

Richard A Goldstein

List of Publications by Year in descending order

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113
papers

6,037
citations

87843

38
h-index

88593

70
g-index

130
all docs

130
docs citations

130
times ranked

7351
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
2	Why are proteins marginally stable?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 105-109.	1.5	327
3	rtREV: An Amino Acid Substitution Matrix for Inference of Retrovirus and Reverse Transcriptase Phylogeny. <i>Journal of Molecular Evolution</i> , 2002, 55, 65-73.	0.8	214
4	Probabilistic reconstruction of ancestral protein sequences. <i>Journal of Molecular Evolution</i> , 1996, 42, 313-320.	0.8	188
5	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
6	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. <i>PLoS Computational Biology</i> , 2006, 2, e69.	1.5	187
7	Amino acid coevolution induces an evolutionary Stokes shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1352-9.	3.3	183
8	Why are proteins so robust to site mutations?. <i>Journal of Molecular Biology</i> , 2002, 315, 479-484.	2.0	146
9	Estimating the total number of protein folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 408-414.	1.5	131
10	Excited states, electron-transfer reactions, and intermediates in bacterial photosynthetic reaction centers. <i>The Journal of Physical Chemistry</i> , 1989, 93, 8280-8294.	2.9	129
11	Why are some proteins structures so common?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 3341-3345.	3.3	126
12	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Site-wise Mutation-Selection Models. <i>Genetics</i> , 2012, 190, 1101-1115.	1.2	114
13	The evolution and evolutionary consequences of marginal thermostability in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1396-1407.	1.5	113
14	Identifying Changes in Selective Constraints: Host Shifts in Influenza. <i>PLoS Computational Biology</i> , 2009, 5, e1000564.	1.5	106
15	Changing Selective Pressure during Antigenic Changes in Human Influenza H3. <i>PLoS Pathogens</i> , 2008, 4, e1000058.	2.1	102
16	Human cytomegalovirus haplotype reconstruction reveals high diversity due to superinfection and evidence of within-host recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5693-5698.	3.3	94
17	On the thermodynamic hypothesis of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 5545-5549.	3.3	92
18	Assessing Predictors of Changes in Protein Stability upon Mutation Using Self-Consistency. <i>PLoS ONE</i> , 2012, 7, e46084.	1.1	91

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19	Evolution of model proteins on a foldability landscape. , 1997, 29, 461-466.		86
20	Context-dependent optimal substitution matrices. Protein Engineering, Design and Selection, 1995, 8, 641-645.	1.0	85
21	The structure of protein evolution and the evolution of protein structure. Current Opinion in Structural Biology, 2008, 18, 170-177.	2.6	85
22	Analysis of Host-Parasite Incongruence in Papillomavirus Evolution Using Importance Sampling. Molecular Biology and Evolution, 2010, 27, 1301-1314.	3.5	85
23	Amino-acid interactions in psychrophiles, mesophiles, thermophiles, and hyperthermophiles: Insights from the quasi-chemical approximation. Protein Science, 2007, 16, 1887-1895.	3.1	76
24	Energetics of initial charge separation in bacterial photosynthesis: The triplet decay rate in very high magnetic fields. Biochimica Et Biophysica Acta - Bioenergetics, 1988, 934, 253-263.	0.5	74
25	Distribution of indel lengths. Proteins: Structure, Function and Bioinformatics, 2001, 45, 102-104.	1.5	73
26	Searching for foldable protein structures using optimized energy functions. Biopolymers, 1995, 36, 43-51.	1.2	72
27	Generalized protein tertiary structure recognition using associative memory hamiltonians. Journal of Molecular Biology, 1991, 222, 1013-1034.	2.0	71
28	Models of natural mutations including site heterogeneity. , 1998, 32, 289-295.		69
29	Optimal local propensities for model proteins. Proteins: Structure, Function and Bioinformatics, 1995, 22, 413-418.	1.5	66
30	Nonadaptive Amino Acid Convergence Rates Decrease over Time. Molecular Biology and Evolution, 2015, 32, 1373-1381.	3.5	66
31	The foldability landscape of model proteins. , 1997, 42, 427-438.		65
32	The distribution of structures in evolving protein populations. Biopolymers, 2000, 53, 1-8.	1.2	65
33	The emerging GII.P16-GII.4 Sydney 2012 norovirus lineage is circulating worldwide, arose by late-2014 and contains polymerase changes that may increase virus transmission. PLoS ONE, 2017, 12, e0179572.	1.1	63
34	Effect of alphabet size and foldability requirements on protein structure designability. Proteins: Structure, Function and Bioinformatics, 1999, 34, 113-124.	1.5	56
35	Effects of Nuclear Spin Polarization on Reaction Dynamics in Photosynthetic Bacterial Reaction Centers. Biophysical Journal, 1987, 51, 937-946.	0.2	54
36	Dynamics of within-host Mycobacterium tuberculosis diversity and heteroresistance during treatment. EBioMedicine, 2020, 55, 102747.	2.7	52

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37	Evolution of functionality in lattice proteins. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 150-156.	1.3	49
38	The Neuronal Replicator Hypothesis. <i>Neural Computation</i> , 2010, 22, 2809-2857.	1.3	48
39	Sequence entropy of folding and the absolute rate of amino acid substitutions. <i>Nature Ecology and Evolution</i> , 2017, 1, 1923-1930.	3.4	46
40	Mutation matrices and physical-chemical properties: Correlations and implications. , 1997, 27, 336-344.		44
41	Population Size Dependence of Fitness Effect Distribution and Substitution Rate Probed by Biophysical Model of Protein Thermostability. <i>Genome Biology and Evolution</i> , 2013, 5, 1584-1593.	1.1	44
42	Mutagenesis in Norovirus in Response to Favipiravir Treatment. <i>New England Journal of Medicine</i> , 2018, 379, 2173-2176.	13.9	43
43	Dimerization in Aminergic G-Protein-Coupled Receptors: Application of a Hidden-Site Class Model of Evolution. <i>Biochemistry</i> , 2003, 42, 14522-14531.	1.2	42
44	Observations of Amino Acid Gain and Loss during Protein Evolution Are Explained by Statistical Bias. <i>Molecular Biology and Evolution</i> , 2006, 23, 1444-1449.	3.5	42
45	The tangled bank of amino acids. <i>Protein Science</i> , 2016, 25, 1354-1362.	3.1	40
46	Predicting solvent accessibility: Higher accuracy using Bayesian statistics and optimized residue substitution classes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 38-47.	1.5	38
47	Probing conformational changes in neurotransmitter transporters: a structural context. <i>European Journal of Pharmacology</i> , 2003, 479, 3-12.	1.7	38
48	Molecular Signatures of Regression of the Canine Transmissible Venereal Tumor. <i>Cancer Cell</i> , 2018, 33, 620-633.e6.	7.7	37
49	Evolution of Taxis Responses in Virtual Bacteria: Non-Adaptive Dynamics. <i>PLoS Computational Biology</i> , 2008, 4, e1000084.	1.5	36
50	Using Non-Homogeneous Models of Nucleotide Substitution to Identify Host Shift Events: Application to the Origin of the 1918 "Spanish" Influenza Pandemic Virus. <i>Journal of Molecular Evolution</i> , 2009, 69, 333-345.	0.8	36
51	Optimizing energy potentials for success in protein tertiary structure prediction. <i>Folding & Design</i> , 1998, 3, 223-228.	4.5	35
52	Surveying determinants of protein structure designability across different energy models and amino-acid alphabets: A consensus. <i>Journal of Chemical Physics</i> , 2000, 112, 2533-2547.	1.2	35
53	Optimization of a new score function for the detection of remote homologs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 498-503.	1.5	33
54	The effect of very high magnetic fields on the reaction dynamics in bacterial reaction centers: Implications for the reaction mechanism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1989, 977, 78-86.	0.5	32

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55	Depicting a protein's two faces: GPCR classification by phylogenetic tree-based HMMs. FEBS Letters, 2003, 554, 95-99.	1.3	32
56	Strong evidence for protein epistasis, weak evidence against it. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1450-E1450.	3.3	31
57	A Model of the Mechanisms of Language Extinction and Revitalization Strategies to Save Endangered Languages. Human Biology, 2010, 82, 47-75.	0.4	29
58	Charting the Host Adaptation of Influenza Viruses. Molecular Biology and Evolution, 2011, 28, 1755-1767.	3.5	28
59	Performance of an iterated T-HMM for homology detection. Bioinformatics, 2004, 20, 2175-2180.	1.8	26
60	Optimization of a new score function for the generation of accurate alignments. Proteins: Structure, Function and Bioinformatics, 2002, 48, 605-610.	1.5	25
61	The effect of very high magnetic fields on the delayed fluorescence from oriented bacterial reaction centers. Biochimica Et Biophysica Acta - Bioenergetics, 1989, 977, 70-77.	0.5	23
62	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	23
63	Predicting protein secondary structure with probabilistic schemata of evolutionarily derived information. Protein Science, 1997, 6, 1963-1975.	3.1	22
64	Predicting Functional Sites in Proteins: Site-specific Evolutionary Models and Their Application to Neurotransmitter Transporters. Journal of Molecular Biology, 2004, 339, 227-242.	2.0	22
65	Preadaptation of pandemic GII.4 Noroviruses in unsampled virus reservoirs years before emergence. Virus Evolution, 2020, 6, veaa067.	2.2	22
66	Constructing amino acid residue substitution classes maximally indicative of local protein structure. , 1996, 25, 28-37.		19
67	Universal correlation between energy gap and foldability for the random energy model and lattice proteins. Journal of Chemical Physics, 1999, 111, 6599-6609.	1.2	19
68	MODELING EVOLUTION AT THE PROTEIN LEVEL USING AN ADJUSTABLE AMINO ACID FITNESS MODEL. , 1999, , 18-29.		19
69	How to generate improved potentials for protein tertiary structure prediction: A lattice model study. Proteins: Structure, Function and Bioinformatics, 2000, 41, 157-163.	1.5	18
70	Detecting distant homologs using phylogenetic tree-based HMMs. Proteins: Structure, Function and Bioinformatics, 2003, 52, 446-453.	1.5	18
71	High Viral Diversity and Mixed Infections in Cerebral Spinal Fluid From Cases of Varicella Zoster Virus Encephalitis. Journal of Infectious Diseases, 2018, 218, 1592-1601.	1.9	18
72	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. Molecular Biology and Evolution, 2020, 37, 2706-2710.	3.5	18

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73	Mixed cytomegalovirus genotypes in HIV-positive mothers show compartmentalization and distinct patterns of transmission to infants. <i>ELife</i> , 2020, 9, .	2.8	18
74	Biophysics and population size constrains speciation in an evolutionary model of developmental system drift. <i>PLoS Computational Biology</i> , 2019, 15, e1007177.	1.5	17
75	A coarse-grained biophysical model of sequence evolution and the population size dependence of the speciation rate. <i>Journal of Theoretical Biology</i> , 2015, 378, 56-64.	0.8	15
76	Finding Direction in the Search for Selection. <i>Journal of Molecular Evolution</i> , 2017, 84, 39-50.	0.8	15
77	Whole genome sequencing of Herpes Simplex Virus 1 directly from human cerebrospinal fluid reveals selective constraints in neurotropic viruses. <i>Virus Evolution</i> , 2020, 6, veaa012.	2.2	15
78	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. <i>Evolutionary Bioinformatics</i> , 2007, 2, 91-101.	0.6	15
79	Simple Biophysical Model Predicts Faster Accumulation of Hybrid Incompatibilities in Small Populations Under Stabilizing Selection. <i>Genetics</i> , 2015, 201, 1525-1537.	1.2	14
80	Positive selection in dNTPase SAMHD1 throughout mammalian evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18647-18654.	3.3	14
81	Evolution of viral variants in remdesivir-treated and untreated SARS-CoV-2-infected pediatric patients. <i>Journal of Medical Virology</i> , 2022, 94, 161-172.	2.5	13
82	The organization of two rRNA (<i>rrn</i>) operons of the slow-growing pathogen <i>Mycobacterium celatum</i> provides key insights into mycobacterial evolution. <i>FEMS Microbiology Letters</i> , 2008, 280, 102-112.	0.7	11
83	<i>In Vivo</i> Emergence of a Novel Protease Inhibitor Resistance Signature in HIV-1 Matrix. <i>MBio</i> , 2020, 11, .	1.8	11
84	Wide variation in susceptibility of transmitted/founder HIV-1 subtype C isolates to protease inhibitors and association with <i>in vitro</i> replication efficiency. <i>Scientific Reports</i> , 2016, 6, 38153.	1.6	10
85	Emergent Robustness in Competition Between Autocatalytic Chemical Networks. <i>Origins of Life and Evolution of Biospheres</i> , 2006, 36, 381-389.	0.8	9
86	Evolution of response dynamics underlying bacterial chemotaxis. <i>BMC Evolutionary Biology</i> , 2011, 11, 240.	3.2	9
87	The Evolution of Collective Restraint: Policing and Obedience among Non-conjugative Plasmids. <i>PLoS Computational Biology</i> , 2013, 9, e1003036.	1.5	9
88	ANALYZING SITE HETEROGENEITY DURING PROTEIN EVOLUTION. , 2000, , 191-202.		9
89	Analytic Markovian Rates for Generalized Protein Structure Evolution. <i>PLoS ONE</i> , 2012, 7, e34228.	1.1	7
90	ChromaClade: combined visualisation of phylogenetic and sequence data. <i>BMC Evolutionary Biology</i> , 2019, 19, 186.	3.2	7

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91	Compaction and folding in model proteins. <i>Journal of Chemical Physics</i> , 1997, 107, 4408-4415.	1.2	5
92	Performance evaluation of a new algorithm for the detection of remote homologs with sequence comparison. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 367-376.	1.5	5
93	Divergence, recombination and retention of functionality during protein evolution. <i>Human Genomics</i> , 2005, 2, 158.	1.4	5
94	Selection for cooperativity causes epistasis predominately between native contacts and enables epistasis-based structure reconstruction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5
95	Effect of alphabet size and foldability requirements on protein structure designability. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 34, 113-124.	1.5	5
96	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. <i>MBio</i> , 2022, 13, e0026922.	1.8	5
97	Positive Selection Analysis of Overlapping Reading Frames Is Invalid. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 947-947.	0.5	4
98	SubRecon: ancestral reconstruction of amino acid substitutions along a branch in a phylogeny. <i>Bioinformatics</i> , 2018, 34, 2297-2299.	1.8	4
99	Reply to Jensen and Kowalik: Consideration of mixed infections is central to understanding HCMV intrahost diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 818-819.	3.3	4
100	The Nature of Excited States and Intermediates in Bacterial Photosynthesis. , 1988, , 165-176.		4
101	Mechanistic Models of Protein Evolution. , 2017, , 277-296.		3
102	Optimal chemotactic responses in stochastic environments. <i>PLoS ONE</i> , 2017, 12, e0179111.	1.1	2
103	Evolutionary Perspectives on Protein Thermodynamics. <i>Lecture Notes in Computer Science</i> , 2004, , 718-727.	1.0	2
104	SELECTIVE ADVANTAGE OF RECOMBINATION IN EVOLVING PROTEIN POPULATIONS: A LATTICE MODEL STUDY. <i>International Journal of Modern Physics C</i> , 2006, 17, 75-90.	0.8	1
105	Mutation matrices and physicalâ€œchemical properties: Correlations and implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 27, 336-344.	1.5	1
106	Models of natural mutations including site heterogeneity. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 289-295.	1.5	1
107	The distribution of structures in evolving protein populations. , 2000, 53, 1.		1
108	The distribution of structures in evolving protein populations. , 2000, 53, 1.		1

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109	USING EVOLUTIONARY METHODS TO STUDY G-PROTEIN COUPLED RECEPTORS. , 2001, , .		1
110	Score functions for structure prediction. , 2005, , .		0
111	Modeling protein evolution. , 2005, , .		0
112	Modeling Protein Evolution. Biological and Medical Physics Series, 2012, , 311-325.	0.3	0
113	Protein Evolution and Structural Genomics. , 1999, , .		0