

# Dan S Tawfik

## List of Publications by Year in descending order

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191  
papers

25,140  
citations

6613  
79  
h-index

7518  
151  
g-index

213  
all docs

213  
docs citations

213  
times ranked

18839  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enzyme Promiscuity: A Mechanistic and Evolutionary Perspective. Annual Review of Biochemistry, 2010, 79, 471-505.	11.1	1,137
2	Kemp elimination catalysts by computational enzyme design. Nature, 2008, 453, 190-195.	27.8	1,130
3	Man-made cell-like compartments for molecular evolution. Nature Biotechnology, 1998, 16, 652-656.	17.5	867
4	The Moderately Efficient Enzyme: Evolutionary and Physicochemical Trends Shaping Enzyme Parameters. Biochemistry, 2011, 50, 4402-4410.	2.5	810
5	Protein Dynamism and Evolvability. Science, 2009, 324, 203-207.	12.6	764
6	The 'evolvability' of promiscuous protein functions. Nature Genetics, 2005, 37, 73-76.	21.4	742
7	Antibody Multispecificity Mediated by Conformational Diversity. Science, 2003, 299, 1362-1367.	12.6	673
8	Stability effects of mutations and protein evolvability. Current Opinion in Structural Biology, 2009, 19, 596-604.	5.7	626
9	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. Nature Structural and Molecular Biology, 2004, 11, 412-419.	8.2	569
10	Enzyme promiscuity: evolutionary and mechanistic aspects. Current Opinion in Chemical Biology, 2006, 10, 498-508.	6.1	550
11	Conformational diversity and protein evolution – a 60-year-old hypothesis revisited. Trends in Biochemical Sciences, 2003, 28, 361-368.	7.5	514
12	How Protein Stability and New Functions Trade Off. PLoS Computational Biology, 2008, 4, e1000002.	3.2	468
13	Local fitness landscape of the green fluorescent protein. Nature, 2016, 533, 397-401.	27.8	438
14	Structure- and Reactivity Studies of Serum Paraoxonase PON1 Suggest that Its Native Activity Is Lactonase. Biochemistry, 2005, 44, 6371-6382.	2.5	403
15	The Stability Effects of Protein Mutations Appear to be Universally Distributed. Journal of Molecular Biology, 2007, 369, 1318-1332.	4.2	396
16	Robustness – epistasis link shapes the fitness landscape of a randomly drifting protein. Nature, 2006, 444, 929-932.	27.8	387
17	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. Molecular Cell, 2016, 63, 337-346.	9.7	363
18	Mutational effects and the evolution of new protein functions. Nature Reviews Genetics, 2010, 11, 572-582.	16.3	358

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19	Amplification of complex gene libraries by emulsion PCR. <i>Nature Methods</i> , 2006, 3, 545-550.	19.0	327
20	Chaperonin overexpression promotes genetic variation and enzyme evolution. <i>Nature</i> , 2009, 459, 668-673.	27.8	315
21	Miniaturising the laboratory in emulsion droplets. <i>Trends in Biotechnology</i> , 2006, 24, 395-402.	9.3	312
22	Directed evolution of mammalian paraoxonases PON1 and PON3 for bacterial expression and catalytic specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 482-487.	7.1	275
23	Directed evolution of an extremely fast phosphotriesterase by in vitro compartmentalization. <i>EMBO Journal</i> , 2003, 22, 24-35.	7.8	267
24	The Latent Promiscuity of Newly Identified Microbial Lactonases Is Linked to a Recently Diverged Phosphotriesterase. <i>Biochemistry</i> , 2006, 45, 13677-13686.	2.5	258
25	Initial Mutations Direct Alternative Pathways of Protein Evolution. <i>PLoS Genetics</i> , 2011, 7, e1001321.	3.5	236
26	Intense Neutral Drifts Yield Robust and Evolvable Consensus Proteins. <i>Journal of Molecular Biology</i> , 2008, 379, 1029-1044.	4.2	232
27	Do viral proteins possess unique biophysical features?. <i>Trends in Biochemical Sciences</i> , 2009, 34, 53-59.	7.5	229
28	Messy biology and the origins of evolutionary innovations. <i>Nature Chemical Biology</i> , 2010, 6, 692-696.	8.0	222
29	Advances in laboratory evolution of enzymes. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 151-158.	6.1	214
30	The molecular basis of phosphate discrimination in arsenate-rich environments. <i>Nature</i> , 2012, 491, 134-137.	27.8	209
31	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. <i>Nature Chemical Biology</i> , 2012, 8, 294-300.	8.0	205
32	Bridging the gaps in design methodologies by evolutionary optimization of the stability and proficiency of designed Kemp eliminase KE59. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10358-10363.	7.1	205
33	The Catalytic Histidine Dyad of High Density Lipoprotein-associated Serum Paraoxonase-1 (PON1) Is Essential for PON1-mediated Inhibition of Low Density Lipoprotein Oxidation and Stimulation of Macrophage Cholesterol Efflux. <i>Journal of Biological Chemistry</i> , 2006, 281, 7657-7665.	3.4	204
34	Identification of the algal dimethyl sulfide-releasing enzyme: A missing link in the marine sulfur cycle. <i>Science</i> , 2015, 348, 1466-1469.	12.6	199
35	High-Throughput Screening of Enzyme Libraries: Thiolactonases Evolved by Fluorescence-Activated Sorting of Single Cells in Emulsion Compartments. <i>Chemistry and Biology</i> , 2005, 12, 1281-1289.	6.0	197
36	Directed evolution by in vitro compartmentalization. <i>Nature Methods</i> , 2006, 3, 561-570.	19.0	196

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37	Diminishing returns and tradeoffs constrain the laboratory optimization of an enzyme. <i>Nature Communications</i> , 2012, 3, 1257.	12.8	196
38	High-throughput screens and selections of enzyme-encoding genes. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 210-216.	6.1	187
39	Off-the-shelf proteins that rival tailor-made antibodies as catalysts. <i>Nature</i> , 1996, 383, 60-63.	27.8	177
40	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. <i>Nature Chemical Biology</i> , 2011, 7, 120-125.	8.0	176
41	The universality of enzymatic rateâ€™temperature dependency. <i>Trends in Biochemical Sciences</i> , 2014, 39, 1-7.	7.5	171
42	Directed enzyme evolution: beyond the low-hanging fruit. <i>Current Opinion in Structural Biology</i> , 2012, 22, 406-412.	5.7	167
43	Noiseâ€™mean relationship in mutated promoters. <i>Genome Research</i> , 2012, 22, 2409-2417.	5.5	167
44	Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. <i>Molecular Cell</i> , 2018, 72, 178-186.e5.	9.7	165
45	Arsenate Replacing Phosphate: Alternative Life Chemistries and Ion Promiscuity. <i>Biochemistry</i> , 2011, 50, 1128-1134.	2.5	160
46	The Histidine 115-Histidine 134 Dyad Mediates the Lactonase Activity of Mammalian Serum Paraoxonases. <i>Journal of Biological Chemistry</i> , 2006, 281, 7649-7656.	3.4	154
47	Evolutionary Optimization of Computationally Designed Enzymes: Kemp Eliminases of the KE07 Series. <i>Journal of Molecular Biology</i> , 2010, 396, 1025-1042.	4.2	154
48	In vitro compartmentalization by double emulsions: sorting and gene enrichment by fluorescence activated cell sorting. <i>Analytical Biochemistry</i> , 2004, 325, 151-157.	2.4	153
49	Optimization of the In-Silico-Designed Kemp Eliminase KE70 by Computational Design and Directed Evolution. <i>Journal of Molecular Biology</i> , 2011, 407, 391-412.	4.2	152
50	Catalytic Versatility and Backups in Enzyme Active Sites: The Case of Serum Paraoxonase 1. <i>Journal of Molecular Biology</i> , 2012, 418, 181-196.	4.2	148
51	What Makes a Protein Fold Amenable to Functional Innovation? Fold Polarity and Stability Trade-offs. <i>Journal of Molecular Biology</i> , 2013, 425, 2609-2621.	4.2	140
52	Protein engineers turned evolutionists. <i>Nature Methods</i> , 2007, 4, 991-994.	19.0	135
53	Latent evolutionary potentials under the neutral mutational drift of an enzyme. <i>HFSP Journal</i> , 2007, 1, 67-78.	2.5	134
54	Reconstructing a Missing Link in the Evolution of a Recently Diverged Phosphotriesterase by Active-Site Loop Remodeling. <i>Biochemistry</i> , 2012, 51, 6047-6055.	2.5	128

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55	Man-made enzymes “from design to in vitro compartmentalisation. Current Opinion in Biotechnology, 2000, 11, 338-353.	6.6	123
56	Directed enzyme evolution via small and effective neutral drift libraries. Nature Methods, 2008, 5, 939-942.	19.0	123
57	Directed evolution of proteins for heterologous expression and stability. Current Opinion in Structural Biology, 2005, 15, 50-56.	5.7	122
58	Shared Promiscuous Activities and Evolutionary Features in Various Members of the Amidohydrolase Superfamily. Biochemistry, 2005, 44, 12728-12736.	2.5	119
59	The specificity of cross-reactivity: Promiscuous antibody binding involves specific hydrogen bonds rather than nonspecific hydrophobic stickiness. Protein Science, 2009, 12, 2183-2193.	7.6	119
60	The 192R/Q polymorphs of serum paraoxonase PON1 differ in HDL binding, lipolactonase stimulation, and cholesterol efflux. Journal of Lipid Research, 2006, 47, 2492-2502.	4.2	118
61	Divergence and Convergence in Enzyme Evolution: Parallel Evolution of Paraoxonases from Quorum-quenching Lactonases. Journal of Biological Chemistry, 2012, 287, 11-20.	3.4	114
62	On the Potential Origins of the High Stability of Reconstructed Ancestral Proteins. Molecular Biology and Evolution, 2016, 33, 2633-2641.	8.9	114
63	Evolution of chalcone isomerase from a noncatalytic ancestor. Nature Chemical Biology, 2018, 14, 548-555.	8.0	113
64	The Evolutionary Origins of Detoxifying Enzymes. Journal of Biological Chemistry, 2013, 288, 23914-23927.	3.4	112
65	The robustness and innovability of protein folds. Current Opinion in Structural Biology, 2014, 26, 131-138.	5.7	108
66	Metabolite“Enzyme Coevolution: From Single Enzymes to Metabolic Pathways and Networks. Annual Review of Biochemistry, 2018, 87, 187-216.	11.1	106
67	Evolution of new protein topologies through multistep gene rearrangements. Nature Genetics, 2006, 38, 168-174.	21.4	103
68	Negative Epistasis and Evolvability in TEM-1 $\beta$ -Lactamase“The Thin Line between an Enzyme's Conformational Freedom and Disorder. Journal of Molecular Biology, 2015, 427, 2396-2409.	4.2	102
69	Accuracy-rate tradeoffs: how do enzymes meet demands of selectivity and catalytic efficiency?. Current Opinion in Chemical Biology, 2014, 21, 73-80.	6.1	101
70	Incorporating Synthetic Oligonucleotides via Gene Reassembly (ISOR): a versatile tool for generating targeted libraries. Protein Engineering, Design and Selection, 2007, 20, 219-226.	2.1	99
71	Microbead display by in vitro compartmentalisation: selection for binding using flow cytometry. FEBS Letters, 2002, 532, 455-458.	2.8	98
72	Structural Convergence in the Active Sites of a Family of Catalytic Antibodies. Science, 1997, 275, 1140-1142.	12.6	97

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73	Altering the sequence specificity of HaeIII methyltransferase by directed evolution using in vitro compartmentalization. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 3-11.	2.1	97
74	Rescue of conformational dynamics in enzyme catalysis by directed evolution. <i>Nature Communications</i> , 2018, 9, 1314.	12.8	97
75	Design and in vitro realization of carbon-conserving photorespiration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11455-E11464.	7.1	97
76	Metamorphic proteins mediate evolutionary transitions of structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7287-7292.	7.1	94
77	Protein engineers turned evolutionists—the quest for the optimal starting point. <i>Current Opinion in Biotechnology</i> , 2019, 60, 46-52.	6.6	93
78	Engineering V-Type Nerve Agents Detoxifying Enzymes Using Computationally Focused Libraries. <i>ACS Chemical Biology</i> , 2013, 8, 2394-2403.	3.4	91
79	Enhanced stereoselective hydrolysis of toxic organophosphates by directly evolved variants of mammalian serum paraoxonase. <i>FEBS Journal</i> , 2006, 273, 1906-1919.	4.7	90
80	The Moderately Efficient Enzyme: Futile Encounters and Enzyme Floppiness. <i>Biochemistry</i> , 2015, 54, 4969-4977.	2.5	89
81	De Novo Evolutionary Emergence of a Symmetrical Protein Is Shaped by Folding Constraints. <i>Cell</i> , 2016, 164, 476-486.	28.9	88
82	A Bird's-Eye View of Enzyme Evolution: Chemical, Physicochemical, and Physiological Considerations. <i>Chemical Reviews</i> , 2018, 118, 8786-8797.	47.7	88
83	Structure and kinetics of a transient antibody binding intermediate reveal a kinetic discrimination mechanism in antigen recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12730-12735.	7.1	87
84	Enzyme engineering: reaching the maximal catalytic efficiency peak. <i>Current Opinion in Structural Biology</i> , 2017, 47, 140-150.	5.7	87
85	An Ancient Fingerprint Indicates the Common Ancestry of Rossmann-Fold Enzymes Utilizing Different Ribose-Based Cofactors. <i>PLoS Biology</i> , 2016, 14, e1002396.	5.6	85
86	Quantifying and understanding the fitness effects of protein mutations: Laboratory versus nature. <i>Protein Science</i> , 2016, 25, 1219-1226.	7.6	84
87	Evolved Stereoselective Hydrolases for Broad-Spectrum G-Type Nerve Agent Detoxification. <i>Chemistry and Biology</i> , 2012, 19, 456-466.	6.0	81
88	Slow protein evolutionary rates are dictated by surface–core association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11151-11156.	7.1	80
89	Characterization of Proton-Transfer Catalysis by Serum Albumins. <i>Journal of the American Chemical Society</i> , 2000, 122, 1022-1029.	13.7	79
90	Systematic Mapping of Protein Mutational Space by Prolonged Drift Reveals the Deleterious Effects of Seemingly Neutral Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004421.	3.2	79

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91	Chromogenic and Fluorogenic Assays for the Lactonase Activity of Serum Paraoxonases. ChemBioChem, 2006, 7, 49-53.	2.6	78
92	The development of human sera tests for HDL-bound serum PON1 and its lipolactonase activity. Journal of Lipid Research, 2007, 48, 1637-1646.	4.2	77
93	Efficient Catalysis of Proton Transfer by Synzymes. Journal of the American Chemical Society, 1997, 119, 9578-9579.	13.7	75
94	Potential role of phenotypic mutations in the evolution of protein expression and stability. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6197-6202.	7.1	75
95	Following evolutionary paths to protein-protein interactions with high affinity and selectivity. Nature Structural and Molecular Biology, 2009, 16, 1049-1055.	8.2	75
96	Enzyme Engineering by Targeted Libraries. Methods in Enzymology, 2013, 523, 257-283.	1.0	73
97	Functional Proteins from Short Peptides: Dayhoff's Hypothesis Turns 50. Angewandte Chemie - International Edition, 2016, 55, 15966-15971.	13.8	73
98	On the Magnitude and Specificity of Medium Effects in Enzyme-like Catalysts for Proton Transfer. Journal of Organic Chemistry, 2001, 66, 5866-5874.	3.2	72
99	Latent evolutionary potentials under the neutral mutational drift of an enzyme. HFSP Journal, 2007, 1, 67.	2.5	71
100	Simple yet functional phosphate-loop proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11943-E11950.	7.1	70
101	Directed Evolution of Protein Inhibitors of DNA-nucleases by in Vitro Compartmentalization (IVC) and Nano-droplet Delivery. Journal of Molecular Biology, 2005, 345, 1015-1026.	4.2	68
102	The evolution of oxygen-utilizing enzymes suggests early biosphere oxygenation. Nature Ecology and Evolution, 2021, 5, 442-448.	7.8	68
103	Ohno's Model Revisited: Measuring the Frequency of Potentially Adaptive Mutations under Various Mutational Drifts. Molecular Biology and Evolution, 2008, 25, 2311-2318.	8.9	66
104	On the evolution of chaperones and cochaperones and the expansion of proteomes across the Tree of Life. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	65
105	Reconstruction of Functional Î²-Propeller Lectins via Homo-oligomeric Assembly of Shorter Fragments. Journal of Molecular Biology, 2007, 365, 10-17.	4.2	64
106	BIOCHEMISTRY: Loop Grafting and the Origins of Enzyme Species. Science, 2006, 311, 475-476.	12.6	63
107	On the emergence of P-Loop NTPase and Rossmann enzymes from a Beta-Alpha-Beta ancestral fragment. ELife, 2020, 9, .	6.0	61
108	Directed Evolution of Sulfotransferases and Paraoxonases by Ancestral Libraries. Journal of Molecular Biology, 2011, 411, 837-853.	4.2	58

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109	Catalytic Metal Ion Rearrangements Underline Promiscuity and Evolvability of a Metalloenzyme. <i>Journal of Molecular Biology</i> , 2013, 425, 1028-1038.	4.2	58
110	Protein Insertions and Deletions Enabled by Neutral Roaming in Sequence Space. <i>Molecular Biology and Evolution</i> , 2013, 30, 761-771.	8.9	58
111	Primordial emergence of a nucleic acid-binding protein via phase separation and statistical ornithine-to-arginine conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15731-15739.	7.1	58
112	Investigating the target recognition of DNA cytosine-5 methyltransferase HhaI by library selection using in vitro compartmentalisation. <i>Nucleic Acids Research</i> , 2002, 30, 4937-4944.	14.5	57
113	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 333-345.	2.1	57
114	DddD Is a CoA-Transferase/Lyase Producing Dimethyl Sulfide in the Marine Environment. <i>Biochemistry</i> , 2014, 53, 5473-5475.	2.5	51
115	Role of Chemistry versus Substrate Binding in Recruiting Promiscuous Enzyme Functions. <i>Biochemistry</i> , 2011, 50, 2683-2690.	2.5	48
116	Functional $\beta^2$ -propeller lectins by tandem duplications of repetitive units. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 185-195.	2.1	48
117	Native Mass Spectrometry of Recombinant Proteins from Crude Cell Lysates. <i>Analytical Chemistry</i> , 2017, 89, 4398-4404.	6.5	47
118	The Evolutionary Potential of Phenotypic Mutations. <i>PLoS Genetics</i> , 2015, 11, e1005445.	3.5	45
119	Conformational changes affect binding and catalysis by ester-hydrolysing antibodies 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 285, 421-430.	4.2	44
120	Directed Evolution of Serum Paraoxonase PON3 by Family Shuffling and Ancestor/Consensus Mutagenesis, and Its Biochemical Characterization. <i>Biochemistry</i> , 2009, 48, 6644-6654.	2.5	43
121	Mechanisms of Protein Sequence Divergence and Incompatibility. <i>PLoS Genetics</i> , 2013, 9, e1003665.	3.5	43
122	Correlated Occurrence and Bypass of Frame-Shifting Insertion-Deletions (InDels) to Give Functional Proteins. <i>PLoS Genetics</i> , 2013, 9, e1003882.	3.5	42
123	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. <i>Archives of Toxicology</i> , 2016, 90, 2711-2724.	4.2	42
124	Post-exposure treatment of VX poisoned guinea pigs with the engineered phosphotriesterase mutant C23: A proof-of-concept study. <i>Toxicology Letters</i> , 2014, 231, 45-54.	0.8	40
125	How evolution shapes enzyme selectivity â€“ lessons from aminoacyl-tRNA synthetases and other amino acid utilizing enzymes. <i>FEBS Journal</i> , 2020, 287, 1284-1305.	4.7	39
126	Catalytic and binding poly-reactivities shared by two unrelated proteins: The potential role of promiscuity in enzyme evolution. <i>Protein Science</i> , 2001, 10, 2600-2607.	7.6	38



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127	Spontaneous Emergence of <i>S</i> -Adenosylmethionine and the Evolution of Methylation. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 343-345.	13.8	38
128	Differences in the biochemical properties of esterolytic antibodies correlate with structural diversity. <i>Molecular Immunology</i> , 1994, 31, 127-137.	2.2	37
129	In vivo administration of BL-3050: highly stable engineered PON1-HDL complexes. <i>BMC Clinical Pharmacology</i> , 2009, 9, 18.	2.5	37
130	Catalytic Stimulation by Restrained Active-Site Floppinessâ€”The Case of High Density Lipoprotein-Bound Serum Paraoxonase-1. <i>Journal of Molecular Biology</i> , 2015, 427, 1359-1374.	4.2	37
131	Evolutionary transitions to new DNA methyltransferases through target site expansion and shrinkage. <i>Nucleic Acids Research</i> , 2012, 40, 11627-11637.	14.5	36
132	Antibiotic resistance evolved via inactivation of a ribosomal RNA methylating enzyme. <i>Nucleic Acids Research</i> , 2016, 44, 8897-8907.	14.5	36
133	Promiscuous methylation of non-canonical DNA sites by HaeIII methyltransferase. <i>Nucleic Acids Research</i> , 2002, 30, 3880-3885.	14.5	35
134	Assessing the prediction fidelity of ancestral reconstruction by a library approach. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 507-518.	2.1	35
135	Dimethyl sulfide mediates microbial predatorâ€”prey interactions between zooplankton and algae in the ocean. <i>Nature Microbiology</i> , 2021, 6, 1357-1366.	13.3	33
136	Enzyme evolution in natural products biosynthesis: target- or diversity-oriented?. <i>Current Opinion in Chemical Biology</i> , 2020, 59, 147-154.	6.1	32
137	Short and simple sequences favored the emergence of N-helix phospho-ligand binding sites in the first enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5310-5318.	7.1	32
138	Bridging Themes: Short Protein Segments Found in Different Architectures. <i>Molecular Biology and Evolution</i> , 2021, 38, 2191-2208.	8.9	32
139	Diadenosine tetraphosphate (Ap4A) â€” an <i>E. coli</i> alarmone or a damage metabolite?. <i>FEBS Journal</i> , 2017, 284, 2194-2215.	4.7	30
140	Methanol-free biosynthesis of fatty acid methyl ester (FAME) in <i>Synechocystis</i> sp. PCC 6803. <i>Metabolic Engineering</i> , 2020, 57, 217-227.	7.0	28
141	Chance and pleiotropy dominate genetic diversity in complex bacterial environments. <i>Nature Microbiology</i> , 2019, 4, 1221-1230.	13.3	27
142	<i>Bacilli</i> glutamate dehydrogenases diverged via coevolution of transcription and enzyme regulation. <i>EMBO Reports</i> , 2017, 18, 1139-1149.	4.5	26
143	Enzyme Evolution: An Epistatic Ratchet versus a Smooth Reversible Transition. <i>Molecular Biology and Evolution</i> , 2020, 37, 1133-1147.	8.9	26
144	A â€œFuzzyâ€•Logic Language for Encoding Multiple Physical Traits in Biomolecules. <i>Journal of Molecular Biology</i> , 2014, 426, 4125-4138.	4.2	25

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145	Single treatment of VX poisoned guinea pigs with the phosphotriesterase mutant C23AL: Intraosseous versus intravenous injection. <i>Toxicology Letters</i> , 2016, 258, 198-206.	0.8	24
146	Efficient and Selective P-nitrophenyl-ester-hydrolyzing Antibodies Elicited by a P-nitrobenzyl Phosphonate Hapten. <i>FEBS Journal</i> , 1997, 244, 619-626.	0.2	23
147	The Dimethylsulfoniopropionate (DMSP) Lyase and Lyase-Like Cupin Family Consists of <i>Bona Fide</i> DMSP lyases as Well as Other Enzymes with Unknown Function. <i>Biochemistry</i> , 2018, 57, 3364-3377.	2.5	22
148	The Limited Information Capacity of Cross-Reactive Sensors Drives the Evolutionary Expansion of Signaling. <i>Cell Systems</i> , 2019, 8, 76-85.e6.	6.2	22
149	Enzyme promiscuity and evolution in light of cellular metabolism. <i>FEBS Journal</i> , 2020, 287, 1260-1261.	4.7	21
150	Determinants of cofactor binding to DNA methyltransferases: insights from a systematic series of structural variants of S-adenosylhomocysteine. <i>Organic and Biomolecular Chemistry</i> , 2005, 3, 152.	2.8	20
151	TRINS: a method for gene modification by randomized tandem repeat insertions. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 437-444.	2.1	20
152	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. <i>Journal of Molecular Biology</i> , 2019, 431, 1284-1297.	4.2	20
153	In vitro detoxification of cyclosarin in human blood pre-incubated ex vivo with recombinant serum paraoxonases. <i>Toxicology Letters</i> , 2011, 206, 24-28.	0.8	17
154	Ambiguous evidence for assigning DddQ as a dimethylsulfoniopropionate lyase and oceanic dimethylsulfide producer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2078-9.	7.1	17
155	A new post-intoxication treatment of paraoxon and parathion poisonings using an evolved PON1 variant and recombinant GOT1. <i>Chemico-Biological Interactions</i> , 2016, 259, 242-251.	4.0	17
156	Gal3 Binds Gal80 Tighter than Gal1 Indicating Adaptive Protein Changes Following Duplication. <i>Molecular Biology and Evolution</i> , 2016, 33, 472-477.	8.9	17
157	Polyamines Mediate Folding of Primordial Hyperacidic Helical Proteins. <i>Biochemistry</i> , 2020, 59, 4456-4462.	2.5	17
158	Nonspecific Catalysis By Protein Surfaces. <i>Applied Biochemistry and Biotechnology</i> , 2000, 83, 173-182.	2.9	15
159	Hopeful (Protein InDel) Monsters?. <i>Structure</i> , 2014, 22, 803-804.	3.3	15
160	Assigning the Algal Source of Dimethylsulfide Using a Selective Lyase Inhibitor. <i>ACS Chemical Biology</i> , 2017, 12, 41-46.	3.4	15
161	Esterolytic Antibodies as Mechanistic and Structural Models of Hydrolasesâ€”A Quantitative Analysis. <i>Journal of Molecular Biology</i> , 2002, 320, 559-572.	4.2	14
162	Helicase-like functions in phosphate loop containing beta-alpha polypeptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	14

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163	A counter-enzyme complex regulates glutamate metabolism in <i>Bacillus subtilis</i> . <i>Nature Chemical Biology</i> , 2022, 18, 161-170.	8.0	14
164	The number and type of oxygen-utilizing enzymes indicates aerobic vs. anaerobic phenotype. <i>Free Radical Biology and Medicine</i> , 2019, 140, 84-92.	2.9	13
165	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. <i>PLoS Computational Biology</i> , 2020, 16, e1008145.	3.2	12
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