Alexander F Yakunin

List of Publications by Year in descending order

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136 papers 12,056 citations

48 h-index

43973

29081 104 g-index

142 all docs $\begin{array}{c} 142 \\ \\ \text{docs citations} \end{array}$

times ranked

142

13711 citing authors

#	Article	IF	CITATIONS
1	Defluorination Capability of <scp>l</scp> â€2â€Haloacid Dehalogenases in the HADâ€Like Hydrolase Superfamily Correlates with Active Site Compactness. ChemBioChem, 2022, 23, .	1.3	12
2	REVOLVER: A low-cost automated protein purifier based on parallel preparative gravity column workflows. HardwareX, 2022, 11, e00291.	1.1	0
3	Metabolite Damage and Damage Control in a Minimal Genome. MBio, 2022, 13, .	1.8	10
4	Lignin-oxidizing activity of bacterial laccases characterized using soluble substrates and polymeric lignin. Journal of Biotechnology, 2021, 325, 128-137.	1.9	21
5	Automation assisted anaerobic phenotyping for metabolic engineering. Microbial Cell Factories, 2021, 20, 184.	1.9	4
6	Structural and biochemical insights into CRISPR RNA processing by the Cas5c ribonuclease SMU1763 from Streptococcus mutans. Journal of Biological Chemistry, 2021, 297, 101251.	1.6	2
7	The HydS C-terminal domain of the Thiocapsa bogorovii HydSL hydrogenase is involved in membrane anchoring and electron transfer. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148492.	0.5	4
8	One-Pot Biocatalytic Transformation of Adipic Acid to 6-Aminocaproic Acid and 1,6-Hexamethylenediamine Using Carboxylic Acid Reductases and Transaminases. Journal of the American Chemical Society, 2020, 142, 1038-1048.	6.6	66
9	Evolutionary classification of CRISPR–Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
10	Rational engineering of 2-deoxyribose-5-phosphate aldolases for the biosynthesis of (R)-1,3-butanediol. Journal of Biological Chemistry, 2020, 295, 597-609.	1.6	16
11	A Bifunctional Polyphosphate Kinase Driving the Regeneration of Nucleoside Triphosphate and Reconstituted Cell-Free Protein Synthesis. ACS Synthetic Biology, 2020, 9, 36-42.	1.9	20
12	A microplate screen to estimate metal-binding affinities of metalloproteins. Analytical Biochemistry, 2020, 609, 113836.	1.1	8
13	A novel C-terminal degron identified in bacterial aldehyde decarbonylases using directed evolution. Biotechnology for Biofuels, 2020, 13, 114.	6.2	8
14	Biocatalytic in Vitro and in Vivo FMN Prenylation and (De)carboxylase Activation. ACS Chemical Biology, 2020, 15, 1874-1882.	1.6	13
15	Proteome Cold-Shock Response in the Extremely Acidophilic Archaeon, Cuniculiplasma divulgatum. Microorganisms, 2020, 8, 759.	1.6	3
16	Extrachromosomal circular elements targeted by CRISPR-Cas in <i>Dehalococcoides mccartyi</i> are linked to mobilization of reductive dehalogenase genes. ISME Journal, 2019, 13, 24-38.	4.4	16
17	Site-directed mutagenesis and stability of the carboxylic acid reductase MAB4714 from Mycobacterium abscessus. Journal of Biotechnology, 2019, 303, 72-79.	1.9	15
18	Prenylated FMN: Biosynthesis, purification, and Fdc1 activation. Methods in Enzymology, 2019, 620, 469-488.	0.4	5

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19	Decoding the ocean's microbiological secrets for marine enzyme biodiscovery. FEMS Microbiology Letters, 2019, 366, .	0.7	26
20	Bisphosphonic acids and related compounds as inhibitors of nucleotide―and polyphosphateâ€processing enzymes: A PPK1 and PPK2 case study. Chemical Biology and Drug Design, 2019, 93, 1197-1206.	1.5	8
21	Biocatalytic production of adipic acid from glucose using engineered Saccharomyces cerevisiae. Metabolic Engineering Communications, 2018, 6, 28-32.	1.9	70
22	Evaluating the effect of enzymatic pretreatment on the anaerobic digestibility of pulp and paper biosludge. Biotechnology Reports (Amsterdam, Netherlands), 2018, 17, 77-85.	2.1	42
23	Direct analysis by timeâ€ofâ€flight secondary ion mass spectrometry reveals action of bacterial laccaseâ€mediator systems on both hardwood and softwood samples. Physiologia Plantarum, 2018, 164, 5-16.	2.6	10
24	The Legionella pneumophila effector Ceg4 is a phosphotyrosine phosphatase that attenuates activation of eukaryotic MAPK pathways. Journal of Biological Chemistry, 2018, 293, 3307-3320.	1.6	12
25	Biosynthesis and Activity of Prenylated FMN Cofactors. Cell Chemical Biology, 2018, 25, 560-570.e6.	2.5	45
26	Determinants and Prediction of Esterase Substrate Promiscuity Patterns. ACS Chemical Biology, 2018, 13, 225-234.	1.6	106
27	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. Environmental Science & Environmental Metagenomes with High Hydrolytic Environmental Metagenomes with High Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. Environmental Science & Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. Environmental Science & Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. Environmental Science &	4.6	56
28	Discovery and Functional Characterization of a Yeast Sugar Alcohol Phosphatase. ACS Chemical Biology, 2018, 13, 3011-3020.	1.6	12
29	Structural Insights into Substrate Selectivity and Activity of Bacterial Polyphosphate Kinases. ACS Catalysis, 2018, 8, 10746-10760.	5.5	48
30	Heavy Metal Removal by Bioaccumulation Using Genetically Engineered Microorganisms. Frontiers in Bioengineering and Biotechnology, 2018, 6, 157.	2.0	203
31	Relationships between Substrate Promiscuity and Chiral Selectivity of Esterases from Phylogenetically and Environmentally Diverse Microorganisms. Catalysts, 2018, 8, 10.	1.6	11
32	Engineering a short, aldolase-based pathway for (R)-1,3-butanediol production in Escherichia coli. Metabolic Engineering, 2018, 48, 13-24.	3.6	49
33	Novel Aldo-Keto Reductases for the Biocatalytic Conversion of 3-Hydroxybutanal to 1,3-Butanediol: Structural and Biochemical Studies. Applied and Environmental Microbiology, 2017, 83, .	1.4	24
34	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. Scientific Reports, 2017, 7, 44103.	1.6	67
35	Refined experimental annotation reveals conserved corrinoid autotrophy in chloroform-respiring <i>Dehalobacter</i> isolates. ISME Journal, 2017, 11, 626-640.	4.4	21
36	Structural and functional characterization of the TYW3/Taw3 class of SAM-dependent methyltransferases. Rna, 2017, 23, 346-354.	1.6	13

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37	SAMHD1 is a biomarker for cytarabine response and a therapeutic target in acute myeloid leukemia. Nature Medicine, 2017, 23, 250-255.	15.2	121
38	Metabolic and evolutionary patterns in the extremely acidophilic archaeon Ferroplasma acidiphilum YT. Scientific Reports, 2017, 7, 3682.	1.6	21
39	Exploring Bacterial Carboxylate Reductases for the Reduction of Bifunctional Carboxylic Acids. Biotechnology Journal, 2017, 12, 1600751.	1.8	74
40	Alkene hydrogenation activity of enoate reductases for an environmentally benign biosynthesis of adipic acid. Chemical Science, 2017, 8, 1406-1413.	3.7	77
41	Arabidopsis <i>TH2</i> Encodes the Orphan Enzyme Thiamin Monophosphate Phosphatase. Plant Cell, 2016, 28, 2683-2696.	3.1	42
42	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in Escherichia coli. Cell Reports, 2016, 14, 648-661.	2.9	34
43	Experimental validation of in silico modelâ€predicted isocitrate dehydrogenase and phosphomannose isomerase from D ehalococcoides mccartyi. Microbial Biotechnology, 2016, 9, 47-60.	2.0	1
44	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. Biomacromolecules, 2016, 17, 2027-2039.	2.6	114
45	Systematic Genetic Screens Reveal the Dynamic Global Functional Organization of the Bacterial Translation Machinery. Cell Reports, 2016, 17, 904-916.	2.9	34
46	Altered stoichiometry i>Escherichia coli / i>Cascade complexes with shortened CRISPR RNA spacers are capable of interference and primed adaptation. Nucleic Acids Research, 2016, 44, 10849-10861.	6.5	37
47	A family of metal-dependent phosphatases implicated in metabolite damage-control. Nature Chemical Biology, 2016, 12, 621-627.	3.9	48
48	The Cas6e ribonuclease is not required for interference and adaptation by the <i>E. coli </i> type I-E CRISPR-Cas system. Nucleic Acids Research, 2015, 43, 6049-6061.	6.5	21
49	Metagenomics as a Tool for Enzyme Discovery: Hydrolytic Enzymes from Marine-Related Metagenomes. Advances in Experimental Medicine and Biology, 2015, 883, 1-20.	0.8	35
50	Identification and Characterization of Carboxyl Esterases of Gill Chamber-Associated Microbiota in the Deep-Sea Shrimp Rimicaris exoculata by Using Functional Metagenomics. Applied and Environmental Microbiology, 2015, 81, 2125-2136.	1.4	35
51	Pressure adaptation is linked to thermal adaptation in saltâ€saturated marine habitats. Environmental Microbiology, 2015, 17, 332-345.	1.8	40
52	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2015, 290, 18678-18698.	1.6	70
53	Structural and functional analysis of betaine aldehyde dehydrogenase from <i>Staphylococcus aureus</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1159-1175.	2.5	16
54	An updated evolutionary classification of CRISPR–Cas systems. Nature Reviews Microbiology, 2015, 13, 722-736.	13.6	2,081

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55	Analysis of Nuclease Activity of Cas1 Proteins Against Complex DNA Substrates. Methods in Molecular Biology, 2015, 1311, 251-264.	0.4	4
56	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian) Tj ETQq0 0 esterases and an arabinopyranosidase. Applied Microbiology and Biotechnology, 2015, 99, 10031-10046.	0 rgBT / 1.7	Overlock 10
57	CRISPR RNA binding and DNA target recognition by purified Cascade complexes from Escherichia coli. Nucleic Acids Research, 2015, 43, 530-543.	6.5	22
58	Role of the Streptococcus mutans CRISPR-Cas Systems in Immunity and Cell Physiology. Journal of Bacteriology, 2015, 197, 749-761.	1.0	59
59	The environment shapes microbial enzymes: five cold-active and salt-resistant carboxylesterases from marine metagenomes. Applied Microbiology and Biotechnology, 2015, 99, 2165-2178.	1.7	83
60	The CRISPR-associated Cas4 protein Pcal_0546 from Pyrobaculum calidifontis contains a [2Fe-2S] cluster: crystal structure and nuclease activity. Nucleic Acids Research, 2014, 42, 11144-11155.	6.5	29
61	Structure-Based Mutational Studies of Substrate Inhibition of Betaine Aldehyde Dehydrogenase BetB from Staphylococcus aureus. Applied and Environmental Microbiology, 2014, 80, 3992-4002.	1.4	52
62	Toroidal Structure and DNA Cleavage by the CRISPR-Associated [4Fe-4S] Cluster Containing Cas4 Nuclease SSO0001 from <i>Sulfolobus solfataricus</i> . Journal of the American Chemical Society, 2013, 135, 17476-17487.	6.6	52
63	Biochemical and Structural Studies of Conserved Maf Proteins Revealed Nucleotide Pyrophosphatases with a Preference for Modified Nucleotides. Chemistry and Biology, 2013, 20, 1386-1398.	6.2	15
64	Genome sequence and functional genomic analysis of the oil-degrading bacterium Oleispira antarctica. Nature Communications, 2013, 4, 2156.	5.8	115
65	Nucleotide degradation and ribose salvage in yeast. Molecular Systems Biology, 2013, 9, 665.	3.2	58
66	Biochemical studies of the multicopper oxidase (small laccase) from <i><scp>S</scp>treptomyces coelicolor</i> using bioactive phytochemicals and siteâ€directed mutagenesis. Microbial Biotechnology, 2013, 6, 588-597.	2.0	50
67	Biochemical Diversity of Carboxyl Esterases and Lipases from Lake Arreo (Spain): a Metagenomic Approach. Applied and Environmental Microbiology, 2013, 79, 3553-3562.	1.4	59
68	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
69	Nuclease Activity of the Human SAMHD1 Protein Implicated in the Aicardi-Goutières Syndrome and HIV-1 Restriction. Journal of Biological Chemistry, 2013, 288, 8101-8110.	1.6	194
70	Structure and activity of the NAD(P) ⁺ â€dependent succinate semialdehyde dehydrogenase Ynel from <i>Salmonella typhimurium</i> . Proteins: Structure, Function and Bioinformatics, 2013, 81, 1031-1041.	1.5	16
71	Structure and activity of the <i>Pseudomonas aeruginosa</i> hotdog-fold thioesterases PA5202 and PA2801. Biochemical Journal, 2012, 444, 445-455.	1.7	6
72	Biochemical and Structural Studies of Uncharacterized Protein PA0743 from Pseudomonas aeruginosa Revealed NAD+-dependent l-Serine Dehydrogenase. Journal of Biological Chemistry, 2012, 287, 1874-1883.	1.6	23

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73	Application of Time-of-Flight-Secondary Ion Mass Spectrometry for the Detection of Enzyme Activity on Solid Wood Substrates. Analytical Chemistry, 2012, 84, 4443-4451.	3.2	38
74	Structure and activity of the cold-active and anion-activated carboxyl esterase OLEI01171 from the oil-degrading marine bacterium <i>Oleispira antarctica</i>). Biochemical Journal, 2012, 445, 193-203.	1.7	31
75	Mapping the Reaction Coordinates of Enzymatic Defluorination. Journal of the American Chemical Society, 2011, 133, 7461-7468.	6.6	73
76	Riboneogenesis in Yeast. Cell, 2011, 145, 969-980.	13.5	105
77	Structure and activity of the Cas3 HD nuclease MJ0384, an effector enzyme of the CRISPR interference. EMBO Journal, 2011, 30, 4616-4627.	3.5	122
78	Evolution and classification of the CRISPR–Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	13.6	2,078
79	An Inserted $\hat{l}\pm/\hat{l}^2$ Subdomain Shapes the Catalytic Pocket of Lactobacillus johnsonii Cinnamoyl Esterase. PLoS ONE, 2011, 6, e23269.	1.1	46
80	A dual function of the CRISPR–Cas system in bacterial antivirus immunity and DNA repair. Molecular Microbiology, 2011, 79, 484-502.	1.2	241
81	Structure and activity of the Saccharomyces cerevisiae dUTP pyrophosphatase DUT1, an essential housekeeping enzyme. Biochemical Journal, 2011, 437, 243-253.	1.7	25
82	Structural and enzymatic characterization of NanS (YjhS), a 9â€∢i>Oâ€Acetyl <i>N</i> â€acetylneuraminic acid esterase from <i>Escherichia coli O157:H7</i> . Protein Science, 2011, 20, 1208-1219.	3.1	33
83	The Chromosomal mazEF Locus of Streptococcus mutans Encodes a Functional Type II Toxin-Antitoxin Addiction System. Journal of Bacteriology, 2011, 193, 1122-1130.	1.0	34
84	Sequence―and activityâ€based screening of microbial genomes for novel dehalogenases. Microbial Biotechnology, 2010, 3, 107-120.	2.0	53
85	Mining bacterial genomes for novel arylesterase activity. Microbial Biotechnology, 2010, 3, 677-690.	2.0	12
86	Structure and Activity of the Metal-independent Fructose-1,6-bisphosphatase YK23 from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2010, 285, 21049-21059.	1.6	21
87	Structural Insight into the Mechanism of c-di-GMP Hydrolysis by EAL Domain Phosphodiesterases. Journal of Molecular Biology, 2010, 402, 524-538.	2.0	121
88	Mass Spectrometry Following Mild Enzymatic Digestion Reveals Phosphorylation of Recombinant Proteins in Escherichia coli Through Mechanisms Involving Direct Nucleotide Binding. Journal of Proteome Research, 2010, 9, 3311-3318.	1.8	7
89	Structure of PhnP, a Phosphodiesterase of the Carbon-Phosphorus Lyase Pathway for Phosphonate Degradation. Journal of Biological Chemistry, 2009, 284, 17216-17226.	1.6	34
90	Structural and Biochemical Characterization of the Type II Fructose-1,6-bisphosphatase GlpX from Escherichia coli. Journal of Biological Chemistry, 2009, 284, 3784-3792.	1.6	49

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91	ADP-dependent 6-Phosphofructokinase from Pyrococcus horikoshii OT3. Journal of Biological Chemistry, 2009, 284, 22664-22671.	1.6	21
92	Crystal structure of human retinoblastoma binding protein 9. Proteins: Structure, Function and Bioinformatics, 2009, 74, 526-529.	1.5	12
93	Genetic and biochemical properties of an alkaline phosphatase PhoX family protein found in many bacteria. Environmental Microbiology, 2009, 11, 1572-1587.	1.8	67
94	Structural and enzymatic characterization of DR1281: A calcineurinâ€like phosphoesterase from ⟨i>Deinococcus radiodurans⟨ i>. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1000-1009.	1.5	15
95	Structural and functional characterization of a novel phosphatase from the <i>Arabidopsis thaliana</i> gene locus At1g05000. Proteins: Structure, Function and Bioinformatics, 2008, 73, 241-253.	1.5	17
96	Biochemical and Structural Characterization of a Novel Family of Cystathionine \hat{l}^2 -Synthase Domain Proteins Fused to a Zn Ribbon-Like Domain. Journal of Molecular Biology, 2008, 375, 301-315.	2.0	44
97	Structural Insight into the Mechanism of Substrate Specificity and Catalytic Activity of an HD-Domain Phosphohydrolase: The 5′-Deoxyribonucleotidase YfbR from Escherichia coli. Journal of Molecular Biology, 2008, 378, 215-226.	2.0	62
98	Functional and Structural Characterization of Four Glutaminases from Escherichia coli and Bacillus subtilis. Biochemistry, 2008, 47, 5724-5735.	1.2	101
99	Functional and Structural Characterization of DR_0079 from <i>Deinococcus radiodurans</i> , a Novel Nudix Hydrolase with a Preference for Cytosine (Deoxy)ribonucleoside 5′-Di- and Triphosphates. Biochemistry, 2008, 47, 6571-6582.	1.2	11
100	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. Journal of Biological Chemistry, 2008, 283, 20361-20371.	1.6	177
101	Polyphosphate-dependent synthesis of ATP and ADP by the family-2 polyphosphate kinases in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17730-17735.	3.3	112
102	High Throughput Screening of Purified Proteins for Enzymatic Activity. Methods in Molecular Biology, 2008, 426, 331-341.	0.4	17
103	Structure of an Amide Bond Forming F420:γĴ³-glutamyl Ligase from Archaeoglobus Fulgidus - A Member of a New Family of Non-ribosomal Peptide Synthases. Journal of Molecular Biology, 2007, 372, 456-469.	2.0	31
104	Molecular Basis of the Antimutagenic Activity of the House-Cleaning Inosine Triphosphate Pyrophosphatase RdgB from Escherichia coli. Journal of Molecular Biology, 2007, 374, 1091-1103.	2.0	26
105	Development of BIATECH-54 standard mixtures for assessment of protein identification and relative expression. Proteomics, 2007, 7, 3693-3698.	1.3	11
106	In situ proteolysis for protein crystallization and structure determination. Nature Methods, 2007, 4, 1019-1021.	9.0	197
107	Structural and biochemical characterization of a novel Mn2+-dependent phosphodiesterase encoded by theyfcEgene. Protein Science, 2007, 16, 1338-1348.	3.1	24
108	Crystal structures of a phosphotransacetylase from Bacillus subtilis and its complex with acetyl phosphate. Journal of Structural and Functional Genomics, 2006, 6, 269-279.	1.2	20

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109	Genome-wide Analysis of Substrate Specificities of the Escherichia coli Haloacid Dehalogenase-like Phosphatase Family. Journal of Biological Chemistry, 2006, 281, 36149-36161.	1.6	249
110	Molecular Basis of Formaldehyde Detoxification. Journal of Biological Chemistry, 2006, 281, 14514-14522.	1.6	118
111	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	87
112	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	104
113	Structural and functional characterization of a 5,10-methenyltetrahydrofolate synthetase from Mycoplasma pneumoniae (Gl: 13508087). Proteins: Structure, Function and Bioinformatics, 2005, 61, 433-443.	1.5	12
114	General Enzymatic Screens Identify Three New Nucleotidases in Escherichia coli. Journal of Biological Chemistry, 2004, 279, 54687-54694.	1.6	118
115	Structural and Functional Characterization of a Novel Phosphodiesterase from Methanococcus jannaschii. Journal of Biological Chemistry, 2004, 279, 31854-31862.	1.6	55
116	The Structural Basis for Methylmalonic Aciduria. Journal of Biological Chemistry, 2004, 279, 23646-23653.	1.6	43
117	The HD Domain of the Escherichia coli tRNA Nucleotidyltransferase Has 2′,3′-Cyclic Phosphodiesterase, 2′-Nucleotidase, and Phosphatase Activities. Journal of Biological Chemistry, 2004, 279, 36819-36827.	1.6	74
118	Fe-responsive accumulation of redox proteins ferredoxin and flavodoxin in a marine cryptomonad. European Journal of Phycology, 2004, 39, 73-82.	0.9	12
119	Structural proteomics: a tool for genome annotation. Current Opinion in Chemical Biology, 2004, 8, 42-48.	2.8	70
120	Structure- and Function-based Characterization of a New Phosphoglycolate Phosphatase from Thermoplasma acidophilum. Journal of Biological Chemistry, 2004, 279, 517-526.	1.6	49
121	Role of GlnB and GlnK in ammonium control of both nitrogenase systems in the phototrophic bacterium Rhodobacter capsulatus. Microbiology (United Kingdom), 2003, 149, 2203-2212.	0.7	86
122	Aspartate Dehydrogenase, a Novel Enzyme Identified from Structural and Functional Studies of TM1643. Journal of Biological Chemistry, 2003, 278, 8804-8808.	1.6	70
123	Integrating Structure, Bioinformatics, and Enzymology to Discover Function. Journal of Biological Chemistry, 2003, 278, 26039-26045.	1.6	115
124	AmtB Is Necessary for NH 4 + -Induced Nitrogenase Switch-Off and ADP-Ribosylation in Rhodobacter capsulatus. Journal of Bacteriology, 2002, 184, 4081-4088.	1.0	57
125	Regulation of nitrogenase in the photosynthetic bacterium <i>Rhodobacter sphaeroides</i> containing <i>draTG</i> and <i>nifHDK</i> genes from <i>Rhodobacter capsulatus</i> Canadian Journal of Microbiology, 2001, 47, 206-212.	0.8	15
126	Regulation of nitrogenase in the photosynthetic bacterium <i>Rhodobacter sphaeroides</i> containing <i>draTG</i> and <i>nifHDK</i> genes from <i>Rhodobacter capsulatus</i> Canadian Journal of Microbiology, 2001, 47, 206-212.	0.8	11

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127	Regulation of nitrogenase activity in Rhodobacter capsulatus under dark microoxic conditions. Archives of Microbiology, 2000, 173, 366-372.	1.0	14
128	ACCUMULATION OF FERREDOXIN AND FLAVODOXIN IN A MARINE DIATOM IN RESPONSE TO FE. Journal of Phycology, 1999, 35, 510-519.	1.0	69
129	The Presence of ADP-Ribosylated Fe Protein of Nitrogenase in <i>Rhodobacter capsulatus</i> Is Correlated with Cellular Nitrogen Status. Journal of Bacteriology, 1999, 181, 1994-2000.	1.0	25
130	A Luminol/Iodophenol Chemiluminescent Detection System for Western Immunoblots. Analytical Biochemistry, 1998, 258, 146-149.	1.1	60
131	Purification and characterization of pyruvate oxidoreductase from the photosynthetic bacterium Rhodobacter capsulatus. Biochimica Et Biophysica Acta - Bioenergetics, 1998, 1409, 39-49.	0.5	52
132	Short-Term Regulation of Nitrogenase Activity by NH ₄ ⁺ in <i>Rhodobacter capsulatus</i> : Multiple In Vivo Nitrogenase Responses to NH ₄ ⁺ Addition. Journal of Bacteriology, 1998, 180, 6392-6395.	1.0	35
133	Electron Transport as a Limiting Factor in Biological Hydrogen Production. , 1998, , 99-104.		0
134	Purification and properties of a bacterial-type ferredoxin from the nitrogen-fixing cyanobacterium Anabaena variabilis ATCC29413. BBA - Proteins and Proteomics, 1993, 1163, 124-130.	2.1	16
135	Purification and properties of a flavodoxin from the heterocystous cyanobacterium Anabaena sphaerica. BBA - Proteins and Proteomics, 1993, 1164, 305-310.	2.1	7
136	Properties and regulation of synthesis of two ferredoxins from Rhodopseudomonas capsulata. Biochimica Et Biophysica Acta - Bioenergetics, 1983, 725, 298-308.	0.5	37