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	The evolutionary history of the HUP domain. Critical Reviews in Biochemistry and Molecular Biology, 2022, 57, 1-15.	2.3	7
2	Directed evolution of the rRNA methylating enzyme Cfr reveals molecular basis of antibiotic resistance. ELife, 2022, 11, .	2.8	10
3	A counter-enzyme complex regulates glutamate metabolism in Bacillus subtilis. Nature Chemical Biology, 2022, 18, 161-170.	3.9	14
4	Innovation and tinkering in the evolution of oxidases. Protein Science, 2022, 31, e4310.	3.1	8
5	Uniform binding and negative catalysis at the origin of enzymes. Protein Science, 2022, 31, .	3.1	5
6	Quinone Methideâ€Based Organophosphate Hydrolases Inhibitors: Trans Proximity Labelers versus Cis Labeling Activityâ€Based Probes. ChemBioChem, 2021, 22, 894-903.	1.3	4
7	Bridging Themes: Short Protein Segments Found in Different Architectures. Molecular Biology and Evolution, 2021, 38, 2191-2208.	3.5	32
8	The evolution of oxygen-utilizing enzymes suggests early biosphere oxygenation. Nature Ecology and Evolution, 2021, 5, 442-448.	3.4	68
9	Protoâ€proteins in Protocells. ChemSystemsChem, 2021, 3, e2100002.	1.1	6
10	Helicase-like functions in phosphate loop containing beta-alpha polypeptides. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
11	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, .	3.3	65
12	Dimethyl sulfide mediates microbial predatorâ€“prey interactions between zooplankton and algae in the ocean. Nature Microbiology, 2021, 6, 1357-1366.	5.9	33
13	Enzyme Evolution: An Epistatic Ratchet versus a Smooth Reversible Transition. Molecular Biology and Evolution, 2020, 37, 1133-1147.	3.5	26
14	How evolution shapes enzyme selectivity â€“ lessons from aminoacylâ€tRNA synthetases and other amino acid utilizing enzymes. FEBS Journal, 2020, 287, 1284-1305.	2.2	39
15	Methanol-free biosynthesis of fatty acid methyl ester (FAME) in Synechocystis sp. PCC 6803. Metabolic Engineering, 2020, 57, 217-227.	3.6	28
16	Polyamines Mediate Folding of Primordial Hyperacidic Helical Proteins. Biochemistry, 2020, 59, 4456-4462.	1.2	17
17	Enzyme evolution in natural products biosynthesis: target- or diversity-oriented?. Current Opinion in Chemical Biology, 2020, 59, 147-154.	2.8	32
18	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. PLoS Computational Biology, 2020, 16, e1008145.	1.5	12

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19	Primordial emergence of a nucleic acid-binding protein via phase separation and statistical ornithine-to-arginine conversion. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15731-15739.	3.3	58
20	Short and simple sequences favored the emergence of N-helix phospho-ligand binding sites in the first enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5310-5318.	3.3	32
21	Enzyme promiscuity and evolution in light of cellular metabolism. FEBS Journal, 2020, 287, 1260-1261.	2.2	21
22	On the emergence of P-Loop NTPase and Rossmann enzymes from a Beta-Alpha-Beta ancestral fragment. ELife, 2020, 9, .	2.8	61
23	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. , 2020, 16, e1008145.		0
24	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. , 2020, 16, e1008145.		0
25	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. , 2020, 16, e1008145.		0
26	Determining the interaction status and evolutionary fate of duplicated homomeric proteins. , 2020, 16, e1008145.		0
27	Bifunctional Substrate Activation via an Arginine Residue Drives Catalysis in Chalcone Isomerases. ACS Catalysis, 2019, 9, 8388-8396.	5.5	11
28	A mixture of three engineered phosphotriesterases enables rapid detoxification of the entire spectrum of known threat nerve agents. Protein Engineering, Design and Selection, 2019, 32, 169-174.	1.0	8
29	A Personal Reflection on the Chemistryâ€Biology Interface. Israel Journal of Chemistry, 2019, 59, 23-28.	1.0	3
30	Chance and pleiotropy dominate genetic diversity in complex bacterial environments. Nature Microbiology, 2019, 4, 1221-1230.	5.9	27
31	The number and type of oxygen-utilizing enzymes indicates aerobic vs. anaerobic phenotype. Free Radical Biology and Medicine, 2019, 140, 84-92.	1.3	13
32	Protein engineers turned evolutionistsâ€"the quest for the optimal starting point. Current Opinion in Biotechnology, 2019, 60, 46-52.	3.3	93
33	The Limited Information Capacity of Cross-Reactive Sensors Drives the Evolutionary Expansion of Signaling. Cell Systems, 2019, 8, 76-85.e6.	2.9	22
34	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. Journal of Molecular Biology, 2019, 431, 1284-1297.	2.0	20
35	Evolution of chalcone isomerase from a noncatalytic ancestor. Nature Chemical Biology, 2018, 14, 548-555.	3.9	113
36	Rescue of conformational dynamics in enzyme catalysis by directed evolution. Nature Communications, 2018, 9, 1314.	5.8	97

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37	The Dimethylsulfoniopropionate (DMSP) Lyase and Lyase-Like Cupin Family Consists of Bona Fide DMSP lyases as Well as Other Enzymes with Unknown Function. Biochemistry, 2018, 57, 3364-3377.	1.2	22
38	Design and in vitro realization of carbon-conserving photorespiration. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11455-E11464.	3.3	97
39	Simple yet functional phosphate-loop proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11943-E11950.	3.3	70
40	Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. Molecular Cell, 2018, 72, 178-186.e5.	4.5	165
41	A Birdâ€™s-Eye View of Enzyme Evolution: Chemical, Physicochemical, and Physiological Considerations. Chemical Reviews, 2018, 118, 8786-8797.	23.0	88
42	Biochemical Profiling of DMSP Lyases. Methods in Enzymology, 2018, 605, 269-289.	0.4	1
43	Metaboliteâ€“Enzyme Coevolution: From Single Enzymes to Metabolic Pathways and Networks. Annual Review of Biochemistry, 2018, 87, 187-216.	5.0	106
44	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. Protein Engineering, Design and Selection, 2017, 30, 333-345.	1.0	57
45	Bacilli glutamate dehydrogenases diverged via coevolution of transcription and enzyme regulation. EMBO Reports, 2017, 18, 1139-1149.	2.0	26
46	Spontaneous Emergence of Sâ€Adenosylmethionine and the Evolution of Methylation. Angewandte Chemie - International Edition, 2017, 56, 343-345.	7.2	38
47	Diadenosine tetraphosphate (Ap4A) â€“ an E. coli alarmone or a damage metabolite?. FEBS Journal, 2017, 284, 2194-2215.	2.2	30
48	Native Mass Spectrometry of Recombinant Proteins from Crude Cell Lysates. Analytical Chemistry, 2017, 89, 4398-4404.	3.2	47
49	Assigning the Algal Source of Dimethylsulfide Using a Selective Lyase Inhibitor. ACS Chemical Biology, 2017, 12, 41-46.	1.6	15
50	Spontaneous Emergence of Sâ€Adenosylmethionine and the Evolution of Methylation. Angewandte Chemie, 2017, 129, 349-351.	1.6	8
51	Enzyme engineering: reaching the maximal catalytic efficiency peak. Current Opinion in Structural Biology, 2017, 47, 140-150.	2.6	87
52	Quantifying and understanding the fitness effects of protein mutations: Laboratory versus nature. Protein Science, 2016, 25, 1219-1226.	3.1	84
53	Editorial. Protein Science, 2016, 25, 1164-1167.	3.1	4
54	Local fitness landscape of the green fluorescent protein. Nature, 2016, 533, 397-401.	13.7	438

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55	Antibiotic resistance evolved via inactivation of a ribosomal RNA methylating enzyme. Nucleic Acids Research, 2016, 44, 8897-8907.	6.5	36
56	Editorial overview: Engineering and design. Current Opinion in Structural Biology, 2016, 39, v-vi.	2.6	1
57	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. Molecular Cell, 2016, 63, 337-346.	4.5	363
58	Single treatment of VX poisoned guinea pigs with the phosphotriesterase mutant C23AL: Intraosseous versus intravenous injection. Toxicology Letters, 2016, 258, 198-206.	0.4	24
59	On the Potential Origins of the High Stability of Reconstructed Ancestral Proteins. Molecular Biology and Evolution, 2016, 33, 2633-2641.	3.5	114
60	Functional Proteins from Short Peptides: Dayhoff's Hypothesis Turns 50. Angewandte Chemie - International Edition, 2016, 55, 15966-15971.	7.2	73
61	Funktionelle Proteine aus kurzen Peptiden: 50 Jahre nach Margaret Dayhoffs Hypothese. Angewandte Chemie, 2016, 128, 16198-16203.	1.6	5
62	Engineering and Directed Evolution of DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2016, 945, 491-509.	0.8	3
63	A new post-intoxication treatment of paraoxon and parathion poisonings using an evolved PON1 variant and recombinant GOT1. Chemico-Biological Interactions, 2016, 259, 242-251.	1.7	17
64	De Novo Evolutionary Emergence of a Symmetrical Protein Is Shaped by Folding Constraints. Cell, 2016, 164, 476-486.	13.5	88
65	Editorial overview: Biocatalysis and Biotransformation: Esoteric, Niche Enzymology. Current Opinion in Chemical Biology, 2016, 31, v-vii.	2.8	7
66	Gal3 Binds Gal80 Tighter than Gal1 Indicating Adaptive Protein Changes Following Duplication. Molecular Biology and Evolution, 2016, 33, 472-477.	3.5	17
67	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. Archives of Toxicology, 2016, 90, 2711-2724.	1.9	42
68	An Ancient Fingerprint Indicates the Common Ancestry of Rossmann-Fold Enzymes Utilizing Different Ribose-Based Cofactors. PLoS Biology, 2016, 14, e1002396.	2.6	85
69	Systematic Mapping of Protein Mutational Space by Prolonged Drift Reveals the Deleterious Effects of Seemingly Neutral Mutations. PLoS Computational Biology, 2015, 11, e1004421.	1.5	79
70	Negative Epistasis and Evolvability in TEM-1 Î²-Lactamaseâ€"The Thin Line between an Enzyme's Conformational Freedom and Disorder. Journal of Molecular Biology, 2015, 427, 2396-2409.	2.0	102
71	Assessing the prediction fidelity of ancestral reconstruction by a library approach. Protein Engineering, Design and Selection, 2015, 28, 507-518.	1.0	35
72	Catalytic Stimulation by Restrained Active-Site Floppinessâ€"The Case of High Density Lipoprotein-Bound Serum Paraoxonase-1. Journal of Molecular Biology, 2015, 427, 1359-1374.	2.0	37

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73	The Moderately Efficient Enzyme: Futile Encounters and Enzyme Floppiness. Biochemistry, 2015, 54, 4969-4977.	1.2	89
74	Identification of the algal dimethyl sulfideâ€“releasing enzyme: A missing link in the marine sulfur cycle. Science, 2015, 348, 1466-1469.	6.0	199
75	The Evolutionary Potential of Phenotypic Mutations. PLoS Genetics, 2015, 11, e1005445.	1.5	45
76	Ambiguous evidence for assigning DddQ as a dimethylsulfoniopropionate lyase and oceanic dimethylsulfide producer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2078-9.	3.3	17
77	A â€œFuzzyâ€•Logic Language for Encoding Multiple Physical Traits in Biomolecules. Journal of Molecular Biology, 2014, 426, 4125-4138.	2.0	25
78	The universality of enzymatic rateâ€“temperature dependency. Trends in Biochemical Sciences, 2014, 39, 1-7.	3.7	171
79	Post-exposure treatment of VX poisoned guinea pigs with the engineered phosphotriesterase mutant C23: A proof-of-concept study. Toxicology Letters, 2014, 231, 45-54.	0.4	40
80	The robustness and innovability of protein folds. Current Opinion in Structural Biology, 2014, 26, 131-138.	2.6	108
81	DddD Is a CoA-Transferase/Lyase Producing Dimethyl Sulfide in the Marine Environment. Biochemistry, 2014, 53, 5473-5475.	1.2	51
82	Accuracy-rate tradeoffs: how do enzymes meet demands of selectivity and catalytic efficiency?. Current Opinion in Chemical Biology, 2014, 21, 73-80.	2.8	101
83	Hopeful (Protein InDel) Monsters?. Structure, 2014, 22, 803-804.	1.6	15
84	Generating Targeted Libraries by the Combinatorial Incorporation of Synthetic Oligonucleotides During Gene Shuffling (ISOR). Methods in Molecular Biology, 2014, 1179, 129-137.	0.4	11
85	Catalytic Metal Ion Rearrangements Underline Promiscuity and Evolvability of a Metalloenzyme. Journal of Molecular Biology, 2013, 425, 1028-1038.	2.0	58
86	Protein Insertions and Deletions Enabled by Neutral Roaming in Sequence Space. Molecular Biology and Evolution, 2013, 30, 761-771.	3.5	58
87	Enzyme Engineering by Targeted Libraries. Methods in Enzymology, 2013, 523, 257-283.	0.4	73
88	What Makes a Protein Fold Amenable to Functional Innovation? Fold Polarity and Stability Trade-offs. Journal of Molecular Biology, 2013, 425, 2609-2621.	2.0	140
89	Engineering V-Type Nerve Agents Detoxifying Enzymes Using Computationally Focused Libraries. ACS Chemical Biology, 2013, 8, 2394-2403.	1.6	91
90	Correlated Occurrence and Bypass of Frame-Shifting Insertion-Deletions (InDels) to Give Functional Proteins. PLoS Genetics, 2013, 9, e1003882.	1.5	42

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91	Mechanisms of Protein Sequence Divergence and Incompatibility. PLoS Genetics, 2013, 9, e1003665.	1.5	43
92	The Evolutionary Origins of Detoxifying Enzymes. Journal of Biological Chemistry, 2013, 288, 23914-23927.	1.6	112
93	Evolutionary transitions to new DNA methyltransferases through target site expansion and shrinkage. Nucleic Acids Research, 2012, 40, 11627-11637.	6.5	36
94	Divergence and Convergence in Enzyme Evolution: Parallel Evolution of Paraoxonases from Quorum-quenching Lactonases. Journal of Biological Chemistry, 2012, 287, 11-20.	1.6	114
95	TRINS: a method for gene modification by randomized tandem repeat insertions. Protein Engineering, Design and Selection, 2012, 25, 437-444.	1.0	20
96	Directed enzyme evolution: beyond the low-hanging fruit. Current Opinion in Structural Biology, 2012, 22, 406-412.	2.6	167
97	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. Nature Chemical Biology, 2012, 8, 294-300.	3.9	205
98	Catalytic Versatility and Backups in Enzyme Active Sites: The Case of Serum Paraoxonase 1. Journal of Molecular Biology, 2012, 418, 181-196.	2.0	148
99	The molecular basis of phosphate discrimination in arsenate-rich environments. Nature, 2012, 491, 134-137.	13.7	209
100	Reconstructing a Missing Link in the Evolution of a Recently Diverged Phosphotriesterase by Active-Site Loop Remodeling. Biochemistry, 2012, 51, 6047-6055.	1.2	128
101	Diminishing returns and tradeoffs constrain the laboratory optimization of an enzyme. Nature Communications, 2012, 3, 1257.	5.8	196
102	Noiseâ€“mean relationship in mutated promoters. Genome Research, 2012, 22, 2409-2417.	2.4	167
103	Bridging the gaps in design methodologies by evolutionary optimization of the stability and proficiency of designed Kemp eliminase KE59. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10358-10363.	3.3	205
104	Evolved Stereoselective Hydrolases for Broad-Spectrum G-Type Nerve Agent Detoxification. Chemistry and Biology, 2012, 19, 456-466.	6.2	81
105	Role of Chemistry versus Substrate Binding in Recruiting Promiscuous Enzyme Functions. Biochemistry, 2011, 50, 2683-2690.	1.2	48
106	Arsenate Replacing Phosphate: Alternative Life Chemistries and Ion Promiscuity. Biochemistry, 2011, 50, 1128-1134.	1.2	160
107	The Moderately Efficient Enzyme: Evolutionary and Physicochemical Trends Shaping Enzyme Parameters. Biochemistry, 2011, 50, 4402-4410.	1.2	810
108	Optimization of the In-Silico-Designed Kemp Eliminase KE70 by Computational Design and Directed Evolution. Journal of Molecular Biology, 2011, 407, 391-412.	2.0	152

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109	Directed Evolution of Sulfotransferases and Paraoxonases by Ancestral Libraries. Journal of Molecular Biology, 2011, 411, 837-853.	2.0	58
110	In vitro detoxification of cyclosarin in human blood pre-incubated ex vivo with recombinant serum paraoxonases. Toxicology Letters, 2011, 206, 24-28.	0.4	17
111	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. Nature Chemical Biology, 2011, 7, 120-125.	3.9	176
112	Functional Î²-propeller lectins by tandem duplications of repetitive units. Protein Engineering, Design and Selection, 2011, 24, 185-195.	1.0	48
113	Slow protein evolutionary rates are dictated by surfaceâ€“core association. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11151-11156.	3.3	80
114	Initial Mutations Direct Alternative Pathways of Protein Evolution. PLoS Genetics, 2011, 7, e1001321.	1.5	236
115	Messy biology and the origins of evolutionary innovations. Nature Chemical Biology, 2010, 6, 692-696.	3.9	222
116	Mutational effects and the evolution of new protein functions. Nature Reviews Genetics, 2010, 11, 572-582.	7.7	358
117	Metamorphic proteins mediate evolutionary transitions of structure. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7287-7292.	3.3	94
118	Evolutionary Optimization of Computationally Designed Enzymes: Kemp Eliminases of the KE07 Series. Journal of Molecular Biology, 2010, 396, 1025-1042.	2.0	154
119	Enzyme Promiscuity: A Mechanistic and Evolutionary Perspective. Annual Review of Biochemistry, 2010, 79, 471-505.	5.0	1,137
120	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.	3.3	75
121	Stability effects of mutations and protein evolvability. Current Opinion in Structural Biology, 2009, 19, 596-604.	2.6	626
122	Do viral proteins possess unique biophysical features?. Trends in Biochemical Sciences, 2009, 34, 53-59.	3.7	229
123	In vivo administration of BL-3050: highly stable engineered PON1-HDL complexes. BMC Clinical Pharmacology, 2009, 9, 18.	2.5	37
124	Chaperonin overexpression promotes genetic variation and enzyme evolution. Nature, 2009, 459, 668-673.	13.7	315
125	Following evolutionary paths to protein-protein interactions with high affinity and selectivity. Nature Structural and Molecular Biology, 2009, 16, 1049-1055.	3.6	75
126	The specificity of cross-reactivity: Promiscuous antibody binding involves specific hydrogen bonds rather than nonspecific hydrophobic stickiness. Protein Science, 2009, 12, 2183-2193.	3.1	119

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127	Directed Evolution of Serum Paraoxonase PON3 by Family Shuffling and Ancestor/Consensus Mutagenesis, and Its Biochemical Characterization. Biochemistry, 2009, 48, 6644-6654.	1.2	43
128	Protein Dynamism and Evolvability. Science, 2009, 324, 203-207.	6.0	764
129	Advances in laboratory evolution of enzymes. Current Opinion in Chemical Biology, 2008, 12, 151-158.	2.8	214
130	Kemp elimination catalysts by computational enzyme design. Nature, 2008, 453, 190-195.	13.7	1,130
131	Directed enzyme evolution via small and effective neutral drift libraries. Nature Methods, 2008, 5, 939-942.	9.0	123
132	Intense Neutral Drifts Yield Robust and Evolvable Consensus Proteins. Journal of Molecular Biology, 2008, 379, 1029-1044.	2.0	232
133	Ohno's Model Revisited: Measuring the Frequency of Potentially Adaptive Mutations under Various Mutational Drifts. Molecular Biology and Evolution, 2008, 25, 2311-2318.	3.5	66
134	How Protein Stability and New Functions Trade Off. PLoS Computational Biology, 2008, 4, e1000002.	1.5	468
135	Serum paraoxonase PON1 and its interactions with HDL. FASEB Journal, 2008, 22, 811.1.	0.2	1
136	The development of human sera tests for HDL-bound serum PON1 and its lipolactonase activity. Journal of Lipid Research, 2007, 48, 1637-1646.	2.0	77
137	Reconstruction of Functional Î²-Propeller Lectins via Homo-oligomeric Assembly of Shorter Fragments. Journal of Molecular Biology, 2007, 365, 10-17.	2.0	64
138	The Stability Effects of Protein Mutations Appear to be Universally Distributed. Journal of Molecular Biology, 2007, 369, 1318-1332.	2.0	396
139	Latent evolutionary potentials under the neutral mutational drift of an enzyme. HFSP Journal, 2007, 1, 67-78.	2.5	134
140	Protein engineers turned evolutionists. Nature Methods, 2007, 4, 991-994.	9.0	135
141	Incorporating Synthetic Oligonucleotides via Gene Reassembly (ISOR): a versatile tool for generating targeted libraries. Protein Engineering, Design and Selection, 2007, 20, 219-226.	1.0	99
142	Latent evolutionary potentials under the neutral mutational drift of an enzyme. , 2007, 1, 67-78.		71
143	The Latent Promiscuity of Newly Identified Microbial Lactonases Is Linked to a Recently Diverged Phosphotriesteraseâ€. Biochemistry, 2006, 45, 13677-13686.	1.2	258
144	High-throughput Screens and Selections of Enzyme-encoding Genes. , 2006, , 163-181.		0

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145	Enhanced stereoselective hydrolysis of toxic organophosphates by directly evolved variants of mammalian serum paraoxonase. FEBS Journal, 2006, 273, 1906-1919.	2.2	90
146	Evolution of new protein topologies through multistep gene rearrangements. Nature Genetics, 2006, 38, 168-174.	9.4	103
147	Amplification of complex gene libraries by emulsion PCR. Nature Methods, 2006, 3, 545-550.	9.0	327
148	Directed evolution by in vitro compartmentalization. Nature Methods, 2006, 3, 561-570.	9.0	196
149	Robustnessâ€“epistasis link shapes the fitness landscape of a randomly drifting protein. Nature, 2006, 444, 929-932.	13.7	387
150	Enzyme promiscuity: evolutionary and mechanistic aspects. Current Opinion in Chemical Biology, 2006, 10, 498-508.	2.8	550
151	Miniaturising the laboratory in emulsion droplets. Trends in Biotechnology, 2006, 24, 395-402.	4.9	312
152	Chromogenic and Fluorogenic Assays for the Lactonase Activity of Serum Paraoxonases. ChemBioChem, 2006, 7, 49-53.	1.3	78
153	BIOCHEMISTRY: Loop Grafting and the Origins of Enzyme Species. Science, 2006, 311, 475-476.	6.0	63
154	The Histidine 115-Histidine 134 Dyad Mediates the Lactonase Activity of Mammalian Serum Paraoxonases. Journal of Biological Chemistry, 2006, 281, 7649-7656.	1.6	154
155	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.	2.0	118
156	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. Journal of Biological Chemistry, 2006, 281, 7657-7665.	1.6	204
157	Catalytic Antibodies as Mechanistic and Structural Models of Hydrolytic Enzymes. , 2005, , 418-453.		1
158	High-throughput screens and selections of enzyme-encoding genes. Current Opinion in Chemical Biology, 2005, 9, 210-216.	2.8	187
159	High-Throughput Screening of Enzyme Libraries: Thiolactonases Evolved by Fluorescence-Activated Sorting of Single Cells in Emulsion Compartments. Chemistry and Biology, 2005, 12, 1281-1289.	6.2	197
160	The 'evolvability' of promiscuous protein functions. Nature Genetics, 2005, 37, 73-76.	9.4	742
161	Directed evolution of proteins for heterologous expression and stability. Current Opinion in Structural Biology, 2005, 15, 50-56.	2.6	122
162	Structure and kinetics of a transient antibody binding intermediate reveal a kinetic discrimination mechanism in antigen recognition. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12730-12735.	3.3	87

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163	Shared Promiscuous Activities and Evolutionary Features in Various Members of the Amidohydrolase Superfamily. Biochemistry, 2005, 44, 12728-12736.	1.2	119
164	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.	2.0	68
165	Structureâ^'Reactivity Studies of Serum Paraoxonase PON1 Suggest that Its Native Activity Is Lactonase. Biochemistry, 2005, 44, 6371-6382.	1.2	403
166	Determinants of cofactor binding to DNA methyltransferases: insights from a systematic series of structural variants of S-adenosylhomocysteine. Organic and Biomolecular Chemistry, 2005, 3, 152.	1.5	20
167	Altering the sequence specificity of HaeIII methyltransferase by directed evolution using in vitro compartmentalization. Protein Engineering, Design and Selection, 2004, 17, 3-11.	1.0	97
168	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. Nature Structural and Molecular Biology, 2004, 11, 412-419.	3.6	569
169	In vitro compartmentalization by double emulsions: sorting and gene enrichment by fluorescence activated cell sorting. Analytical Biochemistry, 2004, 325, 151-157.	1.1	153
170	Directed evolution of mammalian paraoxonases PON1 and PON3 for bacterial expression and catalytic specialization. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 482-487.	3.3	275
171	In vitro compartmentalization (IVC): A high-throughput screening technology using emulsions and FACS. Discovery Medicine, 2004, 4, 49-53.	0.5	2
172	Directed evolution of an extremely fast phosphotriesterase by in vitro compartmentalization. EMBO Journal, 2003, 22, 24-35.	3.5	267
173	Conformational diversity and protein evolution â€“ a 60-year-old hypothesis revisited. Trends in Biochemical Sciences, 2003, 28, 361-368.	3.7	514
174	Antibody Multispecificity Mediated by Conformational Diversity. Science, 2003, 299, 1362-1367.	6.0	673
175	Promiscuous methylation of non-canonical DNA sites by HaeIII methyltransferase. Nucleic Acids Research, 2002, 30, 3880-3885.	6.5	35
176	Investigating the target recognition of DNA cytosine-5 methyltransferase HhaI by library selection using in vitro compartmentalisation. Nucleic Acids Research, 2002, 30, 4937-4944.	6.5	57
177	Microbead display by in vitro compartmentalisation: selection for binding using flow cytometry. FEBS Letters, 2002, 532, 455-458.	1.3	98
178	Esterolytic Antibodies as Mechanistic and Structural Models of Hydrolasesâ€”A Quantitative Analysis. Journal of Molecular Biology, 2002, 320, 559-572.	2.0	14
179	On the Magnitude and Specificity of Medium Effects in Enzyme-like Catalysts for Proton Transfer. Journal of Organic Chemistry, 2001, 66, 5866-5874.	1.7	72
180	Catalytic and binding polyâ€reactivities shared by two unrelated proteins: The potential role of promiscuity in enzyme evolution. Protein Science, 2001, 10, 2600-2607.	3.1	38

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181	Man-made enzymes â€" from design to in vitro compartmentalisation. Current Opinion in Biotechnology, 2000, 11, 338-353.	3.3	123
182	Nonspecific Catalysis By Protein Surfaces. Applied Biochemistry and Biotechnology, 2000, 83, 173-182.	1.4	15
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