

Thomas J Magliery

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	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
4	Determinant roles of dendritic cell-expressed Notch Delta-like and Jagged ligands on anti-tumor T cell immunity. , 2019, 7, 95.		31
5	Stoichiometry of triple-sieve tRNA editing complex ensures fidelity of aminoacyl-tRNA formation. <i>Nucleic Acids Research</i> , 2019, 47, 929-940.	14.5	13
6	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
7	Linker engineering in anti-TAG-72 antibody fragments optimizes biophysical properties, serum half-life, and high-specificity tumor imaging. <i>Journal of Biological Chemistry</i> , 2018, 293, 9030-9040.	3.4	15
8	A 3E8.scFv.Cys-IR800 Conjugate Targeting TAG-72 in an Orthotopic Colorectal Cancer Model. <i>Molecular Imaging and Biology</i> , 2018, 20, 47-54.	2.6	17
9	Insights into the mechanism of paraoxonase-1: Comparing the reactivity of the six-bladed β^2 -propeller hydrolases. <i>Biochemistry</i> , 2018, , .	2.5	6
10	Resonance assignments of wild-type and two cysteine-free variants of the four-helix bundle protein, Rop. <i>Biomolecular NMR Assignments</i> , 2018, 12, 345-350.	0.8	1
11	Cover Image, Volume 86, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C4-C4.	2.6	0
12	^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
13	Using thermal scanning assays to test protein-protein interactions of inner-ear cadherins. <i>PLoS ONE</i> , 2017, 12, e0189546.	2.5	14
14	Protein stability: computation, sequence statistics, and new experimental methods. <i>Current Opinion in Structural Biology</i> , 2015, 33, 161-168.	5.7	128
15	Addressing the unmet need for visualizing conditional random fields in biological data. <i>BMC Bioinformatics</i> , 2014, 15, 202.	2.6	4
16	Understanding the sequence requirements of protein families: insights from the BioVis 2013 contests. <i>BMC Proceedings</i> , 2014, 8, S1.	1.6	4
17	An Antibody with a Variable ϵ Region Coiled α Knob ϵ Domain. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 132-135.	13.8	25
18	Characterization of an Italian Founder Mutation in the RING-Finger Domain of BRCA1. <i>PLoS ONE</i> , 2014, 9, e86924.	2.5	24

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19	Somatic hypermutation maintains antibody thermodynamic stability during affinity maturation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4261-4266.	7.1	59
20	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
21	Protein Engineering and Stabilization from Sequence Statistics. Methods in Enzymology, 2013, 523, 237-256.	1.0	25
22	Solubilization and Humanization of Paraoxonase-1. Journal of Lipids, 2012, 2012, 1-13.	4.8	9
23	Simplifying protein expression with ligation-free, traceless and tag-switching plasmids. Protein Expression and Purification, 2012, 85, 9-17.	1.3	21
24	Stabilizing Proteins from Sequence Statistics: The Interplay of Conservation and Correlation in Triosephosphate Isomerase Stability. Journal of Molecular Biology, 2012, 420, 384-399.	4.2	91
25	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
26	Synthetic Approach to Stop-Codon Scanning Mutagenesis. Journal of the American Chemical Society, 2011, 133, 6177-6186.	13.7	10
27	Triosephosphate Isomerase by Consensus Design: Dramatic Differences in Physical Properties and Activity of Related Variants. Journal of Molecular Biology, 2011, 413, 195-208.	4.2	59
28	Protein stability by number: high-throughput and statistical approaches to one of protein science's most difficult problems. Current Opinion in Chemical Biology, 2011, 15, 443-451.	6.1	53
29	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
30	Expression and purification of a recombinant amyloidogenic peptide from transthyretin for solid-state NMR spectroscopy. Protein Expression and Purification, 2010, 70, 101-108.	1.3	5
31	Direct single-molecule observation of a protein living in two opposed native structures. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10153-10158.	7.1	72
32	Dramatic Differences in Organophosphorus Hydrolase Activity between Human and Chimeric Recombinant Mammalian Paraoxonase-1 Enzymes. Biochemistry, 2009, 48, 10416-10422.	2.5	42
33	High-Throughput Thermal Scanning: A General, Rapid Dye-Binding Thermal Shift Screen for Protein Engineering. Journal of the American Chemical Society, 2009, 131, 3794-3795.	13.7	196
34	Re-engineering a split-GFP reassembly screen to examine RING-domain interactions between BARD1 and BRCA1 mutants observed in cancer patients. Molecular BioSystems, 2008, 4, 599.	2.9	36
35	Reassembled GFP: Detecting Protein-Protein Interactions and Protein Expression Patterns. Methods of Biochemical Analysis, 2005, 47, 391-405.	0.2	18
36	Sequence variation in ligand binding sites in proteins. BMC Bioinformatics, 2005, 6, 240.	2.6	72

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37	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
38	A cell-based screen for function of the four-helix bundle protein Rop: a new tool for combinatorial experiments in biophysics. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 77-83.	2.1	14
39	Expanding the Genetic Code in Vitro and in Vivo. , 2004, , 221-249.		0
40	Combinatorial approaches to protein stability and structure. <i>FEBS Journal</i> , 2004, 271, 1595-1608.	0.2	29
41	Library approaches to biophysical problems. <i>FEBS Journal</i> , 2004, 271, 1593-1594.	0.2	1
42	Detecting protein-protein interactions with GFP-fragment reassembly. <i>Nature Methods</i> , 2004, 1, 255-262.	19.0	118
43	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
44	Exploring the Limits of Codon and Anticodon Size. <i>Chemistry and Biology</i> , 2002, 9, 237-244.	6.0	78
45	Expanding the genetic code: selection of efficient suppressors of four-base codons and identification of "shifty" 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
46	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
47	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
48	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
49	Characterization of an "orthogonal"™ suppressor tRNA derived from <i>E. coli</i> tRNA ^{2Gln} . <i>Chemistry and Biology</i> , 1997, 4, 685-691.	6.0	35