Debora S Marks

List of Publications by Year
in descending order

75 papers	**22,266** citations	57758 **44** h-index	79698 **73** g-index
107 all docs	**107** docs citations	**107** times ranked	**26400** citing authors

#	Article	IF	Citations
1	Human MicroRNA Targets. PLoS Biology, 2004, 2, e363.	5.6	3,253
2	MicroRNA targets in Drosophila. Genome Biology, 2003, 5, R1.	9.6	3,023
3	The microRNA.org resource: targets and expression. Nucleic Acids Research, 2007, 36, D149-D153.	14.5	2,280
4	Identification of Virus-Encoded MicroRNAs. Science, 2004, 304, 734-736.	12.6	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.	7.1	1,231
6	Protein 3D Structure Computed from Evolutionary Sequence Variation. PLoS ONE, 2011, 6, e28766.	2.5	975
7	The Small RNA Profile during Drosophila melanogaster Development. Developmental Cell, 2003, 5, 337-350.	7.0	866
8	miR-122, a Mammalian Liver-Specific microRNA, is Processed from hcr mRNA and MayDownregulate the High Affinity Cationic Amino Acid Transporter CAT-1. RNA Biology, 2004, 1, 106-113.	3.1	758
9	Protein structure prediction from sequence variation. Nature Biotechnology, 2012, 30, 1072-1080.	17.5	569
10	Mutation effects predicted from sequence co-variation. Nature Biotechnology, 2017, 35, 128-135.	17.5	543
11	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. Cell, 2012, 149, 1607-1621.	28.9	478
12	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. Nature Biotechnology, 2009, 27, 549-555.	17.5	470
13	Sequence co-evolution gives 3D contacts and structures of protein complexes. ELife, 2014, 3, .	6.0	452
14	Deep generative models of genetic variation capture the effects of mutations. Nature Methods, 2018, 15, 816-822.	19.0	395
15	MicroRNA control of protein expression noise. Science, 2015, 348, 128-132.	12.6	337
16	Disease variant prediction with deep generative models of evolutionary data. Nature, 2021, 599, 91-95.	27.8	306
17	Antisense-Mediated Depletion Reveals Essential and Specific Functions of MicroRNAs in Drosophila Development. Cell, 2005, 121, 1097-1108.	28.9	304
18	The developmental miRNA profiles of zebrafish as determined by small RNA cloning. Genes and Development, 2005, 19, 1288-1293.	5.9	301

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19	Target mRNA abundance dilutes microRNA and siRNA activity. Molecular Systems Biology, 2010, 6, 363.	7.2	299
20	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
21	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000â€"2013. Journal of Infectious Diseases, 2016, 214, 1579-1587.	4.0	186
22	The EVcouplings Python framework for coevolutionary sequence analysis. Bioinformatics, 2019, 35, 1582-1584.	4.1	180
23	A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. Molecular Cell, 2018, 71, 178-190.e8.	9.7	177
24	Protein design and variant prediction using autoregressive generative models. Nature Communications, 2021, 12, 2403.	12.8	168
25	3D RNA and Functional Interactions from Evolutionary Couplings. Cell, 2016, 165, 963-975.	28.9	152
26	Cryoâ€"electron microscopy structure of the lipid dropletâ€"formation protein seipin. Journal of Cell Biology, 2018, 217, 4080-4091.	5.2	147
27	FreeContact: fast and free software for protein contact prediction from residue co-evolution. BMC Bioinformatics, 2014, 15, 85.	2.6	146
28	Structured States of Disordered Proteins from Genomic Sequences. Cell, 2016, 167, 158-170.e12.	28.9	127
29	Inferring protein 3D structure from deep mutation scans. Nature Genetics, 2019, 51, 1170-1176.	21.4	124
30	Amino acid coevolution reveals three-dimensional structure and functional domains of insect odorant receptors. Nature Communications, 2015, 6, 6077.	12.8	113
31	Structure of the peptidoglycan polymerase RodA resolved by evolutionary coupling analysis. Nature, 2018, 556, 118-121.	27.8	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 PhenothiazinesÂ§. Journal of Medicinal Chemistry, 2000, 43, 3148-3156.	6.4	108
33	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. Genome Research, 2010, 20, 1010-1019.	5.5	102
34	Can sequencing shed light on cell cycling?. Nature, 2001, 409, 844-846.	27.8	97
35	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. PLoS Computational Biology, 2015, 11, e1004182.	3.2	97
36	mRNA turnover rate limits siRNA and microRNA efficacy. Molecular Systems Biology, 2010, 6, 433.	7.2	94

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37	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	4.1	92
38	Structural coordination of polymerization and crosslinking by a SEDS–bPBP peptidoglycan synthase complex. Nature Microbiology, 2020, 5, 813-820.	13.3	91
39	Computational Analysis of Mouse piRNA Sequence and Biogenesis. PLoS Computational Biology, 2007, 3, e222.	3.2	83
40	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF-β pathway and reveal microRNA regulation of TGFBR2. Silence: A Journal of RNA Regulation, 2011, 2, 3.	8.1	78
41	Protein structure determination by combining sparse NMR data with evolutionary couplings. Nature Methods, 2015, 12, 751-754.	19.0	75
42	Large-scale discovery of protein interactions at residue resolution using co-evolution calculated from genomic sequences. Nature Communications, 2021, 12, 1396.	12.8	68
43	CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. Cell Systems, 2021, 12, 128-140.e4.	6.2	67
44	Structure and Sequence Analyses of Clustered Protocadherins Reveal Antiparallel Interactions that Mediate Homophilic Specificity. Structure, 2015, 23, 2087-2098.	3.3	65
45	Core Genes Evolve Rapidly in the Long-Term Evolution Experiment with Escherichia coli. Genome Biology and Evolution, 2017, 9, 1072-1083.	2.5	64
46	Rapid generation of potent antibodies by autonomous hypermutation in yeast. Nature Chemical Biology, 2021, 17, 1057-1064.	8.0	59
47	Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. ELife, 2020, 9, .	6.0	58
48	All-atom 3D structure prediction of transmembrane β-barrel proteins from sequences. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5413-5418.	7.1	53
49	Antiparallel protocadherin homodimers use distinct affinity- and specificity-mediating regions in cadherin repeats 1-4. ELife, 2016, 5, .	6.0	53
50	Structure and mutagenic analysis of the lipid II flippase MurJ from <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6709-6714.	7.1	52
51	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
52	Genome-wide discovery of epistatic loci affecting antibiotic resistance in Neisseria gonorrhoeae using evolutionary couplings. Nature Microbiology, 2019, 4, 328-338.	13.3	41
53	Protein Structure from Experimental Evolution. Cell Systems, 2020, 10, 15-24.e5.	6.2	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. Journal of Biological Chemistry, 1999, 274, 3632-3641.	3.4	35

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55	Regulated spatial organization and sensitivity of cytosolic protein oxidation in Caenorhabditis elegans. Nature Communications, 2014, 5, 5020.	12.8	34
56	Interaction specificity of clustered protocadherins inferred from sequence covariation and structural analysis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17825-17830.	7.1	29
57	Co-evolution of interacting proteins through non-contacting and non-specific mutations. Nature Ecology and Evolution, 2022, 6, 590-603.	7.8	23
58	Dormant spores sense amino acids through the B subunits of their germination receptors. Nature Communications, 2021, 12, 6842.	12.8	22
59	The SpoVA membrane complex is required for dipicolinic acid import during sporulation and export during germination. Genes and Development, 2022, 36, 634-646.	5.9	17
60	Population-specific design of de-immunized protein biotherapeutics. PLoS Computational Biology, 2018, 14, e1005983.	3.2	16
61	mRNA turnover rate limits siRNA and microRNA efficacy. Molecular Systems Biology, 2010, 6, 454.	7.2	14
62	Gainâ€ofâ€function experiments with bacteriophage lambda uncover residues under diversifying selection in nature. Evolution; International Journal of Organic Evolution, 2018, 72, 2234-2243.	2.3	14
63	Structural Studies by High-Field NMR Spectroscopy of a Binary-Addressed Complementary Oligonucleotide System Juxtaposing Pyrene and Perfluoro-Azide Units. Journal of Biomolecular Structure and Dynamics, 1997, 15, 307-320.	3.5	13
64	Mechanical gating of the auditory transduction channel TMC1 involves the fourth and sixth transmembrane helices. Science Advances, 2022, 8, .	10.3	13
65	Evidence that regulation of intramembrane proteolysis is mediated by substrate gating during sporulation in Bacillus subtilis. PLoS Genetics, 2018, 14, e1007753.	3.5	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. Journal of Biomolecular Structure and Dynamics, 1999, 17, 193-211.	3.5	10
67	Structure, Dynamics and Implied Gating Mechanism of a Human Cyclic Nucleotide-Gated Channel. PLoS Computational Biology, 2014, 10, e1003976.	3.2	9
68	Natural and Designed Proteins Inspired by Extremotolerant Organisms Can Form Condensates and Attenuate Apoptosis in Human Cells. ACS Synthetic Biology, 2022, 11, 1292-1302.	3.8	9
69	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. Methods in Enzymology, 2019, 614, 363-392.	1.0	8
70	A Hybrid Approach for Protein Structure Determination Combining Sparse NMR with Evolutionary Coupling Sequence Data. Advances in Experimental Medicine and Biology, 2018, 1105, 153-169.	1.6	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. MSystems, 2022, 7, e0146621.	3.8	5

#	ARTICLE	IF	CITATIONS
73	Solutions to the computational protein folding problem. FASEB Journal, 2018, 32, 377.1.	0.5	1
74	Computational analysis of mouse piRNA sequence and biogenesis. PLoS Computational Biology, 2005, preprint, e222.	3.2	0
75	Democratizing the mapping of gene mutations to protein biophysics. Nature, 2022, 604, 47-48.	27.8	0