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	A Closed Form Model for Molecular Ratchet-Type Chemically Induced Dimerization Modules. Biochemistry, 2023, 62, 281-291.	2.5	4
2	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
3	Facile Assembly of Combinatorial Mutagenesis Libraries Using Nicking Mutagenesis. Methods in Molecular Biology, 2022, , 85-109.	0.9	1
4	Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. Nature Biotechnology, 2022, 40, 1855-1861.	17.5	34
5	Optimization of multi-site nicking mutagenesis for generation of large, user-defined combinatorial libraries. Protein Engineering, Design and Selection, 2021, 34, .	2.1	10
6	The inner workings of an enzyme. Science, 2021, 373, 391-392.	12.6	1
7	One-shot identification of SARS-CoV-2ÂS RBD escape mutants using yeast screening. Cell Reports, 2021, 36, 109627.	6.4	35
8	Identification of SARS-CoV-2ÂS RBD escape mutants using yeast screening and deep mutational scanning. STAR Protocols, 2021, 2, 100869.	1.2	4
9	Regulatory Approved Monoclonal Antibodies Contain Framework Mutations Predicted From Human Antibody Repertoires. Frontiers in Immunology, 2021, 12, 728694.	4.8	7
10	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
11	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
12	A yeast surface display platform for plant hormone receptors: Toward directed evolution of new biosensors. AICHE Journal, 2020, 66, e16767.	3.6	6
13	Saturation Mutagenesis Genome Engineering of Infective Î¦X174 Bacteriophage <i>via</i> Unamplified Oligo Pools and Golden Gate Assembly. ACS Synthetic Biology, 2020, 9, 125-131.	3.8	8
14	Feline Interleukin-31 Shares Overlapping Epitopes with the Oncostatin M Receptor and IL-31RA. Biochemistry, 2020, 59, 2171-2181.	2.5	3
15	The importance and future of biochemical engineering. Biotechnology and Bioengineering, 2020, 117, 2305-2318.	3.3	13
16	A Method for User-defined Mutagenesis by Integrating Oligo Pool Synthesis Technology with Nicking Mutagenesis. Bio-protocol, 2020, 10, e3697.	0.4	5
17	Impact of In Vivo Protein Folding Probability on Local Fitness Landscapes. Molecular Biology and Evolution, 2019, 36, 2764-2777.	8.9	16
18	User-defined single pot mutagenesis using unamplified oligo pools. Protein Engineering, Design and Selection, 2019, 32, 41-45.	2.1	19

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19	An Automated Data-Driven Pipeline for Improving Heterologous Enzyme Expression. ACS Synthetic Biology, 2019, 8, 474-481.	3.8	24
20	Data-driven engineering of protein therapeutics. Current Opinion in Biotechnology, 2019, 60, 104-110.	6.6	22
21	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
22	Characterizing Protein-Protein Interactions Using Deep Sequencing Coupled to Yeast Surface Display. Methods in Molecular Biology, 2018, 1764, 101-121.	0.9	21
23	Characterization of Individual Human Antibodies That Bind Pertussis Toxin Stimulated by Acellular Immunization. Infection and Immunity, 2018, 86, .	2.2	13
24	Fine Epitope Mapping of Two Antibodies Neutralizing the <i>Bordetella</i> Adenylate Cyclase Toxin. Biochemistry, 2017, 56, 1324-1336.	2.5	14
25	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
26	Single-mutation fitness landscapes for an enzyme on multiple substrates reveal specificity is globally encoded. Nature Communications, 2017, 8, 15695.	12.8	102
27	Negatively Supercharging Cellulases Render Them Lignin-Resistant. ACS Sustainable Chemistry and Engineering, 2017, 5, 6247-6252.	6.7	32
28	A peptide mimic of an antibody. Science, 2017, 358, 450-451.	12.6	6
29	Insights into cellulase€lignin non€specific binding revealed by computational redesign of the surface of green fluorescent protein. Biotechnology and Bioengineering, 2017, 114, 740-750.	3.3	25
30	Deep sequencing methods for protein engineering and design. Current Opinion in Structural Biology, 2017, 45, 36-44.	5.7	88
31	Plasmid-based one-pot saturation mutagenesis. Nature Methods, 2016, 13, 928-930.	19.0	130
32	Determination of binding affinity upon mutation for type I dockerin€"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
33	High-throughput evaluation of synthetic metabolic pathways. Technology, 2016, 04, 9-14.	1.4	2
34	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. PLoS ONE, 2016, 11, e0147229.	2.5	29
35	Producing Glucose 6-Phosphate from Cellulosic Biomass. Journal of Biological Chemistry, 2015, 290, 26638-26648.	3.4	17
36	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

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37	Comprehensive Sequence-Flux Mapping of a Levoglucosan Utilization Pathway in <i>E. coli</i>. ACS Synthetic Biology, 2015, 4, 1235-1243.	3.8	51
38	Rapid Fine Conformational Epitope Mapping Using Comprehensive Mutagenesis and Deep Sequencing. Journal of Biological Chemistry, 2015, 290, 26457-26470.	3.4	67
39	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
40	High-Resolution Sequence-Function Mapping of Full-Length Proteins. PLoS ONE, 2015, 10, e0118193.	2.5	57
41	Introduction to the Rosetta Special Collection. PLoS ONE, 2015, 10, e0144326.	2.5	2
42	The Interrelationship between Promoter Strength, Gene Expression, and Growth Rate. PLoS ONE, 2014, 9, e109105.	2.5	67
43	Lignin triggers irreversible cellulase loss during pretreated lignocellulosic biomass saccharification. Biotechnology for Biofuels, 2014, 7, 175.	6.2	90
44	Computational Design of Novel Protein Binders and Experimental Affinity Maturation. Methods in Enzymology, 2013, 523, 1-19.	1.0	38
45	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. Nature Biotechnology, 2012, 30, 543-548.	17.5	342
46	Hotspot-Centric De Novo Design of Protein Binders. Journal of Molecular Biology, 2011, 413, 1047-1062.	4.2	41
47	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
48	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. Science, 2011, 332, 816-821.	12.6	527
49	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
50	Rational shape engineering of the filamentous protein Î³ prefoldin through incremental gene truncation. Biopolymers, 2009, 91, 496-503.	2.4	14
51	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
52	Biotemplated Metal Nanowires Using Hyperthermophilic Protein Filaments. Small, 2009, 5, 2038-2042.	10.0	32
53	Controlling the Selfâ€Assembly of a Filamentous Hyperthermophilic Chaperone by an Engineered Capping Protein. Small, 2008, 4, 956-960.	10.0	12
54	A filamentous molecular chaperone of the prefoldin family from the deep-sea hyperthermophile Methanocaldococcus jannaschii. Protein Science, 2007, 16, 626-634.	7.6	36

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55	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
56	Minimal protein-folding systems in hyperthermophilic archaea. Nature Reviews Microbiology, 2004, 2, 315-324.	28.6	68
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