Colin J Jackson

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

151 papers	4,404 citations	37 h-index	61 g-index
179 ext. papers	5,606 ext. citations	7.8 avg, IF	5.52 L-index

#	Paper	IF	Citations
151	Genomic and metagenomic surveys of hydrogenase distribution indicate H2 is a widely utilised energy source for microbial growth and survival. *ISME Journal*, **2016**, 10, 761-77	11.9	319
150	Biochemistry of microbial degradation of hexachlorocyclohexane and prospects for bioremediation. *Microbiology and Molecular Biology Reviews*, **2010**, 74, 58-80	13.2	281
149	The role of protein dynamics in the evolution of new enzyme function. *Nature Chemical Biology*, **2016**, 12, 944-950	11.7	166
148	Diminishing returns and tradeoffs constrain the laboratory optimization of an enzyme. *Nature Communications*, **2012**, 3, 1257	17.4	156
147	Evolutionary optimization of computationally designed enzymes: Kemp eliminases of the KE07 series. *Journal of Molecular Biology*, **2010**, 396, 1025-42	6.5	132
146	The enzymatic basis for pesticide bioremediation. *Indian Journal of Microbiology*, **2008**, 48, 65-79	3.7	120
145	Reconstructing a missing link in the evolution of a recently diverged phosphotriesterase by active-site loop remodeling. *Biochemistry*, **2012**, 51, 6047-55	3.2	109
144	Identification and characterization of two families of F420 H2-dependent reductases from Mycobacteria that catalyse aflatoxin degradation. *Molecular Microbiology*, **2010**, 78, 561-75	4.1	105
143	Sensing and signaling of oxidative stress in chloroplasts by inactivation of the SAL1 phosphoadenosine phosphatase. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4567-76	11.5	101
142	Conformational sampling, catalysis, and evolution of the bacterial phosphotriesterase. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 21631-6	11.5	93
141	Physiology, Biochemistry, and Applications of F420- and Fo-Dependent Redox Reactions. *Microbiology and Molecular Biology Reviews*, **2016**, 80, 451-93	13.2	88
140	Structure and function of an insect carboxylesterase (Esterase7) associated with insecticide resistance. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 10177-82	11.5	84
139	The evolution of new enzyme function: lessons from xenobiotic metabolizing bacteria versus insecticide-resistant insects. *Evolutionary Applications*, **2011**, 4, 225-48	4.8	78
138	In crystallo capture of a Michaelis complex and product-binding modes of a bacterial phosphotriesterase. *Journal of Molecular Biology*, **2008**, 375, 1189-96	6.5	78
137	Improving a natural enzyme activity through incorporation of unnatural amino acids. *Journal of the American Chemical Society*, **2011**, 133, 326-33	16.4	67
136	LTP Induction Boosts Glutamate Spillover by Driving Withdrawal of Perisynaptic Astroglia. *Neuron*, **2020**, 108, 919-936.e11	13.9	65
135	Substrate-promoted formation of a catalytically competent binuclear center and regulation of reactivity in a glycerophosphodiesterase from Enterobacter aerogenes. *Journal of the American Chemical Society*, **2008**, 130, 14129-38	16.4	64

134	The structure of an enzyme-product complex reveals the critical role of a terminal hydroxide nucleophile in the bacterial phosphotriesterase mechanism. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2005**, 1752, 56-64	4	64
133	Protein engineering with unnatural amino acids. *Current Opinion in Structural Biology*, **2013**, 23, 581-7	8.1	63
132	The structure and function of a novel glycerophosphodiesterase from Enterobacter aerogenes. *Journal of Molecular Biology*, **2007**, 367, 1047-62	6.5	62
131	Growth of Escherichia coli coexpressing phosphotriesterase and glycerophosphodiester phosphodiesterase, using paraoxon as the sole phosphorus source. *Applied and Environmental Microbiology*, **2004**, 70, 404-12	4.8	62
130	Ancestral Protein Reconstruction Yields Insights into Adaptive Evolution of Binding Specificity in Solute-Binding Proteins. *Cell Chemical Biology*, **2016**, 23, 236-245	8.2	59
129	Laboratory evolution of protein conformational dynamics. *Current Opinion in Structural Biology*, **2018**, 50, 49-57	8.1	56
128	Catalytic improvement and evolution of atrazine chlorohydrolase. *Applied and Environmental Microbiology*, **2009**, 75, 2184-91	4.8	54
127	Anomalous scattering analysis of Agrobacterium radiobacter phosphotriesterase: the prominent role of iron in the heterobinuclear active site. *Biochemical Journal*, **2006**, 397, 501-8	3.8	52
126	Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein. *Nature Chemical Biology*, **2018**, 14, 542-547	11.7	51
125	Use of engineered enzymes to identify organophosphate and pyrethroid-related toxicity in toxicity identification evaluations. *Environmental Science & Technology*, **2009**, 43, 5514-20	10.3	51
124	Reverse evolution leads to genotypic incompatibility despite functional and active site convergence. *ELife*, **2015**, 4,	8.9	51
123	Characterization of the phenylurea hydrolases A and B: founding members of a novel amidohydrolase subgroup. *Biochemical Journal*, **2009**, 418, 431-41	3.8	50
122	The evolution of multiple active site configurations in a designed enzyme. *Nature Communications*, **2018**, 9, 3900	17.4	50
121	Sequence-Structure-Function Classification of a Catalytically Diverse Oxidoreductase Superfamily in Mycobacteria. *Journal of Molecular Biology*, **2015**, 427, 3554-3571	6.5	47
120	Construction of a robust and sensitive arginine biosensor through ancestral protein reconstruction. *Protein Science*, **2015**, 24, 1412-22	6.3	47
119	Bridging the synaptic gap: neuroligins and neurexin I in Apis mellifera. *PLoS ONE*, **2008**, 3, e3542	3.7	46
118	The methanogenic redox cofactor F is widely synthesized by aerobic soil bacteria. *ISME Journal*, **2017**, 11, 125-137	11.9	43
117	Intramolecular epistasis and the evolution of a new enzymatic function. *PLoS ONE*, **2012**, 7, e39822	3.7	42

116	A polymer surfactant corona dynamically replaces water in solvent-free protein liquids and ensures macromolecular flexibility and activity. *Journal of the American Chemical Society*, **2012**, 134, 13168-71	16.4	41
115	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. *Molecular Psychiatry*, **2019**, 24, 1707-1719	15.1	38
114	Monitoring hippocampal glycine with the computationally designed optical sensor GlyFS. *Nature Chemical Biology*, **2018**, 14, 861-869	11.7	36
113	T-dependent B cell responses to Plasmodium induce antibodies that form a high-avidity multivalent complex with the circumsporozoite protein. *PLoS Pathogens*, **2017**, 13, e1006469	7.6	36
112	A revised biosynthetic pathway for the cofactor F in prokaryotes. *Nature Communications*, **2019**, 10, 1558	17.4	35
111	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. *Nature Chemical Biology*, **2019**, 15, 1120-1128	11.7	35
110	Protein engineering: the potential of remote mutations. *Biochemical Society Transactions*, **2019**, 47, 701-711	5.1	34
109	Testing the evolvability of an insect carboxylesterase for the detoxification of synthetic pyrethroid insecticides. *Insect Biochemistry and Molecular Biology*, **2012**, 42, 343-52	4.5	34
108	Molecular basis for the behavioral effects of the odorant degrading enzyme Esterase 6 in Drosophila. *Scientific Reports*, **2017**, 7, 46188	4.9	33
107	Conformational Tinkering Drives Evolution of a Promiscuous Activity through Indirect Mutational Effects. *Biochemistry*, **2016**, 55, 4583-93	3.2	33
106	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. *Nature Immunology*, **2019**, 20, 1299-1310	19.1	29
105	A 5000-fold increase in the specificity of a bacterial phosphotriesterase for malathion through combinatorial active site mutagenesis. *PLoS ONE*, **2014**, 9, e94177	3.7	28
104	Structure-based rational design of a phosphotriesterase. *Applied and Environmental Microbiology*, **2009**, 75, 5153-6	4.8	28
103	The effects of substrate orientation on the mechanism of a phosphotriesterase. *Organic and Biomolecular Chemistry*, **2005**, 3, 4343-50	3.9	27
102	The Structure and Stability of the Disulfide-Linked [illegible]-Crystallin Dimer Provide Insight into Oxidation Products Associated with Lens Cataract Formation. *Journal of Molecular Biology*, **2019**, 431, 483-497	6.5	27
101	Evolution of Protein Quaternary Structure in Response to Selective Pressure for Increased Thermostability. *Journal of Molecular Biology*, **2016**, 428, 2359-2371	6.5	26
100	Increased expression of a bacterial phosphotriesterase in Escherichia coli through directed evolution. *Protein Expression and Purification*, **2005**, 41, 433-40	2	25
99	Kistamicin biosynthesis reveals the biosynthetic requirements for production of highly crosslinked glycopeptide antibiotics. *Nature Communications*, **2019**, 10, 2613	17.4	24

98	The Redox Cofactor F Protects Mycobacteria from Diverse Antimicrobial Compounds and Mediates a Reductive Detoxification System. *Applied and Environmental Microbiology*, **2016**, 82, 6810-6818	4.8	23
97	Malonate-bound structure of the glycerophosphodiesterase from Enterobacter aerogenes (GpdQ) and characterization of the native Fe2+ metal-ion preference. *Acta Crystallographica Section F: Structural Biology Communications*, **2008**, 64, 681-5		21
96	Mycobacterial FH-Dependent Reductases Promiscuously Reduce Diverse Compounds through a Common Mechanism. *Frontiers in Microbiology*, **2017**, 8, 1000	5.7	20
95	Probing the mechanisms for the selectivity and promiscuity of methyl parathion hydrolase. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2016**, 374,	3	19
94	Mining electron density for functionally relevant protein polysterism in crystal structures. *Cellular and Molecular Life Sciences*, **2011**, 68, 1829-41	10.3	19
93	Structural and evolutionary approaches to the design and optimization of fluorescence-based small molecule biosensors. *Current Opinion in Structural Biology*, **2019**, 57, 31-38	8.1	18
92	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. *PLoS Pathogens*, **2020**, 16, e1008287	7.6	18
91	Pharmacokinetics of OpdA, an organophosphorus hydrolase, in the African green monkey. *Biochemical Pharmacology*, **2010**, 80, 1075-9	6	18
90	Cryptic genetic variation shapes the adaptive evolutionary potential of enzymes. *ELife*, **2019**, 8,	8.9	18
89	Rv2074 is a novel F420 H2 -dependent biliverdin reductase in Mycobacterium tuberculosis. *Protein Science*, **2016**, 25, 1692-709	6.3	18
88	Ancestral sequence reconstruction for protein engineers. *Current Opinion in Structural Biology*, **2021**, 69, 131-141	8.1	18
87	Conformational Disorganization within the Active Site of a Recently Evolved Organophosphate Hydrolase Limits Its Catalytic Efficiency. *Biochemistry*, **2016**, 55, 1408-17	3.2	17
86	Synthesis of a D-ring isomer of galanthamine via a radical-based Smiles rearrangement reaction. *Journal of Organic Chemistry*, **2014**, 79, 6759-64	4.2	17
85	Competing S(N)2 and E2 reaction pathways for hexachlorocyclohexane degradation in the gas phase, solution and enzymes. *Chemical Communications*, **2011**, 47, 976-8	5.8	17
84	Local Efficacy of Glutamate Uptake Decreases with Synapse Size. *Cell Reports*, **2020**, 32, 108182	10.6	17
83	Overcoming insecticide resistance through computational inhibitor design. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 21012-21021	11.5	16
82	Evolutionary expansion of the amidohydrolase superfamily in bacteria in response to the synthetic compounds molinate and diuron. *Applied and Environmental Microbiology*, **2015**, 81, 2612-24	4.8	16
81	Mutation of outer-shell residues modulates metal ion co-ordination strength in a metalloenzyme. *Biochemical Journal*, **2010**, 429, 313-21	3.8	16

80	Use of OpdA, an organophosphorus (OP) hydrolase, prevents lethality in an African green monkey model of acute OP poisoning. *Toxicology*, **2014**, 317, 1-5	4.4	15
79	Protonation state of F420H2 in the prodrug-activating deazaflavin dependent nitroreductase (Ddn) from Mycobacterium tuberculosis. *Molecular BioSystems*, **2016**, 12, 1110-3		15
78	Structure of an Insecticide Sequestering Carboxylesterase from the Disease Vector Culex quinquefasciatus: What Makes an Enzyme a Good Insecticide Sponge?. *Biochemistry*, **2017**, 56, 5512-5525	3.2	14
77	Kinetic and sequence-structure-function analysis of known LinA variants with different hexachlorocyclohexane isomers. *PLoS ONE*, **2011**, 6, e25128	3.7	14
76	Altered conformational sampling along an evolutionary trajectory changes the catalytic activity of an enzyme. *Nature Communications*, **2020**, 11, 5945	17.4	14
75	Classification and substrate head-group specificity of membrane fatty acid desaturases. *Computational and Structural Biotechnology Journal*, **2016**, 14, 341-349	6.8	14
74	Structural Basis for the Allosteric Regulation of the SbtA Bicarbonate Transporter by the P-like Protein, SbtB, from sp. PCC7001. *Biochemistry*, **2019**, 58, 5030-5039	3.2	14
73	Kinetics and efficacy of an organophosphorus hydrolase in a rodent model of methyl-parathion poisoning. *Academic Emergency Medicine*, **2010**, 17, 736-40	3.4	12
72	Mapping the Accessible Conformational Landscape of an Insect Carboxylesterase Using Conformational Ensemble Analysis and Kinetic Crystallography. *Structure*, **2016**, 24, 977-87	5.2	12
71	Cofactor F420-Dependent Enzymes: An Under-Explored Resource for Asymmetric Redox Biocatalysis. *Catalysts*, **2019**, 9, 868	4	12
70	nonribosomal peptide synthetase Ebony encodes an atypical condensation domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 2913-2918	11.5	11
69	Iron(III) located in the dinuclear metallo-βlactamase IMP-1 by pseudocontact shifts. *Angewandte Chemie - International Edition*, **2014**, 53, 14269-72	16.4	11
68	Phosphorescent oxygen-sensing and singlet oxygen production by a biosynthetic silk. *RSC Advances* , **2016**, 6, 39530-39533	3.7	11
67	Rangefinder: A Semisynthetic FRET Sensor Design Algorithm. *ACS Sensors*, **2016**, 1, 1286-1290	9.2	10
66	300-Fold increase in production of the Zn2+-dependent dechlorinase TrzN in soluble form via apoenzyme stabilization. *Applied and Environmental Microbiology*, **2014**, 80, 4003-11	4.8	10
65	Cofactor Tail Length Modulates Catalysis of Bacterial F-Dependent Oxidoreductases. *Frontiers in Microbiology*, **2017**, 8, 1902	5.7	10
64	Strategies for Increasing Protein Stability. *Methods in Molecular Biology*, **2020**, 2073, 163-181	1.4	10
63	Total Syntheses of the 3-Pyrrolo[2,3-]quinolone-Containing Alkaloids Marinoquinolines A-F, K, and Aplidiopsamine A Using a Palladium-Catalyzed Ullmann Cross-Coupling/Reductive Cyclization Pathway. *Journal of Organic Chemistry*, **2020**, 85, 650-663	4.2	10

62	Structural and functional characterization of a putative de novo gene in Drosophila. *Nature Communications*, **2021**, 12, 1667	17.4	10
61	The Synthesis of Certain Derivatives and Analogues of (-)- and (+)-Galanthamine and an Assessment of their Capacities to Inhibit Acetylcholine Esterase. *Journal of Organic Chemistry*, **2017**, 82, 7869-7886	4.2	9
60	Predicting X-ray diffuse scattering from translation-libration-screw structural ensembles. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1657-67		9
59	Structures of a non-ribosomal peptide synthetase condensation domain suggest the basis of substrate selectivity. *Nature Communications*, **2021**, 12, 2511	17.4	9
58	Consensus Mutagenesis and Ancestral Reconstruction Provide Insight into the Substrate Specificity and Evolution of the Front-End ⍰-Desaturase Family. *Biochemistry*, **2020**, 59, 1398-1409	3.2	8
57	Hydrophobic Shielding Drives Catalysis of Hydride Transfer in a Family of FH-Dependent Enzymes. *Biochemistry*, **2016**, 55, 6908-6918	3.2	8
56	The purification, crystallization and preliminary diffraction of a glycerophosphodiesterase from Enterobacter aerogenes. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 659-61		8
55	Immunizations with diverse sarbecovirus receptor-binding domains elicit SARS-CoV-2 neutralizing antibodies against a conserved site of vulnerability. *Immunity*, **2021**,	32.3	8
54	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. *Molecular Biology and Evolution*, **2021**, 38, 2915-2929	8.3	8
53	Constrained evolution of a bispecific enzyme: lessons for biocatalyst design. *Organic and Biomolecular Chemistry*, **2017**, 15, 937-946	3.9	7
52	Active Site Desolvation and Thermostability Trade-Offs in the Evolution of Catalytically Diverse Triazine Hydrolases. *Biochemistry*, **2016**, 55, 6304-6313	3.2	7
51	FAD-sequestering proteins protect mycobacteria against hypoxic and oxidative stress. *Journal of Biological Chemistry*, **2019**, 294, 2903-2912	5.4	7
50	Bacterial catabolism of s-triazine herbicides: biochemistry, evolution and application. *Advances in Microbial Physiology*, **2020**, 76, 129-186	4.4	6
49	Sequential Electrostatic Assembly of a Polymer Surfactant Corona Increases Activity of the Phosphotriesterase arPTE. *Bioconjugate Chemistry*, **2019**, 30, 2771-2776	6.3	6
48	Enzyme dynamics and engineering: one step at a time. *Chemistry and Biology*, **2014**, 21, 1259-1260		6
47	Hydrogel-Immobilized Supercharged Proteins. *Advanced Biology*, **2018**, 2, 1700240	3.5	6
46	Ancestral Protein Reconstruction and Circular Permutation for Improving the Stability and Dynamic Range of FRET Sensors. *Methods in Molecular Biology*, **2017**, 1596, 71-87	1.4	5
45	Structural reconstruction of protein ancestry. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 3897-3902	11.5	5

44	Crystal structure of the mouse interleukin-3 □receptor: insights into interleukin-3 binding and receptor activation. *Biochemical Journal*, **2014**, 463, 393-403	3.8	5
43	The NK Landscape as a Versatile Benchmark for Machine Learning Driven Protein Engineering		5
42	The Evolution of New Catalytic Mechanisms for Xenobiotic Hydrolysis in Bacterial Metalloenzymes. *Australian Journal of Chemistry*, **2016**, 69, 1383	1.2	5
41	The molecular basis for the neofunctionalization of the juvenile hormone esterase duplication in Drosophila. *Insect Biochemistry and Molecular Biology*, **2019**, 106, 10-18	4.5	5
40	Total Syntheses of the Amaryllidaceae Alkaloids Zephycandidine III and Lycosinine A and Their Evaluation as Inhibitors of Acetylcholinesterase. *European Journal of Organic Chemistry*, **2017**, 2017, 4044-4053	3.2	4
39	Devising New Syntheses of the Alkaloid Galanthamine, a Potent and Clinically Deployed Inhibitor of Acetylcholine Esterase. *Strategies and Tactics in Organic Synthesis*, **2015**, 29-50	0.2	4
38	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F-0 in Mycobacteria. *MSystems*, **2020**, 5,	7.6	4
37	Avid binding by B cells to the Plasmodium circumsporozoite protein repeat suppresses responses to protective subdominant epitopes. *Cell Reports*, **2021**, 35, 108996	10.6	4
36	Challenges of short substrate analogues as SARS-CoV-2 main protease inhibitors. *Bioorganic and Medicinal Chemistry Letters*, **2021**, 50, 128333	2.9	4
35	The evolution and engineering of enzyme activity through tuning conformational landscapes. *Protein Engineering, Design and Selection*, **2021**, 34,	1.9	4
34	Engineering a solid-state metalloprotein hydrogen evolution catalyst. *Scientific Reports*, **2020**, 10, 3774	4.9	3
33	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. *PLoS ONE*, **2015**, 10, e0140219	3.7	3
32	Through-Space Scalar F-F Couplings between Fluorinated Noncanonical Amino Acids for the Detection of Specific Contacts in Proteins. *Journal of the American Chemical Society*, **2021**, 143, 19587-19598	16.4	3
31	Altered conformational sampling along an evolutionary trajectory changes the catalytic activity of an enzyme		3
30	A computationally designed fluorescent biosensor for D-serine		3
29	Potent Cyclic Peptide Inhibitors of FXIIa Discovered by mRNA Display with Genetic Code Reprogramming. *Journal of Medicinal Chemistry*, **2021**, 64, 7853-7876	8.3	3
28	Resonant Dielectric Metagratings for Response Intensified Optical Sensing. *Advanced Functional Materials*, **2021**, 2103143	15.6	3
27	Carboxylesterases in the Metabolism and Toxicity of Pesticides **2011**, 57-75		2

26	Directed Evolution of Enzymes **2010**, 723-749		2
25	Cloning, expression, purification, crystallization and preliminary X-ray studies of a pyridoxine 5Sphosphate oxidase from Mycobacterium smegmatis. *Acta Crystallographica Section F: Structural Biology Communications*, **2008**, 64, 435-7		2
24	Adventures on the routes of protein evolution - in memoriam Dan Salah Tawfik (1955 - 2021).. *Journal of Molecular Biology*, **2022**, 434, 167462	6.5	2
23	Avid binding by B cells to the Plasmodium circumsporozoite protein repeat suppresses responses to protective subdominant epitopes		2
22	Higher-order epistatic networks underlie the evolutionary fitness landscape of a xenobiotic-degrading enzyme		2
21	The evolution of nitroimidazole antibiotic resistance in Mycobacterium tuberculosis		2
20	High avidity drives the interaction between the streptococcal C1 phage endolysin, PlyC, with the cell surface carbohydrates of Group A Streptococcus. *Molecular Microbiology*, **2021**, 116, 397-415	4.1	2
19	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. *Molecular Biology and Evolution*, **2021**, 38, 545-556	8.3	2
18	Regulatory adenylnucleotide-mediated binding of the PII-like protein SbtB to the cyanobacterial bicarbonate transporter SbtA is controlled by the cellular energy state		2
17	Antiviral cyclic peptides targeting the main protease of SARS-CoV-2.. *Chemical Science*, **2022**, 13, 3826-3836	9.4	2
16	Method for Developing Optical Sensors Using a Synthetic Dye-Fluorescent Protein FRET Pair and Computational Modeling and Assessment. *Methods in Molecular Biology*, **2017**, 1596, 89-99	1.4	1
15	Pseudokontaktverschiebungen lokalisieren Eisen(III) in der zweikernigen Metallo-βLaktamase IMP-1. *Angewandte Chemie*, **2014**, 126, 14494-14497	3.6	1
14	A Rationally and Computationally Designed Fluorescent Biosensor for d-Serine. *ACS Sensors*, **2021**, 6, 4193-4205	9.2	1
13	Directed Evolution of Enzymes **2010**, 654-673		1
12	Cellular and structural basis of synthesis of the unique intermediate dehydro-F420-0 in mycobacteria		1
11	Enhancement of metallomacrocycle-based oxygen reduction catalysis through immobilization in a tunable silk-protein scaffold. *Journal of Inorganic Biochemistry*, **2020**, 204, 110960	4.2	1
10	Potency boost of a dihydrofolate reductase inhibitor by multienzyme FH-dependent reduction. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	1
9	Mutational and biophysical robustness in a prestabilized monobody. *Journal of Biological Chemistry*, **2021**, 296, 100447	5.4	1

8	Improved production of the non-native cofactor F in Escherichia coli. *Scientific Reports*, **2021**, 11, 21774	4.9	0
7	Substrate Dynamics Contribute to Enzymatic Specificity in Human and Bacterial Methionine Adenosyltransferases.. *Jacs Au*, **2021**, 1, 2349-2360		0
6	Computational design and experimental characterisation of a stable human heparanase variant.. *RSC Chemical Biology*, **2022**, 3, 341-349	3	0
5	Evo-velocity: Protein language modeling accelerates the study of evolution.. *Cell Systems*, **2022**, 13, 271-273	10.6	0
4	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering **2020**, 16, e1008287		
3	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering **2020**, 16, e1008287		
2	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering **2020**, 16, e1008287		
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