

Eric A Gaucher

List of Publications by Year in descending order

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53
papers

3,785
citations

126907

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175258

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docs citations

54
times ranked

4270
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic Articulation of Uric Acid Evolution in Mammals and How It Informs a Therapeutic Uricase. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	11
2	Ancestral Sequence Reconstruction: From Chemical Paleogenetics to Maximum Likelihood Algorithms and Beyond. <i>Journal of Molecular Evolution</i> , 2021, 89, 157-164.	1.8	25
3	Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. <i>Nature Communications</i> , 2021, 12, 380.	12.8	20
4	Molecular coevolution of coagulation factor VIII and von Willebrand factor. <i>Blood Advances</i> , 2021, 5, 812-822.	5.2	4
5	Evolution of bacterial steroid biosynthesis and its impact on eukaryogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
6	Identification of coagulation factor IX variants with enhanced activity through ancestral sequence reconstruction. <i>Blood Advances</i> , 2021, 5, 3333-3343.	5.2	6
7	Brief report: The uricase mutation in humans increases our risk for cancer growth. <i>Cancer & Metabolism</i> , 2021, 9, 32.	5.0	9
8	CRISPR-Cas9-mediated reactivation of the uricase pseudogene in human cells prevents acute hyperuricemia. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 25, 578-584.	5.1	1
9	Combining Ancestral Reconstruction with Folding-Landscape Simulations to Engineer Heterologous Protein Expression. <i>Journal of Molecular Biology</i> , 2021, 433, 167321.	4.2	5
10	Stabilization of Near-Infrared Fluorescent Proteins by Packaging in Virus-like Particles. <i>Biomacromolecules</i> , 2020, 21, 2432-2439.	5.4	10
11	Incorporation of Modified Amino Acids by Engineered Elongation Factors with Expanded Substrate Capabilities. <i>ACS Synthetic Biology</i> , 2019, 8, 287-296.	3.8	10
12	Non-conservation of folding rates in the thioredoxin family reveals degradation of ancestral unassisted-folding. <i>Biochemical Journal</i> , 2019, 476, 3631-3647.	3.7	16
13	On the Origin of Isoprenoid Biosynthesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 2185-2197.	8.9	54
14	Experimental Evolution of <i>Escherichia coli</i> Harboring an Ancient Translation Protein. <i>Journal of Molecular Evolution</i> , 2017, 84, 69-84.	1.8	40
15	De novo active sites for resurrected Precambrian enzymes. <i>Nature Communications</i> , 2017, 8, 16113.	12.8	60
16	Enhancing the pharmaceutical properties of protein drugs by ancestral sequence reconstruction. <i>Nature Biotechnology</i> , 2017, 35, 35-37.	17.5	87
17	Coevolution of URAT1 and Uricase during Primate Evolution: Implications for Serum Urate Homeostasis and Gout. <i>Molecular Biology and Evolution</i> , 2016, 33, 2193-2200.	8.9	60
18	An experimental phylogeny to benchmark ancestral sequence reconstruction. <i>Nature Communications</i> , 2016, 7, 12847.	12.8	62

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19	Selection for Protein Kinetic Stability Connects Denaturation Temperatures to Organismal Temperatures and Provides Clues to Archaean Life. <i>PLoS ONE</i> , 2016, 11, e0156657.	2.5	16
20	Mutational Studies on Resurrected Ancestral Proteins Reveal Conservation of Site-Specific Amino Acid Preferences throughout Evolutionary History. <i>Molecular Biology and Evolution</i> , 2015, 32, 440-455.	8.9	71
21	Molecular Evolution Directs Protein Translation Using Unnatural Amino Acids. <i>Current Protocols in Chemical Biology</i> , 2015, 7, 223-228.	1.7	2
22	Bioengineering Coagulation Factor VIII through Ancestral Protein Reconstruction. <i>Blood</i> , 2015, 126, 123-123.	1.4	2
23	Phenotypic comparisons of consensus variants versus laboratory resurrections of Precambrian proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 887-896.	2.6	56
24	Uric acid-dependent inhibition of AMP kinase induces hepatic glucose production in diabetes and starvation: evolutionary implications of the uricase loss in hominids. <i>FASEB Journal</i> , 2014, 28, 3339-3350.	0.5	145
25	Evolutionary history and metabolic insights of ancient mammalian uricases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3763-3768.	7.1	238
26	Interchanging Functionality Among Homologous Elongation Factors Using Signatures of Heterotachy. <i>Journal of Molecular Evolution</i> , 2013, 76, 4-12.	1.8	9
27	Conservation of Protein Structure over Four Billion Years. <i>Structure</i> , 2013, 21, 1690-1697.	3.3	115
28	Hyperstability and Substrate Promiscuity in Laboratory Resurrections of Precambrian β -Lactamases. <i>Journal of the American Chemical Society</i> , 2013, 135, 2899-2902.	13.7	212
29	Directed Evolution of Polymerases To Accept Nucleotides with Nonstandard Hydrogen Bond Patterns. <i>Biochemistry</i> , 2013, 52, 5288-5294.	2.5	56
30	Hydrophobic environment is a key factor for the stability of thermophilic proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 715-721.	2.6	98
31	Secondary structure and domain architecture of the 23S and 5S rRNAs. <i>Nucleic Acids Research</i> , 2013, 41, 7522-7535.	14.5	78
32	Reconstitution of translation from <i>Thermus thermophilus</i> reveals a minimal set of components sufficient for protein synthesis at high temperatures and functional conservation of modern and ancient translation components. <i>Nucleic Acids Research</i> , 2012, 40, 7932-7945.	14.5	45
33	RNA-Magnesium-Protein Interactions in Large Ribosomal Subunit. <i>Journal of Physical Chemistry B</i> , 2012, 116, 8113-8120.	2.6	42
34	Uric Acid: A Danger Signal From the RNA World That May Have a Role in the Epidemic of Obesity, Metabolic Syndrome, and Cardiorenal Disease: Evolutionary Considerations. <i>Seminars in Nephrology</i> , 2011, 31, 394-399.	1.6	93
35	Single-molecule paleoenzymology probes the chemistry of resurrected enzymes. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 592-596.	8.2	182
36	Exploiting Models of Molecular Evolution to Efficiently Direct Protein Engineering. <i>Journal of Molecular Evolution</i> , 2011, 72, 193-203.	1.8	47

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37	Utilizing natural diversity to evolve protein function: applications towards thermostability. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 399-406.	6.1	52
38	The Molecular Evolution of the p120-Catenin Subfamily and Its Functional Associations. <i>PLoS ONE</i> , 2010, 5, e15747.	2.5	61
39	Reconstructed evolutionary adaptive paths give polymerases accepting reversible terminators for sequencing and SNP detection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1948-1953.	7.1	71
40	Deep Phylogeny--How a Tree Can Help Characterize Early Life on Earth. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a002238-a002238.	5.5	53
41	Diversity of chemical mechanisms in thioredoxin catalysis revealed by single-molecule force spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 890-896.	8.2	91
42	Palaeotemperature trend for Precambrian life inferred from resurrected proteins. <i>Nature</i> , 2008, 451, 704-707.	27.8	338
43	The planetary biology of ascorbate and uric acid and their relationship with the epidemic of obesity and cardiovascular disease. <i>Medical Hypotheses</i> , 2008, 71, 22-31.	1.5	67
44	Ancestral sequence reconstruction as a tool to understand natural history and guide synthetic biology: realizing and extending the vision of Zuckerkandl and Pauling. , 2007, , 20-33.		11
45	The Diverse Biological Functions of Phosphatidylinositol Transfer Proteins in Eukaryotes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2006, 41, 21-49.	5.2	93
46	A call for likelihood phylogenetics even when the process of sequence evolution is heterogeneous. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 928-931.	2.7	68
47	Resurrecting ancestral alcohol dehydrogenases from yeast. <i>Nature Genetics</i> , 2005, 37, 630-635.	21.4	290
48	Inferring the palaeoenvironment of ancient bacteria on the basis of resurrected proteins. <i>Nature</i> , 2003, 425, 285-288.	27.8	227
49	Evolutionary, Structural and Biochemical Evidence for a New Interaction Site of the Leptin Obesity Protein. <i>Genetics</i> , 2003, 163, 1549-1553.	2.9	32
50	Planetary Biology--Paleontological, Geological, and Molecular Histories of Life. <i>Science</i> , 2002, 296, 864-868.	12.6	105
51	Complex glycosylation of Skp1 in <i>Dictyostelium</i> : implications for the modification of other eukaryotic cytoplasmic and nuclear proteins. <i>Glycobiology</i> , 2002, 12, 17R-27R.	2.5	35
52	The Crystal Structure of eEF1A Refines the Functional Predictions of an Evolutionary Analysis of Rate Changes Among Elongation Factors. <i>Molecular Biology and Evolution</i> , 2002, 19, 569-573.	8.9	27
53	Predicting functional divergence in protein evolution by site-specific rate shifts. <i>Trends in Biochemical Sciences</i> , 2002, 27, 315-321.	7.5	141