

Andrew F Neuwald

List of Publications by Year in descending order

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47
papers

2,833
citations

430874

18
h-index

243625

44
g-index

51
all docs

51
docs citations

51
times ranked

2902
citing authors

#	ARTICLE	IF	CITATIONS
1	A superfamily of conserved domains in DNA damage-responsive cell cycle checkpoint proteins. <i>FASEB Journal</i> , 1997, 11, 68-76.	0.5	684
2	Gibbs motif sampling: Detection of bacterial outer membrane protein repeats. <i>Protein Science</i> , 1995, 4, 1618-1632.	7.6	371
3	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. <i>Journal of the American Statistical Association</i> , 1995, 90, 1156-1170.	3.1	235
4	Extracting protein alignment models from the sequence database. <i>Nucleic Acids Research</i> , 1997, 25, 1665-1677.	14.5	206
5	The hallmark of AGC kinase functional divergence is its C-terminal tail, a cis-acting regulatory module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1272-1277.	7.1	199
6	An unexpected structural relationship between integral membrane phosphatases and soluble haloperoxidases. <i>Protein Science</i> , 1997, 6, 1764-1767.	7.6	142
7	Evolutionary constraints associated with functional specificity of the CMGC protein kinases MAPK, CDK, GSK, SRPK, DYRK, and CK2±. <i>Protein Science</i> , 2004, 13, 2059-2077.	7.6	142
8	Did Protein Kinase Regulatory Mechanisms Evolve Through Elaboration of a Simple Structural Component?. <i>Journal of Molecular Biology</i> , 2005, 351, 956-972.	4.2	137
9	Detecting Patterns in Protein Sequences. <i>Journal of Molecular Biology</i> , 1994, 239, 698-712.	4.2	96
10	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. <i>Journal of the American Statistical Association</i> , 1995, 90, 1156.	3.1	77
11	Rapid detection, classification and accurate alignment of up to a million or more related protein sequences. <i>Bioinformatics</i> , 2009, 25, 1869-1875.	4.1	62
12	Markovian Structures in Biological Sequence Alignments. <i>Journal of the American Statistical Association</i> , 1999, 94, 1-15.	3.1	60
13	Ran's C-terminal, Basic Patch, and Nucleotide Exchange Mechanisms in Light of a Canonical Structure for Rab, Rho, Ras, and Ran GTPases. <i>Genome Research</i> , 2003, 13, 673-692.	5.5	41
14	Gapped alignment of protein sequence motifs through Monte Carlo optimization of a hidden Markov model. <i>BMC Bioinformatics</i> , 2004, 5, 157.	2.6	34
15	A survey of TIR domain sequence and structure divergence. <i>Immunogenetics</i> , 2020, 72, 181-203.	2.4	31
16	A Bayesian Sampler for Optimization of Protein Domain Hierarchies. <i>Journal of Computational Biology</i> , 2014, 21, 269-286.	1.6	30
17	Markovian Structures in Biological Sequence Alignments. <i>Journal of the American Statistical Association</i> , 1999, 94, 1.	3.1	21
18	Ataxin-2, global regulators and bacterial gene expression, and spliceosomal snRNP proteins share a conserved domain. <i>Journal of Molecular Medicine</i> , 1997, 76, 3-5.	3.9	19

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19	The CHAIN program: forging evolutionary links to underlying mechanisms. <i>Trends in Biochemical Sciences</i> , 2007, 32, 487-493.	7.5	18
20	Bayesian Top-Down Protein Sequence Alignment with Inferred Position-Specific Gap Penalties. <i>PLoS Computational Biology</i> , 2016, 12, e1004936.	3.2	17
21	Surveying the Manifold Divergence of an Entire Protein Class for Statistical Clues to Underlying Biochemical Mechanisms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, Article 36.	0.6	16
22	Identification and classification of small molecule kinases: insights into substrate recognition and specificity. <i>BMC Evolutionary Biology</i> , 2016, 16, 7.	3.2	16
23	Cleaning structural and functional information from correlations in protein multiple sequence alignments. <i>Current Opinion in Structural Biology</i> , 2016, 38, 1-8.	5.7	15
24	Bayesian shadows of molecular mechanisms cast in the light of evolution. <i>Trends in Biochemical Sciences</i> , 2006, 31, 374-382.	7.5	14
25	Inferring joint sequence-structural determinants of protein functional specificity. <i>ELife</i> , 2018, 7, .	6.0	14
26	G12 dissociation may be due to retraction of a buried lysine and disruption of an aromatic cluster by a GTP-sensing Arg-Trp pair. <i>Protein Science</i> , 2007, 16, 2570-2577.	7.6	13
27	The glycine brace: a component of Rab, Rho, and Ran GTPases associated with hinge regions of guanine- and phosphate-binding loops. <i>BMC Structural Biology</i> , 2009, 9, 11.	2.3	12
28	Deep Analysis of Residue Constraints (DARC): identifying determinants of protein functional specificity. <i>Scientific Reports</i> , 2020, 10, 1691.	3.3	12
29	Automated hierarchical classification of protein domain subfamilies based on functionally-divergent residue signatures. <i>BMC Bioinformatics</i> , 2012, 13, 144.	2.6	11
30	Protein domain hierarchy Gibbs sampling strategies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 497-517.	0.6	11
31	The Charge-dipole Pocket: A Defining Feature of Signaling Pathway GTPase On/Off Switches. <i>Journal of Molecular Biology</i> , 2009, 390, 142-153.	4.2	10
32	Bayesian classification of residues associated with protein functional divergence: Arf and Arf-like GTPases. <i>Biology Direct</i> , 2010, 5, 66.	4.6	9
33	Inference of Functionally-Relevant N-acetyltransferase Residues Based on Statistical Correlations. <i>PLoS Computational Biology</i> , 2016, 12, e1005294.	3.2	9
34	Hypothesis: bacterial clamp loader ATPase activation through DNA-dependent repositioning of the catalytic base and of a trans-acting catalytic threonine. <i>Nucleic Acids Research</i> , 2006, 34, 5280-5290.	14.5	8
35	Statistical investigations of protein residue direct couplings. <i>PLoS Computational Biology</i> , 2018, 14, e1006237.	3.2	8
36	Evaluating, Comparing, and Interpreting Protein Domain Hierarchies. <i>Journal of Computational Biology</i> , 2014, 21, 287-302.	1.6	7

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37	Initial Cluster Analysis. <i>Journal of Computational Biology</i> , 2018, 25, 121-129.	1.6	7
38	Identifying intracellular signaling modules and exploring pathways associated with breast cancer recurrence. <i>Scientific Reports</i> , 2021, 11, 385.	3.3	6
39	Obtaining extremely large and accurate protein multiple sequence alignments from curated hierarchical alignments. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	4
40	Identifying Function Determining Residues in Neuroimmune Semaphorin 4A. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3024.	4.1	3
41	BICORN: An R package for integrative inference of de novo cis-regulatory modules. <i>Scientific Reports</i> , 2020, 10, 7960.	3.3	2
42	ChIP-GSM: Inferring active transcription factor modules to predict functional regulatory elements. <i>PLoS Computational Biology</i> , 2021, 17, e1009203.	3.2	2
43	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. <i>Bioinformatics</i> , 2021, 37, 650-658.	4.1	1
44	A Bayesian approach for accurate de novo transcriptome assembly. <i>Scientific Reports</i> , 2021, 11, 17663.	3.3	1
45	ChIP-BIT2: a software tool to detect weak binding events using a Bayesian integration approach. <i>BMC Bioinformatics</i> , 2021, 22, 193.	2.6	0
46	eCOMPASS: evaluative comparison of multiple protein alignments by statistical score. <i>Bioinformatics</i> , 2021, 37, 3456-3463.	4.1	0
47	SPARC: Structural properties associated with residue constraints. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1702-1715.	4.1	0