

Thomas J Magliery

List of Publications by Year in descending order

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49
papers

2,329
citations

304743

22
h-index

223800

46
g-index

52
all docs

52
docs citations

52
times ranked

3309
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting Protein-Protein Interactions with a Green Fluorescent Protein Fragment Reassembly Trap: Scope and Mechanism. <i>Journal of the American Chemical Society</i> , 2005, 127, 146-157.	13.7	391
2	High-Throughput Thermal Scanning: A General, Rapid Dye-Binding Thermal Shift Screen for Protein Engineering. <i>Journal of the American Chemical Society</i> , 2009, 131, 3794-3795.	13.7	196
3	Engineering a tRNA and aminoacyl-tRNA synthetase for the site-specific incorporation of unnatural amino acids into proteins in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 10092-10097.	7.1	168
4	A New Functional Suppressor tRNA/Aminoacyl-tRNA Synthetase Pair for the in Vivo Incorporation of Unnatural Amino Acids into Proteins. <i>Journal of the American Chemical Society</i> , 2000, 122, 5010-5011.	13.7	130
5	Protein stability: computation, sequence statistics, and new experimental methods. <i>Current Opinion in Structural Biology</i> , 2015, 33, 161-168.	5.7	128
6	Expanding the genetic code: selection of efficient suppressors of four-base codons and identification of "shifted" four-base codons with a library approach in <i>Escherichia coli</i> . Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 2001, 307, 755-769.	4.2	123
7	Detecting protein-protein interactions with GFP-fragment reassembly. <i>Nature Methods</i> , 2004, 1, 255-262.	19.0	118
8	Stabilizing Proteins from Sequence Statistics: The Interplay of Conservation and Correlation in Triosephosphate Isomerase Stability. <i>Journal of Molecular Biology</i> , 2012, 420, 384-399.	4.2	91
9	Exploring the Limits of Codon and Anticodon Size. <i>Chemistry and Biology</i> , 2002, 9, 237-244.	6.0	78
10	Beyond Consensus: Statistical Free Energies Reveal Hidden Interactions in the Design of a TPR Motif. <i>Journal of Molecular Biology</i> , 2004, 343, 731-745.	4.2	77
11	Sequence variation in ligand binding sites in proteins. <i>BMC Bioinformatics</i> , 2005, 6, 240.	2.6	72
12	Direct single-molecule observation of a protein living in two opposed native structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10153-10158.	7.1	72
13	Triosephosphate Isomerase by Consensus Design: Dramatic Differences in Physical Properties and Activity of Related Variants. <i>Journal of Molecular Biology</i> , 2011, 413, 195-208.	4.2	59
14	Somatic hypermutation maintains antibody thermodynamic stability during affinity maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4261-4266.	7.1	59
15	Protein stability by number: high-throughput and statistical approaches to one of protein science's most difficult problems. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 443-451.	6.1	53
16	A New Orthogonal Suppressor tRNA/Aminoacyl-tRNA Synthetase Pair for Evolving an Organism with an Expanded Genetic Code. <i>Helvetica Chimica Acta</i> , 2000, 83, 2277-2286.	1.6	45
17	Dramatic Differences in Organophosphorus Hydrolase Activity between Human and Chimeric Recombinant Mammalian Paraoxonase-1 Enzymes. <i>Biochemistry</i> , 2009, 48, 10416-10422.	2.5	42
18	Re-engineering a split-GFP reassembly screen to examine RING-domain interactions between BARD1 and BRCA1 mutants observed in cancer patients. <i>Molecular BioSystems</i> , 2008, 4, 599.	2.9	36

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19	Characterization of an "orthogonal" suppressor tRNA derived from E. coli tRNA ^{2Gln} . Chemistry and Biology, 1997, 4, 685-691.	6.0	35
20	Determinant roles of dendritic cell-expressed Notch Delta-like and Jagged ligands on anti-tumor T cell immunity. , 2019, 7, 95.		31
21	Combinatorial approaches to protein stability and structure. FEBS Journal, 2004, 271, 1595-1608.	0.2	29
22	Protein Engineering and Stabilization from Sequence Statistics. Methods in Enzymology, 2013, 523, 237-256.	1.0	25
23	An Antibody with a Variable Region Coiled-Coil "Knob" Domain. Angewandte Chemie - International Edition, 2014, 53, 132-135.	13.8	25
24	Characterization of an Italian Founder Mutation in the RING-Finger Domain of BRCA1. PLoS ONE, 2014, 9, e86924.	2.5	24
25	Mutational Analysis of 48G7 Reveals that Somatic Hypermutation Affects Both Antibody Stability and Binding Affinity. Journal of the American Chemical Society, 2013, 135, 9980-9983.	13.7	22
26	Simplifying protein expression with ligation-free, traceless and tag-switching plasmids. Protein Expression and Purification, 2012, 85, 9-17.	1.3	21
27	Reassembled GFP: Detecting Protein-Protein Interactions and Protein Expression Patterns. Methods of Biochemical Analysis, 2005, 47, 391-405.	0.2	18
28	A 3E8.scFv.Cys-IR800 Conjugate Targeting TAG-72 in an Orthotopic Colorectal Cancer Model. Molecular Imaging and Biology, 2018, 20, 47-54.	2.6	17
29	Mechanistic insights into the hydrolysis of organophosphorus compounds by paraoxonase-1: exploring the limits of substrate tolerance in a promiscuous enzyme. Journal of Physical Organic Chemistry, 2012, 25, 1247-1260.	1.9	15
30	Linker engineering in anti-TAG-72 antibody fragments optimizes biophysical properties, serum half-life, and high-specificity tumor imaging. Journal of Biological Chemistry, 2018, 293, 9030-9040.	3.4	15
31	A cell-based screen for function of the four-helix bundle protein Rop: a new tool for combinatorial experiments in biophysics. Protein Engineering, Design and Selection, 2004, 17, 77-83.	2.1	14
32	Using thermal scanning assays to test protein-protein interactions of inner-ear cadherins. PLoS ONE, 2017, 12, e0189546.	2.5	14
33	Stoichiometry of triple-sieve tRNA editing complex ensures fidelity of aminoacyl-tRNA formation. Nucleic Acids Research, 2019, 47, 929-940.	14.5	13
34	Cysteine-free rop: A four-helix bundle core mutant has wild-type stability and structure but dramatically different unfolding kinetics. Protein Science, 2010, 19, 670-679.	7.6	11
35	Synthetic Approach to Stop-Codon Scanning Mutagenesis. Journal of the American Chemical Society, 2011, 133, 6177-6186.	13.7	10
36	Solubilization and Humanization of Paraoxonase-1. Journal of Lipids, 2012, 2012, 1-13.	4.8	9

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37	Phylogenetic spread of sequence data affects fitness of SOD1 consensus enzymes: Insights from sequence statistics and structural analyses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 609-620.	2.6	6
38	Insights into the mechanism of paraoxonase-1: Comparing the reactivity of the six-bladed \hat{I}^2 -propeller hydrolases. <i>Biochemistry</i> , 2018, , .	2.5	6
39	Expression and purification of a recombinant amyloidogenic peptide from transthyretin for solid-state NMR spectroscopy. <i>Protein Expression and Purification</i> , 2010, 70, 101-108.	1.3	5
40	Addressing the unmet need for visualizing conditional random fields in biological data. <i>BMC Bioinformatics</i> , 2014, 15, 202.	2.6	4
41	Understanding the sequence requirements of protein families: insights from the BioVis 2013 contests. <i>BMC Proceedings</i> , 2014, 8, S1.	1.6	4
42	An efficient and quantitative assay for epitope-tagged therapeutic protein development with a capillary western system. <i>Bioanalysis</i> , 2019, 11, 471-483.	1.5	3
43	Phylogenetic spread of sequence data affects fitness of consensus enzymes: Insights from triosephosphate isomerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 274-283.	2.6	2
44	Library approaches to biophysical problems. <i>FEBS Journal</i> , 2004, 271, 1593-1594.	0.2	1
45	Resonance assignments of wild-type and two cysteine-free variants of the four-helix bundle protein, <i>Rop</i> . <i>Biomolecular NMR Assignments</i> , 2018, 12, 345-350.	0.8	1
46	Editorial overview: From powerful tools to useful products: protein engineering after 35 years of directed evolution. <i>Current Opinion in Structural Biology</i> , 2020, 63, vi-viii.	5.7	1
47	Expanding the Genetic Code in Vitro and in Vivo. , 2004, , 221-249.		0
48	Cover Image, Volume 86, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C4-C4.	2.6	0
49	^1H , ^{13}C , ^{15}N resonance assignment of recombinant <i>Euplotes raikovi</i> protein Er-23. <i>Biomolecular NMR Assignments</i> , 2018, 12, 291-295.	0.8	0