelandii nitrogenase MoFe protein and their relationship to physiological function. Journal of Inorganic Biochemistry, 2007, 101, 1649-1656.	3.5	23
53	Vanadium(v) is reduced by the †as isolated' nitrogenase Fe-protein at neutral pH. Chemical Communications, 2006, , 2807-2809.	4.1	5
54	Azotobacter vinelandiiVanadium Nitrogenase:Â Formaldehyde Is a Product of Catalyzed HCN Reduction, and Excess Ammonia Arises Directly from Catalyzed Azide Reductionâ€. Biochemistry, 2006, 45, 4190-4198.	2.5	29

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55	How Nitrogenase Shakes â^' Initial Information about Pâ^'Cluster and FeMo-cofactor Normal Modes from Nuclear Resonance Vibrational Spectroscopy (NRVS). Journal of the American Chemical Society, 2006, 128, 7608-7612.	13.7	73
56	Evidence for a dynamic role for homocitrate during nitrogen fixation: the effect of substitution at the α-Lys426 position in MoFe-protein of Azotobacter vinelandii. Biochemical Journal, 2006, 397, 261-270.	3.7	25
57	Nitrogenase proteins from Gluconacetobacter diazotrophicus, a sugarcane-colonizing bacterium. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1750, 154-165.	2.3	18
58	Variant MoFe proteins of Azotobacter vinelandii: effects of carbon monoxide on electron paramagnetic resonance spectra generated during enzyme turnover. Journal of Biological Inorganic Chemistry, 2005, 10, 394-406.	2.6	30
59	Mn2+-adenosine nucleotide complexes in the presence of the nitrogenase iron-protein: detection of conformational rearrangements directly at the nucleotide binding site by EPR and 2D-ESEEM (two-dimensional electron spin-echo envelope modulation spectroscopy). Biochemical Journal, 2005, 391, 527-539.	3.7	14
60	Nitrogen Fixation – A General Overview. , 2002, , 1-34.		18
61	Multiple Inequivalent Metalâ^'Nucleotide Coordination Environments in the Presence of the VO2+-Inhibited Nitrogenase Iron Protein:  pH-Dependent Structural Rearrangements at the Nucleotide Binding Site. Biochemistry, 2002, 41, 13253-13263.	2.5	8
62	Electron Paramagnetic Resonance Analysis of DifferentAzotobacter vinelandiiNitrogenase MoFe-Protein Conformations Generated during Enzyme Turnover:Â Evidence forS=3/2Spin States from Reduced MoFe-Protein Intermediatesâ€. Biochemistry, 2001, 40, 3333-3339.	2.5	52
63	Differential Effects on N2Binding and Reduction, HD Formation, and Azide Reduction with α-195His- and α-191Gln-Substituted MoFe Proteins ofAzotobacter vinelandiiNitrogenaseâ€. Biochemistry, 2000, 39, 15570-15577.	2.5	84
64	Azotobacter vinelandii Nitrogenases with Substitutions in the FeMo-Cofactor Environment of the MoFe Protein:  Effects of Acetylene or Ethylene on Interactions with H+, HCN, and CN Biochemistry, 2000, 39, 10855-10865.	2.5	38
65	Azotobacter vinelandiiNitrogenases Containing Altered MoFe Proteins with Substitutions in the FeMo-Cofactor Environment: Effects on the Catalyzed Reduction of Acetylene and Ethyleneâ€. Biochemistry, 2000, 39, 2970-2979.	2.5	50
66	Effects on Substrate Reduction of Substitution of Histidine-195 by Glutamine in the α-Subunit of the MoFe Protein of Azotobacter vinelandii Nitrogenase. Biochemistry, 1998, 37, 17495-17505.	2.5	68
67	Evidence for Electron Transfer-dependent Formation of a Nitrogenase Iron Protein-Molybdenum-Iron Protein Tight Complex. Journal of Biological Chemistry, 1997, 272, 4157-4165.	3.4	40
68	Evidence for Electron Transfer from the Nitrogenase Iron Protein to the Molybdenumâ^'Iron Protein without MgATP Hydrolysis:  Characterization of a Tight Proteinâ^'Protein Complex. Biochemistry, 1996, 35, 7188-7196.	2.5	78
69	Involvement of the P Cluster in Intramolecular Electron Transfer within the Nitrogenase MoFe Protein. Journal of Biological Chemistry, 1995, 270, 27007-27013.	3.4	70
70	Kinetics and mechanism of the reaction of cyanide with molybdenum nitrogenase from Azotobacter vinelandii. Biochemistry, 1989, 28, 8460-8466.	2.5	42