Timothy A Whitehead

List of Publications by Year
in descending order

57 papers	2,662 citations	257450 24 h-index	206112 48 g-index
65 all docs	65 docs citations	65 times ranked	3505 citing authors

#	Article	IF	Citations
1	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. Science, 2011, 332, 816-821.	12.6	527
2	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. Nature Biotechnology, 2012, 30, 543-548.	17.5	342
3	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
4	Plasmid-based one-pot saturation mutagenesis. Nature Methods, 2016, 13, 928-930.	19.0	130
5	Trade-offs between enzyme fitness and solubility illuminated by deep mutational scanning. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2265-2270.	7.1	114
6	Single-mutation fitness landscapes for an enzyme on multiple substrates reveal specificity is globally encoded. Nature Communications, 2017, 8, 15695.	12.8	102
7	Lignin triggers irreversible cellulase loss during pretreated lignocellulosic biomass saccharification. Biotechnology for Biofuels, 2014, 7, 175.	6.2	90
8	Deep sequencing methods for protein engineering and design. Current Opinion in Structural Biology, 2017, 45, 36-44.	5.7	88
9	Minimal protein-folding systems in hyperthermophilic archaea. Nature Reviews Microbiology, 2004, 2, 315-324.	28.6	68
10	The Interrelationship between Promoter Strength, Gene Expression, and Growth Rate. PLoS ONE, 2014, 9, e109105.	2.5	67
11	Rapid Fine Conformational Epitope Mapping Using Comprehensive Mutagenesis and Deep Sequencing. Journal of Biological Chemistry, 2015, 290, 26457-26470.	3.4	67
12	High-Resolution Sequence-Function Mapping of Full-Length Proteins. PLoS ONE, 2015, 10, e0118193.	2.5	57
13	Transcriptional profiling of the hyperthermophilic methanarchaeon Methanococcus jannaschii in response to lethal heat and non-lethal cold shock. Environmental Microbiology, 2005, 7, 789-797.	3.8	56
14	Comprehensive Sequence-Flux Mapping of a Levoglucosan Utilization Pathway in <i>E. coli</i>. ACS Synthetic Biology, 2015, 4, 1235-1243.	3.8	51
15	Hotspot-Centric De Novo Design of Protein Binders. Journal of Molecular Biology, 2011, 413, 1047-1062.	4.2	41
16	Computational Design of Novel Protein Binders and Experimental Affinity Maturation. Methods in Enzymology, 2013, 523, 1-19.	1.0	38
17	Paired heavy- and light-chain signatures contribute to potent SARS-CoV-2 neutralization in public antibody responses. Cell Reports, 2021, 37, 109771.	6.4	38
18	Selfâ€renaturing enzymes: Design of an enzymeâ€chaperone chimera as a new approach to enzyme stabilization. Biotechnology and Bioengineering, 2009, 102, 1316-1322.	3.3	37

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19	A filamentous molecular chaperone of the prefoldin family from the deep-sea hyperthermophile Methanocaldococcus jannaschii. Protein Science, 2007, 16, 626-634.	7.6	36
20	One-shot identification of SARS-CoV-2ÂS RBD escape mutants using yeast screening. Cell Reports, 2021, 36, 109627.	6.4	35
21	Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. Nature Biotechnology, 2022, 40, 1855-1861.	17.5	34
22	Biotemplated Metal Nanowires Using Hyperthermophilic Protein Filaments. Small, 2009, 5, 2038-2042.	10.0	32
23	Negatively Supercharging Cellulases Render Them Lignin-Resistant. ACS Sustainable Chemistry and Engineering, 2017, 5, 6247-6252.	6.7	32
24	Tying up the loose ends: circular permutation decreases the proteolytic susceptibility of recombinant proteins. Protein Engineering, Design and Selection, 2009, 22, 607-613.	2.1	31
25	Computational redesign of the lipid-facing surface of the outer membrane protein OmpA. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9632-9637.	7.1	30
26	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. PLoS ONE, 2016, 11, e0147229.	2.5	29
27	Insights into cellulaseâ€lignin nonâ€specific binding revealed by computational redesign of the surface of green fluorescent protein. Biotechnology and Bioengineering, 2017, 114, 740-750.	3.3	25
28	An Automated Data-Driven Pipeline for Improving Heterologous Enzyme Expression. ACS Synthetic Biology, 2019, 8, 474-481.	3.8	24
29	Data-driven engineering of protein therapeutics. Current Opinion in Biotechnology, 2019, 60, 104-110.	6.6	22
30	Characterizing Protein-Protein Interactions Using Deep Sequencing Coupled to Yeast Surface Display. Methods in Molecular Biology, 2018, 1764, 101-121.	0.9	21
31	Determination of binding affinity upon mutation for type I dockerinâ€"cohesin complexes from <scp> <i>C</i> </scp> <i>lostridium thermocellum</i> and <scp> <i>C</i> </scp> <i>lostridium cellulolyticum</i> using deep sequencing. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1914-1928.	2.6	19
32	User-defined single pot mutagenesis using unamplified oligo pools. Protein Engineering, Design and Selection, 2019, 32, 41-45.	2.1	19
33	Producing Glucose 6-Phosphate from Cellulosic Biomass. Journal of Biological Chemistry, 2015, 290, 26638-26648.	3.4	17
34	Impact of In Vivo Protein Folding Probability on Local Fitness Landscapes. Molecular Biology and Evolution, 2019, 36, 2764-2777.	8.9	16
35	Removal and upgrading of lignocellulosic fermentation inhibitors by in situ biocatalysis and liquidâ€liquid extraction. Biotechnology and Bioengineering, 2015, 112, 627-632.	3.3	15
36	Rational shape engineering of the filamentous protein Î³ prefoldin through incremental gene truncation. Biopolymers, 2009, 91, 496-503.	2.4	14

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37	Fine Epitope Mapping of Two Antibodies Neutralizing the <i>Bordetella</i> Adenylate Cyclase Toxin. Biochemistry, 2017, 56, 1324-1336.	2.5	14
38	Characterization of Individual Human Antibodies That Bind Pertussis Toxin Stimulated by Acellular Immunization. Infection and Immunity, 2018, 86, .	2.2	13
39	The importance and future of biochemical engineering. Biotechnology and Bioengineering, 2020, 117, 2305-2318.	3.3	13
40	Controlling the Self‐Assembly of a Filamentous Hyperthermophilic Chaperone by an Engineered Capping Protein. Small, 2008, 4, 956-960.	10.0	12
41	Pro region engineering of nerve growth factor by deep mutational scanning enables a yeast platform for conformational epitope mapping of anti‐NGF monoclonal antibodies. Biotechnology and Bioengineering, 2018, 115, 1925-1937.	3.3	12
42	Optimization of multi-site nicking mutagenesis for generation of large, user-defined combinatorial libraries. Protein Engineering, Design and Selection, 2021, 34, .	2.1	10
43	Saturation Mutagenesis Genome Engineering of Infective Φ X174 Bacteriophage <i>via</i> Unamplified Oligo Pools and Golden Gate Assembly. ACS Synthetic Biology, 2020, 9, 125-131.	3.8	8
44	Stabilization of the SARS-CoV-2 receptor binding domain by protein core redesign and deep mutational scanning. Protein Engineering, Design and Selection, 2022, 35, .	2.1	8
45	Regulatory Approved Monoclonal Antibodies Contain Framework Mutations Predicted From Human Antibody Repertoires. Frontiers in Immunology, 2021, 12, 728694.	4.8	7
46	A peptide mimic of an antibody. Science, 2017, 358, 450-451.	12.6	6
47	A yeast surface display platform for plant hormone receptors: Toward directed evolution of new biosensors. AICHE Journal, 2020, 66, e16767.	3.6	6
48	A Method for User-defined Mutagenesis by Integrating Oligo Pool Synthesis Technology with Nicking Mutagenesis. Bio-protocol, 2020, 10, e3697.	0.4	5
49	Identification of SARS-CoV-2 RBD escape mutants using yeast screening and deep mutational scanning. STAR Protocols, 2021, 2, 100869.	1.2	4
50	An overview of methods for the structural and functional mapping of epitopes recognized by anti-SARS-CoV-2 antibodies. RSC Chemical Biology, 2021, 2, 1580-1589.	4.1	4
51	A Closed Form Model for Molecular Ratchet-Type Chemically Induced Dimerization Modules. Biochemistry, 2023, 62, 281-291.	2.5	4
52	Feline Interleukin-31 Shares Overlapping Epitopes with the Oncostatin M Receptor and IL-31RA. Biochemistry, 2020, 59, 2171-2181.	2.5	3
53	High-throughput evaluation of synthetic metabolic pathways. Technology, 2016, 04, 9-14.	1.4	2
54	Introduction to the Rosetta Special Collection. PLoS ONE, 2015, 10, e0144326.	2.5	2

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55	The inner workings of an enzyme. Science, 2021, 373, 391-392.	12.6	1
56	Facile Assembly of Combinatorial Mutagenesis Libraries Using Nicking Mutagenesis. Methods in Molecular Biology, 2022, , 85-109.	0.9	1
57	Pro region engineering of nerve growth factor by deep mutational scanning enables a yeast platform for conformational epitope mapping of anti-NGF monoclonal antibodies. Biotechnology and Bioengineering, 0, , .	3.3	0