

Dan S Tawfik

List of Publications by Year in descending order

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191
papers

25,140
citations

6592

79
h-index

7718

150
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. <i>Annual Review of Biochemistry</i> , 2010, 79, 471-505.	5.0	1,137
2	Kemp elimination catalysts by computational enzyme design. <i>Nature</i> , 2008, 453, 190-195.	13.7	1,130
3	Man-made cell-like compartments for molecular evolution. <i>Nature Biotechnology</i> , 1998, 16, 652-656.	9.4	867
4	The Moderately Efficient Enzyme: Evolutionary and Physicochemical Trends Shaping Enzyme Parameters. <i>Biochemistry</i> , 2011, 50, 4402-4410.	1.2	810
5	Protein Dynamism and Evolvability. <i>Science</i> , 2009, 324, 203-207.	6.0	764
6	The 'evolvability' of promiscuous protein functions. <i>Nature Genetics</i> , 2005, 37, 73-76.	9.4	742
7	Antibody Multispecificity Mediated by Conformational Diversity. <i>Science</i> , 2003, 299, 1362-1367.	6.0	673
8	Stability effects of mutations and protein evolvability. <i>Current Opinion in Structural Biology</i> , 2009, 19, 596-604.	2.6	626
9	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 412-419.	3.6	569
10	Enzyme promiscuity: evolutionary and mechanistic aspects. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 498-508.	2.8	550
11	Conformational diversity and protein evolution – a 60-year-old hypothesis revisited. <i>Trends in Biochemical Sciences</i> , 2003, 28, 361-368.	3.7	514
12	How Protein Stability and New Functions Trade Off. <i>PLoS Computational Biology</i> , 2008, 4, e1000002.	1.5	468
13	Local fitness landscape of the green fluorescent protein. <i>Nature</i> , 2016, 533, 397-401.	13.7	438
14	Structure-Reactivity Studies of Serum Paraoxonase PON1 Suggest that Its Native Activity Is Lactonase. <i>Biochemistry</i> , 2005, 44, 6371-6382.	1.2	403
15	The Stability Effects of Protein Mutations Appear to be Universally Distributed. <i>Journal of Molecular Biology</i> , 2007, 369, 1318-1332.	2.0	396
16	Robustness-epistasis link shapes the fitness landscape of a randomly drifting protein. <i>Nature</i> , 2006, 444, 929-932.	13.7	387
17	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. <i>Molecular Cell</i> , 2016, 63, 337-346.	4.5	363
18	Mutational effects and the evolution of new protein functions. <i>Nature Reviews Genetics</i> , 2010, 11, 572-582.	7.7	358

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19	Amplification of complex gene libraries by emulsion PCR. <i>Nature Methods</i> , 2006, 3, 545-550.	9.0	327
20	Chaperonin overexpression promotes genetic variation and enzyme evolution. <i>Nature</i> , 2009, 459, 668-673.	13.7	315
21	Miniaturising the laboratory in emulsion droplets. <i>Trends in Biotechnology</i> , 2006, 24, 395-402.	4.9	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.	3.3	275
23	Directed evolution of an extremely fast phosphotriesterase by in vitro compartmentalization. <i>EMBO Journal</i> , 2003, 22, 24-35.	3.5	267
24	The Latent Promiscuity of Newly Identified Microbial Lactonases Is Linked to a Recently Diverged Phosphotriesterase. <i>Biochemistry</i> , 2006, 45, 13677-13686.	1.2	258
25	Initial Mutations Direct Alternative Pathways of Protein Evolution. <i>PLoS Genetics</i> , 2011, 7, e1001321.	1.5	236
26	Intense Neutral Drifts Yield Robust and Evolvable Consensus Proteins. <i>Journal of Molecular Biology</i> , 2008, 379, 1029-1044.	2.0	232
27	Do viral proteins possess unique biophysical features?. <i>Trends in Biochemical Sciences</i> , 2009, 34, 53-59.	3.7	229
28	Messy biology and the origins of evolutionary innovations. <i>Nature Chemical Biology</i> , 2010, 6, 692-696.	3.9	222
29	Advances in laboratory evolution of enzymes. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 151-158.	2.8	214
30	The molecular basis of phosphate discrimination in arsenate-rich environments. <i>Nature</i> , 2012, 491, 134-137.	13.7	209
31	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. <i>Nature Chemical Biology</i> , 2012, 8, 294-300.	3.9	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.	3.3	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.	1.6	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.	6.0	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.	6.2	197
36	Directed evolution by in vitro compartmentalization. <i>Nature Methods</i> , 2006, 3, 561-570.	9.0	196

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37	Diminishing returns and tradeoffs constrain the laboratory optimization of an enzyme. <i>Nature Communications</i> , 2012, 3, 1257.	5.8	196
38	High-throughput screens and selections of enzyme-encoding genes. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 210-216.	2.8	187
39	Off-the-shelf proteins that rival tailor-made antibodies as catalysts. <i>Nature</i> , 1996, 383, 60-63.	13.7	177
40	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. <i>Nature Chemical Biology</i> , 2011, 7, 120-125.	3.9	176
41	The universality of enzymatic rate-temperature dependency. <i>Trends in Biochemical Sciences</i> , 2014, 39, 1-7.	3.7	171
42	Directed enzyme evolution: beyond the low-hanging fruit. <i>Current Opinion in Structural Biology</i> , 2012, 22, 406-412.	2.6	167
43	Noise-mean relationship in mutated promoters. <i>Genome Research</i> , 2012, 22, 2409-2417.	2.4	167
44	Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. <i>Molecular Cell</i> , 2018, 72, 178-186.e5.	4.5	165
45	Arsenate Replacing Phosphate: Alternative Life Chemistries and Ion Promiscuity. <i>Biochemistry</i> , 2011, 50, 1128-1134.	1.2	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.	1.6	154
47	Evolutionary Optimization of Computationally Designed Enzymes: Kemp Eliminases of the KE07 Series. <i>Journal of Molecular Biology</i> , 2010, 396, 1025-1042.	2.0	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.	1.1	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.	2.0	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.	2.0	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.	2.0	140
52	Protein engineers turned evolutionists. <i>Nature Methods</i> , 2007, 4, 991-994.	9.0	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.	1.2	128

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55	Man-made enzymes "from design to in vitro compartmentalisation. <i>Current Opinion in Biotechnology</i> , 2000, 11, 338-353.	3.3	123
56	Directed enzyme evolution via small and effective neutral drift libraries. <i>Nature Methods</i> , 2008, 5, 939-942.	9.0	123
57	Directed evolution of proteins for heterologous expression and stability. <i>Current Opinion in Structural Biology</i> , 2005, 15, 50-56.	2.6	122
58	Shared Promiscuous Activities and Evolutionary Features in Various Members of the Amidohydrolase Superfamily. <i>Biochemistry</i> , 2005, 44, 12728-12736.	1.2	119
59	The specificity of cross-reactivity: Promiscuous antibody binding involves specific hydrogen bonds rather than nonspecific hydrophobic stickiness. <i>Protein Science</i> , 2009, 12, 2183-2193.	3.1	119
60	The 192R/Q polymorphs of serum paraoxonase PON1 differ in HDL binding, lipolactonase stimulation, and cholesterol efflux. <i>Journal of Lipid Research</i> , 2006, 47, 2492-2502.	2.0	118
61	Divergence and Convergence in Enzyme Evolution: Parallel Evolution of Paraoxonases from Quorum-quenching Lactonases. <i>Journal of Biological Chemistry</i> , 2012, 287, 11-20.	1.6	114
62	On the Potential Origins of the High Stability of Reconstructed Ancestral Proteins. <i>Molecular Biology and Evolution</i> , 2016, 33, 2633-2641.	3.5	114
63	Evolution of chalcone isomerase from a noncatalytic ancestor. <i>Nature Chemical Biology</i> , 2018, 14, 548-555.	3.9	113
64	The Evolutionary Origins of Detoxifying Enzymes. <i>Journal of Biological Chemistry</i> , 2013, 288, 23914-23927.	1.6	112
65	The robustness and innovability of protein folds. <i>Current Opinion in Structural Biology</i> , 2014, 26, 131-138.	2.6	108
66	Metabolite-Enzyme Coevolution: From Single Enzymes to Metabolic Pathways and Networks. <i>Annual Review of Biochemistry</i> , 2018, 87, 187-216.	5.0	106
67	Evolution of new protein topologies through multistep gene rearrangements. <i>Nature Genetics</i> , 2006, 38, 168-174.	9.4	103
68	Negative Epistasis and Evolvability in TEM-1 β -Lactamase "The Thin Line between an Enzyme's Conformational Freedom and Disorder. <i>Journal of Molecular Biology</i> , 2015, 427, 2396-2409.	2.0	102
69	Accuracy-rate tradeoffs: how do enzymes meet demands of selectivity and catalytic efficiency?. <i>Current Opinion in Chemical Biology</i> , 2014, 21, 73-80.	2.8	101
70	Incorporating Synthetic Oligonucleotides via Gene Reassembly (ISOR): a versatile tool for generating targeted libraries. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 219-226.	1.0	99
71	Microbead display by in vitro compartmentalisation: selection for binding using flow cytometry. <i>FEBS Letters</i> , 2002, 532, 455-458.	1.3	98
72	Structural Convergence in the Active Sites of a Family of Catalytic Antibodies. <i>Science</i> , 1997, 275, 1140-1142.	6.0	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.	1.0	97
74	Rescue of conformational dynamics in enzyme catalysis by directed evolution. <i>Nature Communications</i> , 2018, 9, 1314.	5.8	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.	3.3	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.	3.3	94
77	Protein engineers turned evolutionistsâ€”the quest for the optimal starting point. <i>Current Opinion in Biotechnology</i> , 2019, 60, 46-52.	3.3	93
78	Engineering V-Type Nerve Agents Detoxifying Enzymes Using Computationally Focused Libraries. <i>ACS Chemical Biology</i> , 2013, 8, 2394-2403.	1.6	91
79	Enhanced stereoselective hydrolysis of toxic organophosphates by directly evolved variants of mammalian serum paraoxonase. <i>FEBS Journal</i> , 2006, 273, 1906-1919.	2.2	90
80	The Moderately Efficient Enzyme: Futile Encounters and Enzyme Floppiness. <i>Biochemistry</i> , 2015, 54, 4969-4977.	1.2	89
81	De Novo Evolutionary Emergence of a Symmetrical Protein Is Shaped by Folding Constraints. <i>Cell</i> , 2016, 164, 476-486.	13.5	88
82	A Birdâ€™s-Eye View of Enzyme Evolution: Chemical, Physicochemical, and Physiological Considerations. <i>Chemical Reviews</i> , 2018, 118, 8786-8797.	23.0	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.	3.3	87
84	Enzyme engineering: reaching the maximal catalytic efficiency peak. <i>Current Opinion in Structural Biology</i> , 2017, 47, 140-150.	2.6	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.	2.6	85
86	Quantifying and understanding the fitness effects of protein mutations: Laboratory versus nature. <i>Protein Science</i> , 2016, 25, 1219-1226.	3.1	84
87	Evolved Stereoselective Hydrolases for Broad-Spectrum G-Type Nerve Agent Detoxification. <i>Chemistry and Biology</i> , 2012, 19, 456-466.	6.2	81
88	Slow protein evolutionary rates are dictated by surfaceâ€™core association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11151-11156.	3.3	80
89	Characterization of Proton-Transfer Catalysis by Serum Albumins. <i>Journal of the American Chemical Society</i> , 2000, 122, 1022-1029.	6.6	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.	1.5	79

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91	Chromogenic and Fluorogenic Assays for the Lactonase Activity of Serum Paraoxonases. <i>ChemBioChem</i> , 2006, 7, 49-53.	1.3	78
92	The development of human sera tests for HDL-bound serum PON1 and its lipolactonase activity. <i>Journal of Lipid Research</i> , 2007, 48, 1637-1646.	2.0	77
93	Efficient Catalysis of Proton Transfer by Synzymes. <i>Journal of the American Chemical Society</i> , 1997, 119, 9578-9579.	6.6	75
94	Potential role of phenotypic mutations in the evolution of protein expression and stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6197-6202.	3.3	75
95	Following evolutionary paths to protein-protein interactions with high affinity and selectivity. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1049-1055.	3.6	75
96	Enzyme Engineering by Targeted Libraries. <i>Methods in Enzymology</i> , 2013, 523, 257-283.	0.4	73
97	Functional Proteins from Short Peptides: Dayhoff's Hypothesis Turns 50. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 15966-15971.	7.2	73
98	On the Magnitude and Specificity of Medium Effects in Enzyme-like Catalysts for Proton Transfer. <i>Journal of Organic Chemistry</i> , 2001, 66, 5866-5874.	1.7	72
99	Latent evolutionary potentials under the neutral mutational drift of an enzyme. , 2007, 1, 67-78.		71
100	Simple yet functional phosphate-loop proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11943-E11950.	3.3	70
101	Directed Evolution of Protein Inhibitors of DNA-nucleases by in Vitro Compartmentalization (IVC) and Nano-droplet Delivery. <i>Journal of Molecular Biology</i> , 2005, 345, 1015-1026.	2.0	68
102	The evolution of oxygen-utilizing enzymes suggests early biosphere oxygenation. <i>Nature Ecology and Evolution</i> , 2021, 5, 442-448.	3.4	68
103	Ohno's Model Revisited: Measuring the Frequency of Potentially Adaptive Mutations under Various Mutational Drifts. <i>Molecular Biology and Evolution</i> , 2008, 25, 2311-2318.	3.5	66
104	On the evolution of chaperones and cochaperones and the expansion of proteomes across the Tree of Life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	65
105	Reconstruction of Functional β^2 -Propeller Lectins via Homo-oligomeric Assembly of Shorter Fragments. <i>Journal of Molecular Biology</i> , 2007, 365, 10-17.	2.0	64
106	BIOCHEMISTRY: Loop Grafting and the Origins of Enzyme Species. <i>Science</i> , 2006, 311, 475-476.	6.0	63
107	On the emergence of P-Loop NTPase and Rossmann enzymes from a Beta-Alpha-Beta ancestral fragment. <i>ELife</i> , 2020, 9, .	2.8	61
108	Directed Evolution of Sulfotransferases and Paraoxonases by Ancestral Libraries. <i>Journal of Molecular Biology</i> , 2011, 411, 837-853.	2.0	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.	2.0	58
110	Protein Insertions and Deletions Enabled by Neutral Roaming in Sequence Space. <i>Molecular Biology and Evolution</i> , 2013, 30, 761-771.	3.5	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.	3.3	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.	6.5	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.	1.0	57
114	DddD Is a CoA-Transferase/Lyase Producing Dimethyl Sulfide in the Marine Environment. <i>Biochemistry</i> , 2014, 53, 5473-5475.	1.2	51
115	Role of Chemistry versus Substrate Binding in Recruiting Promiscuous Enzyme Functions. <i>Biochemistry</i> , 2011, 50, 2683-2690.	1.2	48
116	Functional β^2 -propeller lectins by tandem duplications of repetitive units. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 185-195.	1.0	48
117	Native Mass Spectrometry of Recombinant Proteins from Crude Cell Lysates. <i>Analytical Chemistry</i> , 2017, 89, 4398-4404.	3.2	47
118	The Evolutionary Potential of Phenotypic Mutations. <i>PLoS Genetics</i> , 2015, 11, e1005445.	1.5	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.	2.0	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.	1.2	43
121	Mechanisms of Protein Sequence Divergence and Incompatibility. <i>PLoS Genetics</i> , 2013, 9, e1003665.	1.5	43
122	Correlated Occurrence and Bypass of Frame-Shifting Insertion-Deletions (InDels) to Give Functional Proteins. <i>PLoS Genetics</i> , 2013, 9, e1003882.	1.5	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.	1.9	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.	0.4	40
125	How evolution shapes enzyme selectivity – lessons from aminoacyl-tRNA synthetases and other amino acid utilizing enzymes. <i>FEBS Journal</i> , 2020, 287, 1284-1305.	2.2	39
126	Catalytic and binding polyreactivities shared by two unrelated proteins: The potential role of promiscuity in enzyme evolution. <i>Protein Science</i> , 2001, 10, 2600-2607.	3.1	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.	7.2	38
128	Differences in the biochemical properties of esterolytic antibodies correlate with structural diversity. <i>Molecular Immunology</i> , 1994, 31, 127-137.	1.0	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 Floppiness—The Case of High Density Lipoprotein-Bound Serum Paraoxonase-1. <i>Journal of Molecular Biology</i> , 2015, 427, 1359-1374.	2.0	37
131	Evolutionary transitions to new DNA methyltransferases through target site expansion and shrinkage. <i>Nucleic Acids Research</i> , 2012, 40, 11627-11637.	6.5	36
132	Antibiotic resistance evolved via inactivation of a ribosomal RNA methylating enzyme. <i>Nucleic Acids Research</i> , 2016, 44, 8897-8907.	6.5	36
133	Promiscuous methylation of non-canonical DNA sites by HaeIII methyltransferase. <i>Nucleic Acids Research</i> , 2002, 30, 3880-3885.	6.5	35
134	Assessing the prediction fidelity of ancestral reconstruction by a library approach. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 507-518.	1.0	35
135	Dimethyl sulfide mediates microbial predator-prey interactions between zooplankton and algae in the ocean. <i>Nature Microbiology</i> , 2021, 6, 1357-1366.	5.9	33
136	Enzyme evolution in natural products biosynthesis: target- or diversity-oriented?. <i>Current Opinion in Chemical Biology</i> , 2020, 59, 147-154.	2.8	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.	3.3	32
138	Bridging Themes: Short Protein Segments Found in Different Architectures. <i>Molecular Biology and Evolution</i> , 2021, 38, 2191-2208.	3.5	32
139	Diadenosine tetraphosphate (Ap ₄ A) — an <i>E. coli</i> alarmone or a damage metabolite?. <i>FEBS Journal</i> , 2017, 284, 2194-2215.	2.2	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.	3.6	28
141	Chance and pleiotropy dominate genetic diversity in complex bacterial environments. <i>Nature Microbiology</i> , 2019, 4, 1221-1230.	5.9	27
142	<i>Bacilli</i> glutamate dehydrogenases diverged via coevolution of transcription and enzyme regulation. <i>EMBO Reports</i> , 2017, 18, 1139-1149.	2.0	26
143	Enzyme Evolution: An Epistatic Ratchet versus a Smooth Reversible Transition. <i>Molecular Biology and Evolution</i> , 2020, 37, 1133-1147.	3.5	26
144	A “Fuzzy” Logic Language for Encoding Multiple Physical Traits in Biomolecules. <i>Journal of Molecular Biology</i> , 2014, 426, 4125-4138.	2.0	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.	0.4	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.	1.2	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.	2.9	22
149	Enzyme promiscuity and evolution in light of cellular metabolism. <i>FEBS Journal</i> , 2020, 287, 1260-1261.	2.2	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.	1.5	20
151	TRINS: a method for gene modification by randomized tandem repeat insertions. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 437-444.	1.0	20
152	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. <i>Journal of Molecular Biology</i> , 2019, 431, 1284-1297.	2.0	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.	0.4	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.	3.3	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.	1.7	17
156	Gal3 Binds Gal80 Tighter than Gal1 Indicating Adaptive Protein Changes Following Duplication. <i>Molecular Biology and Evolution</i> , 2016, 33, 472-477.	3.5	17
157	Polyamines Mediate Folding of Primordial Hyperacidic Helical Proteins. <i>Biochemistry</i> , 2020, 59, 4456-4462.	1.2	17
158	Nonspecific Catalysis By Protein Surfaces. <i>Applied Biochemistry and Biotechnology</i> , 2000, 83, 173-182.	1.4	15
159	Hopeful (Protein InDel) Monsters?. <i>Structure</i> , 2014, 22, 803-804.	1.6	15
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