

Debora S Marks

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

22,266
citations

66250

44
h-index

90395

73
g-index

107
all docs

107
docs citations

107
times ranked

29311
citing authors

#	ARTICLE	IF	CITATIONS
1	Human MicroRNA Targets. PLoS Biology, 2004, 2, e363.	2.6	3,253
2	MicroRNA targets in Drosophila. Genome Biology, 2003, 5, R1.	13.9	3,023
3	The microRNA.org resource: targets and expression. Nucleic Acids Research, 2007, 36, D149-D153.	6.5	2,280
4	Identification of Virus-Encoded MicroRNAs. Science, 2004, 304, 734-736.	6.0	1,474
5	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1293-301.	3.3	1,231
6	Protein 3D Structure Computed from Evolutionary Sequence Variation. PLoS ONE, 2011, 6, e28766.	1.1	975
7	The Small RNA Profile during Drosophila melanogaster Development. Developmental Cell, 2003, 5, 337-350.	3.1	866
8	miR-122, a Mammalian Liver-Specific microRNA, is Processed from hcr mRNA and May Downregulate the High Affinity Cationic Amino Acid Transporter CAT-1. RNA Biology, 2004, 1, 106-113.	1.5	758
9	Protein structure prediction from sequence variation. Nature Biotechnology, 2012, 30, 1072-1080.	9.4	569
10	Mutation effects predicted from sequence co-variation. Nature Biotechnology, 2017, 35, 128-135.	9.4	543
11	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. Cell, 2012, 149, 1607-1621.	13.5	478
12	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. Nature Biotechnology, 2009, 27, 549-555.	9.4	470
13	Sequence co-evolution gives 3D contacts and structures of protein complexes. ELife, 2014, 3, .	2.8	452
14	Deep generative models of genetic variation capture the effects of mutations. Nature Methods, 2018, 15, 816-822.	9.0	395
15	MicroRNA control of protein expression noise. Science, 2015, 348, 128-132.	6.0	337
16	Disease variant prediction with deep generative models of evolutionary data. Nature, 2021, 599, 91-95.	13.7	306
17	Antisense-Mediated Depletion Reveals Essential and Specific Functions of MicroRNAs in Drosophila Development. Cell, 2005, 121, 1097-1108.	13.5	304
18	The developmental miRNA profiles of zebrafish as determined by small RNA cloning. Genes and Development, 2005, 19, 1288-1293.	2.7	301

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19	Target mRNA abundance dilutes microRNA and siRNA activity. <i>Molecular Systems Biology</i> , 2010, 6, 363.	3.2	299
20	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	9.0	297
21	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000–2013. <i>Journal of Infectious Diseases</i> , 2016, 214, 1579-1587.	1.9	186
22	The EVcouplings Python framework for coevolutionary sequence analysis. <i>Bioinformatics</i> , 2019, 35, 1582-1584.	1.8	180
23	A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. <i>Molecular Cell</i> , 2018, 71, 178-190.e8.	4.5	177
24	Protein design and variant prediction using autoregressive generative models. <i>Nature Communications</i> , 2021, 12, 2403.	5.8	168
25	3D RNA and Functional Interactions from Evolutionary Couplings. <i>Cell</i> , 2016, 165, 963-975.	13.5	152
26	Cryo-electron microscopy structure of the lipid droplet formation protein seipin. <i>Journal of Cell Biology</i> , 2018, 217, 4080-4091.	2.3	147
27	FreeContact: fast and free software for protein contact prediction from residue co-evolution. <i>BMC Bioinformatics</i> , 2014, 15, 85.	1.2	146
28	Structured States of Disordered Proteins from Genomic Sequences. <i>Cell</i> , 2016, 167, 158-170.e12.	13.5	127
29	Inferring protein 3D structure from deep mutation scans. <i>Nature Genetics</i> , 2019, 51, 1170-1176.	9.4	124
30	Amino acid coevolution reveals three-dimensional structure and functional domains of insect odorant receptors. <i>Nature Communications</i> , 2015, 6, 6077.	5.8	113
31	Structure of the peptidoglycan polymerase RodA resolved by evolutionary coupling analysis. <i>Nature</i> , 2018, 556, 118-121.	13.7	110
32	Use of an Additional Hydrophobic Binding Site, the Z Site, in the Rational Drug Design of a New Class of Stronger Trypanothione Reductase Inhibitor, Quaternary Alkylammonium Phenothiazines. <i>Journal of Medicinal Chemistry</i> , 2000, 43, 3148-3156.	2.9	108
33	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. <i>Genome Research</i> , 2010, 20, 1010-1019.	2.4	102
34	Can sequencing shed light on cell cycling?. <i>Nature</i> , 2001, 409, 844-846.	13.7	97
35	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004182.	1.5	97
36	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010, 6, 433.	3.2	94

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37	PconsFold: improved contact predictions improve protein models. <i>Bioinformatics</i> , 2014, 30, i482-i488.	1.8	92
38	Structural coordination of polymerization and crosslinking by a SEDS- β BPB peptidoglycan synthase complex. <i>Nature Microbiology</i> , 2020, 5, 813-820.	5.9	91
39	Computational Analysis of Mouse piRNA Sequence and Biogenesis. <i>PLoS Computational Biology</i> , 2007, 3, e222.	1.5	83
40	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- β 2 pathway and reveal microRNA regulation of TGFBR2. <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 3.	8.0	78
41	Protein structure determination by combining sparse NMR data with evolutionary couplings. <i>Nature Methods</i> , 2015, 12, 751-754.	9.0	75
42	Large-scale discovery of protein interactions at residue resolution using co-evolution calculated from genomic sequences. <i>Nature Communications</i> , 2021, 12, 1396.	5.8	68
43	CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. <i>Cell Systems</i> , 2021, 12, 128-140.e4.	2.9	67
44	Structure and Sequence Analyses of Clustered Protocadherins Reveal Antiparallel Interactions that Mediate Homophilic Specificity. <i>Structure</i> , 2015, 23, 2087-2098.	1.6	65
45	Core Genes Evolve Rapidly in the Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1072-1083.	1.1	64
46	Rapid generation of potent antibodies by autonomous hypermutation in yeast. <i>Nature Chemical Biology</i> , 2021, 17, 1057-1064.	3.9	59
47	Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. <i>ELife</i> , 2020, 9, .	2.8	58
48	All-atom 3D structure prediction of transmembrane β -barrel proteins from sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5413-5418.	3.3	53
49	Antiparallel protocadherin homodimers use distinct affinity- and specificity-mediating regions in cadherin repeats 1-4. <i>ELife</i> , 2016, 5, .	2.8	53
50	Structure and mutagenic analysis of the lipid II flippase MurJ from <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6709-6714.	3.3	52
51	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
52	Genome-wide discovery of epistatic loci affecting antibiotic resistance in <i>Neisseria gonorrhoeae</i> using evolutionary couplings. <i>Nature Microbiology</i> , 2019, 4, 328-338.	5.9	41
53	Protein Structure from Experimental Evolution. <i>Cell Systems</i> , 2020, 10, 15-24.e5.	2.9	39
54	Metaphyseal Chondrodysplasia Type Schmid Mutations Are Predicted to Occur in Two Distinct Three-dimensional Clusters within Type X Collagen NC1 Domains That Retain the Ability to Trimerize. <i>Journal of Biological Chemistry</i> , 1999, 274, 3632-3641.	1.6	35

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55	Regulated spatial organization and sensitivity of cytosolic protein oxidation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2014, 5, 5020.	5.8	34
56	Interaction specificity of clustered protocadherins inferred from sequence covariation and structural analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17825-17830.	3.3	29
57	Co-evolution of interacting proteins through non-contacting and non-specific mutations. <i>Nature Ecology and Evolution</i> , 2022, 6, 590-603.	3.4	23
58	Dormant spores sense amino acids through the B subunits of their germination receptors. <i>Nature Communications</i> , 2021, 12, 6842.	5.8	22
59	The SpoVA membrane complex is required for dipicolinic acid import during sporulation and export during germination. <i>Genes and Development</i> , 2022, 36, 634-646.	2.7	17
60	Population-specific design of de-immunized protein biotherapeutics. <i>PLoS Computational Biology</i> , 2018, 14, e1005983.	1.5	16
61	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010, 6, 454.	3.2	14
62	Gain-of-function experiments with bacteriophage lambda uncover residues under diversifying selection in nature. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 2234-2243.	1.1	14
63	Structural Studies by High-Field NMR Spectroscopy of a Binary-Addressed Complementary Oligonucleotide System Juxtaposing Pyrene and Perfluoro-Azide Units. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 15, 307-320.	2.0	13
64	Mechanical gating of the auditory transduction channel TMC1 involves the fourth and sixth transmembrane helices. <i>Science Advances</i> , 2022, 8, .	4.7	13
65	Evidence that regulation of intramembrane proteolysis is mediated by substrate gating during sporulation in <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2018, 14, e1007753.	1.5	11
66	Refined High-Field NMR Solution Structure of a Binary-Addressed Pyrene/Perfluoro-Azide Complementary DNA Oligonucleotide System Shows Extensive Distortion in the Central Nick Region. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 17, 193-211.	2.0	10
67	Structure, Dynamics and Implied Gating Mechanism of a Human Cyclic Nucleotide-Gated Channel. <i>PLoS Computational Biology</i> , 2014, 10, e1003976.	1.5	9
68	Natural and Designed Proteins Inspired by Extremotolerant Organisms Can Form Condensates and Attenuate Apoptosis in Human Cells. <i>ACS Synthetic Biology</i> , 2022, 11, 1292-1302.	1.9	9
69	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. <i>Methods in Enzymology</i> , 2019, 614, 363-392.	0.4	8
70	A Hybrid Approach for Protein Structure Determination Combining Sparse NMR with Evolutionary Coupling Sequence Data. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 153-169.	0.8	7
71	Protein Structures, Interactions and Function from Evolutionary Couplings. , 2017, , 37-58.		6
72	High-Content Screening and Computational Prediction Reveal Viral Genes That Suppress the Innate Immune Response. <i>MSystems</i> , 2022, 7, e0146621.	1.7	5

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73	Solutions to the computational protein folding problem. FASEB Journal, 2018, 32, 377.1.	0.2	1
74	Computational analysis of mouse piRNA sequence and biogenesis. PLoS Computational Biology, 2005, preprint, e222.	1.5	0
75	Democratizing the mapping of gene mutations to protein biophysics. Nature, 2022, 604, 47-48.	13.7	0