

Colin J Jackson

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/550535/colin-j-jackson-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Adventures on the routes of protein evolution - in memoriam Dan Salah Tawfik (1955 - 2021).. <i>Journal of Molecular Biology</i> , 2022 , 434, 167462	6.5	2
150	Antiviral cyclic peptides targeting the main protease of SARS-CoV-2.. <i>Chemical Science</i> , 2022 , 13, 3826-3836	9.4	2
149	Computational design and experimental characterisation of a stable human heparanase variant.. <i>RSC Chemical Biology</i> , 2022 , 3, 341-349	3	0
148	Evo-velocity: Protein language modeling accelerates the study of evolution.. <i>Cell Systems</i> , 2022 , 13, 271-273	20.3	0
147	Improved production of the non-native cofactor F in Escherichia coli. <i>Scientific Reports</i> , 2021 , 11, 21774	4.9	0
146	A Rationally and Computationally Designed Fluorescent Biosensor for d-Serine. <i>ACS Sensors</i> , 2021 , 6, 4193-4205	9.2	1
145	Through-Space Scalar F-F Couplings between Fluorinated Noncanonical Amino Acids for the Detection of Specific Contacts in Proteins. <i>Journal of the American Chemical Society</i> , 2021 , 143, 19587-19598	16.4	3
144	Substrate Dynamics Contribute to Enzymatic Specificity in Human and Bacterial Methionine Adenosyltransferases.. <i>Jacs Au</i> , 2021 , 1, 2349-2360		0
143	Immunizations with diverse sarbecovirus receptor-binding domains elicit SARS-CoV-2 neutralizing antibodies against a conserved site of vulnerability. <i>Immunity</i> , 2021 ,	32.3	8
142	Structural and functional characterization of a putative de novo gene in Drosophila. <i>Nature Communications</i> , 2021 , 12, 1667	17.4	10
141	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2915-2929	8.3	8
140	Avid binding by B cells to the Plasmodium circumsporozoite protein repeat suppresses responses to protective subdominant epitopes. <i>Cell Reports</i> , 2021 , 35, 108996	10.6	4
139	High avidity drives the interaction between the streptococcal C1 phage endolysin, PlyC, with the cell surface carbohydrates of Group A Streptococcus. <i>Molecular Microbiology</i> , 2021 , 116, 397-415	4.1	2
138	Structures of a non-ribosomal peptide synthetase condensation domain suggest the basis of substrate selectivity. <i>Nature Communications</i> , 2021 , 12, 2511	17.4	9
137	Potent Cyclic Peptide Inhibitors of FXIIa Discovered by mRNA Display with Genetic Code Reprogramming. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 7853-7876	8.3	3
136	Potency boost of a dihydrofolate reductase inhibitor by multienzyme FH-dependent reduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
135	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. <i>Molecular Biology and Evolution</i> , 2021 , 38, 545-556	8.3	2

134	Resonant Dielectric Metagratings for Response Intensified Optical Sensing. <i>Advanced Functional Materials</i> , 2021 , 2103143	15.6	3
133	Ancestral sequence reconstruction for protein engineers. <i>Current Opinion in Structural Biology</i> , 2021 , 69, 131-141	8.1	18
132	Challenges of short substrate analogues as SARS-CoV-2 main protease inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 50, 128333	2.9	4
131	Mutational and biophysical robustness in a prestabilized monobody. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100447	5.4	1
130	The evolution and engineering of enzyme activity through tuning conformational landscapes. <i>Protein Engineering, Design and Selection</i> , 2021 , 34,	1.9	4
129	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F-0 in Mycobacteria. <i>MSystems</i> , 2020 , 5,	7.6	4
128	Bacterial catabolism of s-triazine herbicides: biochemistry, evolution and application. <i>Advances in Microbial Physiology</i> , 2020 , 76, 129-186	4.4	6
127	Consensus Mutagenesis and Ancestral Reconstruction Provide Insight into the Substrate Specificity and Evolution of the Front-End β -Desaturase Family. <i>Biochemistry</i> , 2020 , 59, 1398-1409	3.2	8
126	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. <i>PLoS Pathogens</i> , 2020 , 16, e1008287	7.6	18
125	Engineering a solid-state metalloprotein hydrogen evolution catalyst. <i>Scientific Reports</i> , 2020 , 10, 3774	4.9	3
124	Strategies for Increasing Protein Stability. <i>Methods in Molecular Biology</i> , 2020 , 2073, 163-181	1.4	10
123	Enhancement of metallomacrocycle-based oxygen reduction catalysis through immobilization in a tunable silk-protein scaffold. <i>Journal of Inorganic Biochemistry</i> , 2020 , 204, 110960	4.2	1
122	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. <i>Journal of Organic Chemistry</i> , 2020 , 85, 650-663	4.2	10
121	Local Efficacy of Glutamate Uptake Decreases with Synapse Size. <i>Cell Reports</i> , 2020 , 32, 108182	10.6	17
120	Altered conformational sampling along an evolutionary trajectory changes the catalytic activity of an enzyme. <i>Nature Communications</i> , 2020 , 11, 5945	17.4	14
119	LTP Induction Boosts Glutamate Spillover by Driving Withdrawal of Perisynaptic Astroglia. <i>Neuron</i> , 2020 , 108, 919-936.e11	13.9	65
118	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		
117	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		

116	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
115	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
114	Overcoming insecticide resistance through computational inhibitor design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21012-21021	11.5	16
113	nonribosomal peptide synthetase Ebony encodes an atypical condensation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 2913-2918	11.5	11
112	Kistamicin biosynthesis reveals the biosynthetic requirements for production of highly crosslinked glycopeptide antibiotics. <i>Nature Communications</i> , 2019 , 10, 2613	17.4	24
111	Protein engineering: the potential of remote mutations. <i>Biochemical Society Transactions</i> , 2019 , 47, 701-711	3.1	34
110	Structural and evolutionary approaches to the design and optimization of fluorescence-based small molecule biosensors. <i>Current Opinion in Structural Biology</i> , 2019 , 57, 31-38	8.1	18
109	A revised biosynthetic pathway for the cofactor F in prokaryotes. <i>Nature Communications</i> , 2019 , 10, 1558	7.4	35
108	Sequential Electrostatic Assembly of a Polymer Surfactant Corona Increases Activity of the Phosphotriesterase arPTE. <i>Bioconjugate Chemistry</i> , 2019 , 30, 2771-2776	6.3	6
107	Cryptic genetic variation shapes the adaptive evolutionary potential of enzymes. <i>ELife</i> , 2019 , 8,	8.9	18
106	Cofactor F420-Dependent Enzymes: An Under-Explored Resource for Asymmetric Redox Biocatalysis. <i>Catalysts</i> , 2019 , 9, 868	4	12
105	Structural Basis for the Allosteric Regulation of the SbtA Bicarbonate Transporter by the P-like Protein, SbtB, from sp. PCC7001. <i>Biochemistry</i> , 2019 , 58, 5030-5039	3.2	14
104	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019 , 15, 1120-1128	11.7	35
103	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019 , 20, 1299-1310	19.1	29
102	The Structure and Stability of the Disulfide-Linked β -Crystallin Dimer Provide Insight into Oxidation Products Associated with Lens Cataract Formation. <i>Journal of Molecular Biology</i> , 2019 , 431, 483-497	6.5	27
101	FAD-sequestering proteins protect mycobacteria against hypoxic and oxidative stress. <i>Journal of Biological Chemistry</i> , 2019 , 294, 2903-2912	5.4	7
100	The molecular basis for the neofunctionalization of the juvenile hormone esterase duplication in <i>Drosophila</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019 , 106, 10-18	4.5	5
99	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2019 , 24, 1707-1719	15.1	38

98	Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein. <i>Nature Chemical Biology</i> , 2018 , 14, 542-547	11.7	51
97	Monitoring hippocampal glycine with the computationally designed optical sensor GlyFS. <i>Nature Chemical Biology</i> , 2018 , 14, 861-869	11.7	36
96	Laboratory evolution of protein conformational dynamics. <i>Current Opinion in Structural Biology</i> , 2018 , 50, 49-57	8.1	56
95	The evolution of multiple active site configurations in a designed enzyme. <i>Nature Communications</i> , 2018 , 9, 3900	17.4	50
94	Hydrogel-Immobilized Supercharged Proteins. <i>Advanced Biology</i> , 2018 , 2, 1700240	3.5	6
93	Molecular basis for the behavioral effects of the odorant degrading enzyme Esterase 6 in <i>Drosophila</i> . <i>Scientific Reports</i> , 2017 , 7, 46188	4.9	33
92	Total Syntheses of the Amaryllidaceae Alkaloids Zephycandidine III and Lycosinine A and Their Evaluation as Inhibitors of Acetylcholinesterase. <i>European Journal of Organic Chemistry</i> , 2017 , 2017, 4044-4053 ⁴	3.2	4
91	Ancestral Protein Reconstruction and Circular Permutation for Improving the Stability and Dynamic Range of FRET Sensors. <i>Methods in Molecular Biology</i> , 2017 , 1596, 71-87	1.4	5
90	Structural reconstruction of protein ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 3897-3902	11.5	5
89	Method for Developing Optical Sensors Using a Synthetic Dye-Fluorescent Protein FRET Pair and Computational Modeling and Assessment. <i>Methods in Molecular Biology</i> , 2017 , 1596, 89-99	1.4	1
88	Constrained evolution of a bispecific enzyme: lessons for biocatalyst design. <i>Organic and Biomolecular Chemistry</i> , 2017 , 15, 937-946	3.9	7
87	Structure of an Insecticide Sequestering Carboxylesterase from the Disease Vector <i>Culex quinquefasciatus</i> : What Makes an Enzyme a Good Insecticide Sponge?. <i>Biochemistry</i> , 2017 , 56, 5512-5525 ^{3,2}	3.2	14
86	The Synthesis of Certain Derivatives and Analogues of (-)- and (+)-Galanthamine and an Assessment of their Capacities to Inhibit Acetylcholine Esterase. <i>Journal of Organic Chemistry</i> , 2017 , 82, 7869-7886	4.2	9
85	The methanogenic redox cofactor F is widely synthesized by aerobic soil bacteria. <i>ISME Journal</i> , 2017 , 11, 125-137	11.9	43
84	Mycobacterial FH-Dependent Reductases Promiscuously Reduce Diverse Compounds through a Common Mechanism. <i>Frontiers in Microbiology</i> , 2017 , 8, 1000	5.7	20
83	Cofactor Tail Length Modulates Catalysis of Bacterial F-Dependent Oxidoreductases. <i>Frontiers in Microbiology</i> , 2017 , 8, 1902	5.7	10
82	T-dependent B cell responses to Plasmodium induce antibodies that form a high-avidity multivalent complex with the circumsporozoite protein. <i>PLoS Pathogens</i> , 2017 , 13, e1006469	7.6	36
81	Hydrophobic Shielding Drives Catalysis of Hydride Transfer in a Family of FH-Dependent Enzymes. <i>Biochemistry</i> , 2016 , 55, 6908-6918	3.2	8

80	The Redox Cofactor F Protects Mycobacteria from Diverse Antimicrobial Compounds and Mediates a Reductive Detoxification System. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 6810-6818	4.8	23
79	The role of protein dynamics in the evolution of new enzyme function. <i>Nature Chemical Biology</i> , 2016 , 12, 944-950	11.7	166
78	Conformational Tinkering Drives Evolution of a Promiscuous Activity through Indirect Mutational Effects. <i>Biochemistry</i> , 2016 , 55, 4583-93	3.2	33
77	Sensing and signaling of oxidative stress in chloroplasts by inactivation of the SAL1 phosphoadenosine phosphatase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4567-76	11.5	101
76	Probing the mechanisms for the selectivity and promiscuity of methyl parathion hydrolase. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016 , 374,	3	19
75	Rangefinder: A Semisynthetic FRET Sensor Design Algorithm. <i>ACS Sensors</i> , 2016 , 1, 1286-1290	9.2	10
74	Active Site Desolvation and Thermostability Trade-Offs in the Evolution of Catalytically Diverse Triazine Hydrolases. <i>Biochemistry</i> , 2016 , 55, 6304-6313	3.2	7
73	Conformational Disorganization within the Active Site of a Recently Evolved Organophosphate Hydrolase Limits Its Catalytic Efficiency. <i>Biochemistry</i> , 2016 , 55, 1408-17	3.2	17
72	Evolution of Protein Quaternary Structure in Response to Selective Pressure for Increased Thermostability. <i>Journal of Molecular Biology</i> , 2016 , 428, 2359-2371	6.5	26
71	Ancestral Protein Reconstruction Yields Insights into Adaptive Evolution of Binding Specificity in Solute-Binding Proteins. <i>Cell Chemical Biology</i> , 2016 , 23, 236-245	8.2	59
70	Genomic and metagenomic surveys of hydrogenase distribution indicate H ₂ is a widely utilised energy source for microbial growth and survival. <i>ISME Journal</i> , 2016 , 10, 761-77	11.9	319
69	The Evolution of New Catalytic Mechanisms for Xenobiotic Hydrolysis in Bacterial Metalloenzymes. <i>Australian Journal of Chemistry</i> , 2016 , 69, 1383	1.2	5
68	Mapping the Accessible Conformational Landscape of an Insect Carboxylesterase Using Conformational Ensemble Analysis and Kinetic Crystallography. <i>Structure</i> , 2016 , 24, 977-87	5.2	12
67	Protonation state of F420H ₂ in the prodrug-activating deazaflavin dependent nitroreductase (Ddn) from <i>Mycobacterium tuberculosis</i> . <i>Molecular BioSystems</i> , 2016 , 12, 1110-3		15
66	Phosphorescent oxygen-sensing and singlet oxygen production by a biosynthetic silk. <i>RSC Advances</i> , 2016 , 6, 39530-39533	3.7	11
65	Physiology, Biochemistry, and Applications of F420- and Fo-Dependent Redox Reactions. <i>Microbiology and Molecular Biology Reviews</i> , 2016 , 80, 451-93	13.2	88
64	Rv2074 is a novel F420 H ₂ -dependent biliverdin reductase in <i>Mycobacterium tuberculosis</i> . <i>Protein Science</i> , 2016 , 25, 1692-709	6.3	18
63	Classification and substrate head-group specificity of membrane fatty acid desaturases. <i>Computational and Structural Biotechnology Journal</i> , 2016 , 14, 341-349	6.8	14

62	Sequence-Structure-Function Classification of a Catalytically Diverse Oxidoreductase Superfamily in Mycobacteria. <i>Journal of Molecular Biology</i> , 2015 , 427, 3554-3571	6.5	47
61	Devising New Syntheses of the Alkaloid Galanthamine, a Potent and Clinically Deployed Inhibitor of Acetylcholine Esterase. <i>Strategies and Tactics in Organic Synthesis</i> , 2015 , 29-50	0.2	4
60	Predicting X-ray diffuse scattering from translation-libration-screw structural ensembles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1657-67		9
59	Construction of a robust and sensitive arginine biosensor through ancestral protein reconstruction. <i>Protein Science</i> , 2015 , 24, 1412-22	6.3	47
58	Evolutionary expansion of the amidohydrolase superfamily in bacteria in response to the synthetic compounds molinate and diuron. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2612-24	4.8	16
57	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. <i>PLoS ONE</i> , 2015 , 10, e0140219	3.7	3
56	Reverse evolution leads to genotypic incompatibility despite functional and active site convergence. <i>ELife</i> , 2015 , 4,	8.9	51
55	Enzyme dynamics and engineering: one step at a time. <i>Chemistry and Biology</i> , 2014 , 21, 1259-1260		6
54	Synthesis of a D-ring isomer of galanthamine via a radical-based Smiles rearrangement reaction. <i>Journal of Organic Chemistry</i> , 2014 , 79, 6759-64	4.2	17
53	300-Fold increase in production of the Zn ²⁺ -dependent dechlorinase TrzN in soluble form via apoenzyme stabilization. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4003-11	4.8	10
52	Iron(III) located in the dinuclear metallo-β-lactamase IMP-1 by pseudocontact shifts. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 14269-72	16.4	11
51	A 5000-fold increase in the specificity of a bacterial phosphotriesterase for malathion through combinatorial active site mutagenesis. <i>PLoS ONE</i> , 2014 , 9, e94177	3.7	28
50	Crystal structure of the mouse interleukin-3 receptor: insights into interleukin-3 binding and receptor activation. <i>Biochemical Journal</i> , 2014 , 463, 393-403	3.8	5
49	Pseudokontaktverschiebungen lokalisieren Eisen(III) in der zweikernigen Metallo-β-Laktamase IMP-1. <i>Angewandte Chemie</i> , 2014 , 126, 14494-14497	3.6	1
48	Use of OpdA, an organophosphorus (OP) hydrolase, prevents lethality in an African green monkey model of acute OP poisoning. <i>Toxicology</i> , 2014 , 317, 1-5	4.4	15
47	Protein engineering with unnatural amino acids. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 581-7	8.1	63
46	Structure and function of an insect β-carboxylesterase (βesterase7) associated with insecticide resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 10177-82	11.5	84
45	Testing the evolvability of an insect carboxylesterase for the detoxification of synthetic pyrethroid insecticides. <i>Insect Biochemistry and Molecular Biology</i> , 2012 , 42, 343-52	4.5	34

44	Reconstructing a missing link in the evolution of a recently diverged phosphotriesterase by active-site loop remodeling. <i>Biochemistry</i> , 2012 , 51, 6047-55	3.2	109
43	Diminishing returns and tradeoffs constrain the laboratory optimization of an enzyme. <i>Nature Communications</i> , 2012 , 3, 1257	17.4	156
42	A polymer surfactant corona dynamically replaces water in solvent-free protein liquids and ensures macromolecular flexibility and activity. <i>Journal of the American Chemical Society</i> , 2012 , 134, 13168-71	16.4	41
41	Intramolecular epistasis and the evolution of a new enzymatic function. <i>PLoS ONE</i> , 2012 , 7, e39822	3.7	42
40	The evolution of new enzyme function: lessons from xenobiotic metabolizing bacteria versus insecticide-resistant insects. <i>Evolutionary Applications</i> , 2011 , 4, 225-48	4.8	78
39	Improving a natural enzyme activity through incorporation of unnatural amino acids. <i>Journal of the American Chemical Society</i> , 2011 , 133, 326-33	16.4	67
38	Mining electron density for functionally relevant protein polysterism in crystal structures. <i>Cellular and Molecular Life Sciences</i> , 2011 , 68, 1829-41	10.3	19
37	Carboxylesterases in the Metabolism and Toxicity of Pesticides 2011 , 57-75		2
36	Competing S(N)2 and E2 reaction pathways for hexachlorocyclohexane degradation in the gas phase, solution and enzymes. <i>Chemical Communications</i> , 2011 , 47, 976-8	5.8	17
35	Kinetic and sequence-structure-function analysis of known LinA variants with different hexachlorocyclohexane isomers. <i>PLoS ONE</i> , 2011 , 6, e25128	3.7	14
34	Kinetics and efficacy of an organophosphorus hydrolase in a rodent model of methyl-parathion poisoning. <i>Academic Emergency Medicine</i> , 2010 , 17, 736-40	3.4	12
33	Identification and characterization of two families of F420 H2-dependent reductases from Mycobacteria that catalyse aflatoxin degradation. <i>Molecular Microbiology</i> , 2010 , 78, 561-75	4.1	105
32	Biochemistry of microbial degradation of hexachlorocyclohexane and prospects for bioremediation. <i>Microbiology and Molecular Biology Reviews</i> , 2010 , 74, 58-80	13.2	281
31	Mutation of outer-shell residues modulates metal ion co-ordination strength in a metalloenzyme. <i>Biochemical Journal</i> , 2010 , 429, 313-21	3.8	16
30	Evolutionary optimization of computationally designed enzymes: Kemp eliminases of the KE07 series. <i>Journal of Molecular Biology</i> , 2010 , 396, 1025-42	6.5	132
29	Directed Evolution of Enzymes 2010 , 723-749		2
28	Pharmacokinetics of OpdA, an organophosphorus hydrolase, in the African green monkey. <i>Biochemical Pharmacology</i> , 2010 , 80, 1075-9	6	18
27	Directed Evolution of Enzymes 2010 , 654-673		1

26	Conformational sampling, catalysis, and evolution of the bacterial phosphotriesterase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21631-6	11.5	93
25	Catalytic improvement and evolution of atrazine chlorohydrolase. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2184-91	4.8	54
24	Structure-based rational design of a phosphotriesterase. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5153-6	4.8	28
23	Use of engineered enzymes to identify organophosphate and pyrethroid-related toxicity in toxicity identification evaluations. <i>Environmental Science & Technology</i> , 2009 , 43, 5514-20	10.3	51
22	Characterization of the phenylurea hydrolases A and B: founding members of a novel amidohydrolase subgroup. <i>Biochemical Journal</i> , 2009 , 418, 431-41	3.8	50
21	In crystallo capture of a Michaelis complex and product-binding modes of a bacterial phosphotriesterase. <i>Journal of Molecular Biology</i> , 2008 , 375, 1189-96	6.5	78
20	Substrate-promoted formation of a catalytically competent binuclear center and regulation of reactivity in a glycerophosphodiesterase from <i>Enterobacter aerogenes</i> . <i>Journal of the American Chemical Society</i> , 2008 , 130, 14129-38	16.4	64
19	Bridging the synaptic gap: neuroligins and neuexin I in <i>Apis mellifera</i> . <i>PLoS ONE</i> , 2008 , 3, e3542	3.7	46
18	The enzymatic basis for pesticide bioremediation. <i>Indian Journal of Microbiology</i> , 2008 , 48, 65-79	3.7	120
17	Cloning, expression, purification, crystallization and preliminary X-ray studies of a pyridoxine 5Sphosphate oxidase from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 435-7		2
16	Malonate-bound structure of the glycerophosphodiesterase from <i>Enterobacter aerogenes</i> (GpdQ) and characterization of the native Fe ²⁺ metal-ion preference. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 681-5		21
15	The structure and function of a novel glycerophosphodiesterase from <i>Enterobacter aerogenes</i> . <i>Journal of Molecular Biology</i> , 2007 , 367, 1047-62	6.5	62
14	Anomalous scattering analysis of <i>Agrobacterium radiobacter</i> phosphotriesterase: the prominent role of iron in the heterobinuclear active site. <i>Biochemical Journal</i> , 2006 , 397, 501-8	3.8	52
13	The purification, crystallization and preliminary diffraction of a glycerophosphodiesterase from <i>Enterobacter aerogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 659-61		8
12	Increased expression of a bacterial phosphotriesterase in <i>Escherichia coli</i> through directed evolution. <i>Protein Expression and Purification</i> , 2005 , 41, 433-40	2	25
11	The effects of substrate orientation on the mechanism of a phosphotriesterase. <i>Organic and Biomolecular Chemistry</i> , 2005 , 3, 4343-50	3.9	27
10	The structure of an enzyme-product complex reveals the critical role of a terminal hydroxide nucleophile in the bacterial phosphotriesterase mechanism. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005 , 1752, 56-64	4	64
9	Growth of <i>Escherichia coli</i> coexpressing phosphotriesterase and glycerophosphodiester phosphodiesterase, using paraoxon as the sole phosphorus source. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 404-12	4.8	62

8	Avid binding by B cells to the Plasmodium circumsporozoite protein repeat suppresses responses to protective subdominant epitopes	2
7	Altered conformational sampling along an evolutionary trajectory changes the catalytic activity of an enzyme	3
6	Cellular and structural basis of synthesis of the unique intermediate dehydro-F420-0 in mycobacteria	1
5	A computationally designed fluorescent biosensor for D-serine	3
4	The NK Landscape as a Versatile Benchmark for Machine Learning Driven Protein Engineering	5
3	Higher-order epistatic networks underlie the evolutionary fitness landscape of a xenobiotic-degrading enzyme	2
2	The evolution of nitroimidazole antibiotic resistance in Mycobacterium tuberculosis	2
1	Regulatory adenylnucleotide-mediated binding of the PII-like protein SbtB to the cyanobacterial bicarbonate transporter SbtA is controlled by the cellular energy state	2