

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	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
2	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. <i>MBio</i> , 2022, 13, e0026922.	1.8	5
3	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
4	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
5	Preadaptation of pandemic GII.4 noroviruses in unsampled virus reservoirs years before emergence. <i>Virus Evolution</i> , 2020, 6, veaa067.	2.2	22
6	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	3.5	18
7	<i>In Vivo</i> Emergence of a Novel Protease Inhibitor Resistance Signature in HIV-1 Matrix. <i>MBio</i> , 2020, 11, .	1.8	11
8	Dynamics of within-host <i>Mycobacterium tuberculosis</i> diversity and heteroresistance during treatment. <i>EBioMedicine</i> , 2020, 55, 102747.	2.7	52
9	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
10	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
11	Mixed cytomegalovirus genotypes in HIV-positive mothers show compartmentalization and distinct patterns of transmission to infants. <i>ELife</i> , 2020, 9, .	2.8	18
12	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
13	ChromaClade: combined visualisation of phylogenetic and sequence data. <i>BMC Evolutionary Biology</i> , 2019, 19, 186.	3.2	7
14	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
15	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
16	SubRecon: ancestral reconstruction of amino acid substitutions along a branch in a phylogeny. <i>Bioinformatics</i> , 2018, 34, 2297-2299.	1.8	4
17	Molecular Signatures of Regression of the Canine Transmissible Venereal Tumor. <i>Cancer Cell</i> , 2018, 33, 620-633.e6.	7.7	37
18	Mutagenesis in Norovirus in Response to Favipiravir Treatment. <i>New England Journal of Medicine</i> , 2018, 379, 2173-2176.	13.9	43

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19	High Viral Diversity and Mixed Infections in Cerebral Spinal Fluid From Cases of Varicella Zoster Virus Encephalitis. <i>Journal of Infectious Diseases</i> , 2018, 218, 1592-1601.	1.9	18
20	Finding Direction in the Search for Selection. <i>Journal of Molecular Evolution</i> , 2017, 84, 39-50.	0.8	15
21	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
22	Mechanistic Models of Protein Evolution. , 2017, , 277-296.		3
23	Optimal chemotactic responses in stochastic environments. <i>PLoS ONE</i> , 2017, 12, e0179111.	1.1	2
24	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. <i>PLoS ONE</i> , 2017, 12, e0179572.	1.1	63
25	The tangled bank of amino acids. <i>Protein Science</i> , 2016, 25, 1354-1362.	3.1	40
26	Wide variation in susceptibility of transmitted/founder HIV-1 subtype C Isolates to protease inhibitors and association with in vitro replication efficiency. <i>Scientific Reports</i> , 2016, 6, 38153.	1.6	10
27	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
28	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
29	Positive Selection Analysis of Overlapping Reading Frames Is Invalid. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 947-947.	0.5	4
30	Nonadaptive Amino Acid Convergence Rates Decrease over Time. <i>Molecular Biology and Evolution</i> , 2015, 32, 1373-1381.	3.5	66
31	Strong evidence for protein epistasis, weak evidence against it. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1450-E1450.	3.3	31
32	The Evolution of Collective Restraint: Policing and Obedience among Non-conjugative Plasmids. <i>PLoS Computational Biology</i> , 2013, 9, e1003036.	1.5	9
33	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
34	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
35	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
36	Analytic Markovian Rates for Generalized Protein Structure Evolution. <i>PLoS ONE</i> , 2012, 7, e34228.	1.1	7

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37	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
38	Assessing Predictors of Changes in Protein Stability upon Mutation Using Self-Consistency. <i>PLoS ONE</i> , 2012, 7, e46084.	1.1	91
39	Modeling Protein Evolution. <i>Biological and Medical Physics Series</i> , 2012, , 311-325.	0.3	0
40	Evolution of response dynamics underlying bacterial chemotaxis. <i>BMC Evolutionary Biology</i> , 2011, 11, 240.	3.2	9
41	The evolution and evolutionary consequences of marginal thermostability in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1396-1407.	1.5	113
42	Charting the Host Adaptation of Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2011, 28, 1755-1767.	3.5	28
43	Analysis of Host-Parasite Incongruence in Papillomavirus Evolution Using Importance Sampling. <i>Molecular Biology and Evolution</i> , 2010, 27, 1301-1314.	3.5	85
44	The Neuronal Replicator Hypothesis. <i>Neural Computation</i> , 2010, 22, 2809-2857.	1.3	48
45	A Model of the Mechanisms of Language Extinction and Revitalization Strategies to Save Endangered Languages. <i>Human Biology</i> , 2010, 82, 47-75.	0.4	29
46	Identifying Changes in Selective Constraints: Host Shifts in Influenza. <i>PLoS Computational Biology</i> , 2009, 5, e1000564.	1.5	106
47	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
48	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
49	The structure of protein evolution and the evolution of protein structure. <i>Current Opinion in Structural Biology</i> , 2008, 18, 170-177.	2.6	85
50	Evolution of Taxis Responses in Virtual Bacteria: Non-Adaptive Dynamics. <i>PLoS Computational Biology</i> , 2008, 4, e1000084.	1.5	36
51	Changing Selective Pressure during Antigenic Changes in Human Influenza H3. <i>PLoS Pathogens</i> , 2008, 4, e1000058.	2.1	102
52	Amino-acid interactions in psychrophiles, mesophiles, thermophiles, and hyperthermophiles: Insights from the quasi-chemical approximation. <i>Protein Science</i> , 2007, 16, 1887-1895.	3.1	76
53	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. <i>Evolutionary Bioinformatics</i> , 2007, 2, 91-101.	0.6	15
54	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	23

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55	Emergent Robustness in Competition Between Autocatalytic Chemical Networks. <i>Origins of Life and Evolution of Biospheres</i> , 2006, 36, 381-389.	0.8	9
56	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
57	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. <i>PLoS Computational Biology</i> , 2006, 2, e69.	1.5	187
58	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
59	Divergence, recombination and retention of functionality during protein evolution. <i>Human Genomics</i> , 2005, 2, 158.	1.4	5
60	Score functions for structure prediction. , 2005, , .		0
61	Modeling protein evolution. , 2005, , .		0
62	Performance of an iterated T-HMM for homology detection. <i>Bioinformatics</i> , 2004, 20, 2175-2180.	1.8	26
63	Predicting Functional Sites in Proteins: Site-specific Evolutionary Models and Their Application to Neurotransmitter Transporters. <i>Journal of Molecular Biology</i> , 2004, 339, 227-242.	2.0	22
64	Evolutionary Perspectives on Protein Thermodynamics. <i>Lecture Notes in Computer Science</i> , 2004, , 718-727.	1.0	2
65	Probing conformational changes in neurotransmitter transporters: a structural context. <i>European Journal of Pharmacology</i> , 2003, 479, 3-12.	1.7	38
66	Detecting distant homologs using phylogenetic tree-based HMMs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 446-453.	1.5	18
67	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
68	Depicting a protein's two faces: GPCR classification by phylogenetic tree-based HMMs. <i>FEBS Letters</i> , 2003, 554, 95-99.	1.3	32
69	Why are proteins so robust to site mutations?. <i>Journal of Molecular Biology</i> , 2002, 315, 479-484.	2.0	146
70	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
71	Why are proteins marginally stable?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 105-109.	1.5	327
72	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

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73	Optimization of a new score function for the generation of accurate alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 605-610.	1.5	25
74	Distribution of indel lengths. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 102-104.	1.5	73
75	Evolution of functionality in lattice proteins. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 150-156.	1.3	49
76	USING EVOLUTIONARY METHODS TO STUDY G-PROTEIN COUPLED RECEPTORS. , 2001, , .		1
77	The distribution of structures in evolving protein populations. <i>Biopolymers</i> , 2000, 53, 1-8.	1.2	65
78	How to generate improved potentials for protein tertiary structure prediction: A lattice model study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 157-163.	1.5	18
79	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
80	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
81	The distribution of structures in evolving protein populations. , 2000, 53, 1.		1
82	The distribution of structures in evolving protein populations. , 2000, 53, 1.		1
83	ANALYZING SITE HETEROGENEITY DURING PROTEIN EVOLUTION. , 2000, , 191-202.		9
84	Universal correlation between energy gap and foldability for the random energy model and lattice proteins. <i>Journal of Chemical Physics</i> , 1999, 111, 6599-6609.	1.2	19
85	Effect of alphabet size and foldability requirements on protein structure designability. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 34, 113-124.	1.5	56
86	Estimating the total number of protein folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 408-414.	1.5	131
87	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
88	Protein Evolution and Structural Genomics. , 1999, , .		0
89	MODELING EVOLUTION AT THE PROTEIN LEVEL USING AN ADJUSTABLE AMINO ACID FITNESS MODEL. , 1999, , 18-29.		19
90	Optimizing energy potentials for success in protein tertiary structure prediction. <i>Folding & Design</i> , 1998, 3, 223-228.	4.5	35

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91	Models of natural mutations including site heterogeneity. , 1998, 32, 289-295.		69
92	On the thermodynamic hypothesis of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5545-5549.	3.3	92
93	Models of natural mutations including site heterogeneity. Proteins: Structure, Function and Bioinformatics, 1998, 32, 289-295.	1.5	1
94	Compaction and folding in model proteins. Journal of Chemical Physics, 1997, 107, 4408-4415.	1.2	5
95	Predicting protein secondary structure with probabilistic schemata of evolutionarily derived information. Protein Science, 1997, 6, 1963-1975.	3.1	22
96	Mutation matrices and physical-chemical properties: Correlations and implications. , 1997, 27, 336-344.		44
97	Evolution of model proteins on a foldability landscape. , 1997, 29, 461-466.		86
98	The foldability landscape of model proteins. , 1997, 42, 427-438.		65
99	Mutation matrices and physical-chemical properties: Correlations and implications. Proteins: Structure, Function and Bioinformatics, 1997, 27, 336-344.	1.5	1
100	Why are some proteins structures so common?. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 3341-3345.	3.3	126
101	Probabilistic reconstruction of ancestral protein sequences. Journal of Molecular Evolution, 1996, 42, 313-320.	0.8	188
102	Constructing amino acid residue substitution classes maximally indicative of local protein structure. , 1996, 25, 28-37.		19
103	Predicting solvent accessibility: Higher accuracy using Bayesian statistics and optimized residue substitution classes. Proteins: Structure, Function and Bioinformatics, 1996, 25, 38-47.	1.5	38
104	Searching for foldable protein structures using optimized energy functions. Biopolymers, 1995, 36, 43-51.	1.2	72
105	Optimal local propensities for model proteins. Proteins: Structure, Function and Bioinformatics, 1995, 22, 413-418.	1.5	66
106	Context-dependent optimal substitution matrices. Protein Engineering, Design and Selection, 1995, 8, 641-645.	1.0	85
107	Generalized protein tertiary structure recognition using associative memory hamiltonians. Journal of Molecular Biology, 1991, 222, 1013-1034.	2.0	71
108	Excited states, electron-transfer reactions, and intermediates in bacterial photosynthetic reaction centers. The Journal of Physical Chemistry, 1989, 93, 8280-8294.	2.9	129

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109	The effect of very high magnetic fields on the delayed fluorescence from oriented bacterial reaction centers. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1989, 977, 70-77.	0.5	23
110	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
111	Energetics of initial charge separation in bacterial photosynthesis: The triplet decay rate in very high magnetic fields. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1988, 934, 253-263.	0.5	74
112	The Nature of Excited States and Intermediates in Bacterial Photosynthesis. , 1988, , 165-176.		4
113	Effects of Nuclear Spin Polarization on Reaction Dynamics in Photosynthetic Bacterial Reaction Centers. <i>Biophysical Journal</i> , 1987, 51, 937-946.	0.2	54