Debora S Marks

List of Publications by Year
in descending order

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	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
2	Natural and Designed Proteins Inspired by Extremotolerant Organisms Can Form Condensates and Attenuate Apoptosis in Human Cells. ACS Synthetic Biology, 2022, 11, 1292-1302.	1.9	9
3	Co-evolution of interacting proteins through non-contacting and non-specific mutations. Nature Ecology and Evolution, 2022, 6, 590-603.	3.4	23
4	Democratizing the mapping of gene mutations to protein biophysics. Nature, 2022, 604, 47-48.	13.7	0
5	High-Content Screening and Computational Prediction Reveal Viral Genes That Suppress the Innate Immune Response. MSystems, 2022, 7, e0146621.	1.7	5
6	The SpoVA membrane complex is required for dipicolinic acid import during sporulation and export during germination. Genes and Development, 2022, 36, 634-646.	2.7	17
7	Mechanical gating of the auditory transduction channel TMC1 involves the fourth and sixth transmembrane helices. Science Advances, 2022, 8, .	4.7	13
8	CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. Cell Systems, 2021, 12, 128-140.e4.	2.9	67
9	Large-scale discovery of protein interactions at residue resolution using co-evolution calculated from genomic sequences. Nature Communications, 2021, 12, 1396.	5.8	68
10	Protein design and variant prediction using autoregressive generative models. Nature Communications, 2021, 12, 2403.	5.8	168
11	Rapid generation of potent antibodies by autonomous hypermutation in yeast. Nature Chemical Biology, 2021, 17, 1057-1064.	3.9	59
12	Disease variant prediction with deep generative models of evolutionary data. Nature, 2021, 599, 91-95.	13.7	306
13	Dormant spores sense amino acids through the B subunits of their germination receptors. Nature Communications, 2021, 12, 6842.	5.8	22
14	Protein Structure from Experimental Evolution. Cell Systems, 2020, 10, 15-24.e5.	2.9	39
15	Structural coordination of polymerization and crosslinking by a SEDS–bPBP peptidoglycan synthase complex. Nature Microbiology, 2020, 5, 813-820.	5.9	91
16	Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. ELife, 2020, 9, .	2.8	58
17	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.	3.3	29
18	Inferring protein 3D structure from deep mutation scans. Nature Genetics, 2019, 51, 1170-1176.	9.4	124

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19	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. Methods in Enzymology, 2019, 614, 363-392.	0.4	8
20	The EVcouplings Python framework for coevolutionary sequence analysis. Bioinformatics, 2019, 35, 1582-1584.	1.8	180
21	Genome-wide discovery of epistatic loci affecting antibiotic resistance in Neisseria gonorrhoeae using evolutionary couplings. Nature Microbiology, 2019, 4, 328-338.	5.9	41
22	Structure of the peptidoglycan polymerase RodA resolved by evolutionary coupling analysis. Nature, 2018, 556, 118-121.	13.7	110
23	Evidence that regulation of intramembrane proteolysis is mediated by substrate gating during sporulation in Bacillus subtilis. PLoS Genetics, 2018, 14, e1007753.	1.5	11
24	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.	0.8	7
25	Deep generative models of genetic variation capture the effects of mutations. Nature Methods, 2018, 15, 816-822.	9.0	395
26	Cryo–electron microscopy structure of the lipid droplet–formation protein seipin. Journal of Cell Biology, 2018, 217, 4080-4091.	2.3	147
27	Gain–of–function experiments with bacteriophage lambda uncover residues under diversifying selection in nature. Evolution; International Journal of Organic Evolution, 2018, 72, 2234-2243.	1.1	14
28	A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. Molecular Cell, 2018, 71, 178-190.e8.	4.5	177
29	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.	3.3	52
30	Population-specific design of de-immunized protein biotherapeutics. PLoS Computational Biology, 2018, 14, e1005983.	1.5	16
31	Solutions to the computational protein folding problem. FASEB Journal, 2018, 32, 377.1.	0.2	1
32	Mutation effects predicted from sequence co-variation. Nature Biotechnology, 2017, 35, 128-135.	9.4	543
33	Protein Structures, Interactions and Function from Evolutionary Couplings. , 2017, , 37-58.		6
34	Core Genes Evolve Rapidly in the Long-Term Evolution Experiment with Escherichia coli. Genome Biology and Evolution, 2017, 9, 1072-1083.	1.1	64
35	3D RNA and Functional Interactions from Evolutionary Couplings. Cell, 2016, 165, 963-975.	13.5	152
36	Structured States of Disordered Proteins from Genomic Sequences. Cell, 2016, 167, 158-170.e12.	13.5	127

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37	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000–2013. Journal of Infectious Diseases, 2016, 214, 1579-1587.	1.9	186
38	Antiparallel protocadherin homodimers use distinct affinity- and specificity-mediating regions in cadherin repeats 1-4. ELife, 2016, 5, .	2.8	53
39	Amino acid coevolution reveals three-dimensional structure and functional domains of insect odorant receptors. Nature Communications, 2015, 6, 6077.	5.8	113
40	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	9.0	297
41	Protein structure determination by combining sparse NMR data with evolutionary couplings. Nature Methods, 2015, 12, 751-754.	9.0	75
42	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.	3.3	53
43	MicroRNA control of protein expression noise. Science, 2015, 348, 128-132.	6.0	337
44	Structure and Sequence Analyses of Clustered Protocadherins Reveal Antiparallel Interactions that Mediate Homophilic Specificity. Structure, 2015, 23, 2087-2098.	1.6	65
45	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. PLoS Computational Biology, 2015, 11, e1004182.	1.5	97
46	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	1.8	92
47	Structure, Dynamics and Implied Gating Mechanism of a Human Cyclic Nucleotide-Gated Channel. PLoS Computational Biology, 2014, 10, e1003976.	1.5	9
48	Regulated spatial organization and sensitivity of cytosolic protein oxidation in Caenorhabditis elegans. Nature Communications, 2014, 5, 5020.	5.8	34
49	FreeContact: fast and free software for protein contact prediction from residue co-evolution. BMC Bioinformatics, 2014, 15, 85.	1.2	146
50	Sequence co-evolution gives 3D contacts and structures of protein complexes. ELife, 2014, 3, .	2.8	452
51	Protein structure prediction from sequence variation. Nature Biotechnology, 2012, 30, 1072-1080.	9.4	569
52	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. Cell, 2012, 149, 1607-1621.	13.5	478
53	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.	8.0	78
54	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

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55	Protein 3D Structure Computed from Evolutionary Sequence Variation. PLoS ONE, 2011, 6, e28766.	1.1	975
56	mRNA turnover rate limits siRNA and microRNA efficacy. Molecular Systems Biology, 2010, 6, 454.	3.2	14
57	mRNA turnover rate limits siRNA and microRNA efficacy. Molecular Systems Biology, 2010, 6, 433.	3.2	94
58	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. Genome Research, 2010, 20, 1010-1019.	2.4	102
59	Target mRNA abundance dilutes microRNA and siRNA activity. Molecular Systems Biology, 2010, 6, 363.	3.2	299
60	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. Nature Biotechnology, 2009, 27, 549-555.	9.4	470
61	Computational Analysis of Mouse piRNA Sequence and Biogenesis. PLoS Computational Biology, 2007, 3, e222.	1.5	83
62	The microRNA.org resource: targets and expression. Nucleic Acids Research, 2007, 36, D149-D153.	6.5	2,280
63	The developmental miRNA profiles of zebrafish as determined by small RNA cloning. Genes and Development, 2005, 19, 1288-1293.	2.7	301
64	Antisense-Mediated Depletion Reveals Essential and Specific Functions of MicroRNAs in Drosophila Development. Cell, 2005, 121, 1097-1108.	13.5	304
65	Computational analysis of mouse piRNA sequence and biogenesis. PLoS Computational Biology, 2005, preprint, e222.	1.5	0
66	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.	1.5	758
67	Human MicroRNA Targets. PLoS Biology, 2004, 2, e363.	2.6	3,253
68	Identification of Virus-Encoded MicroRNAs. Science, 2004, 304, 734-736.	6.0	1,474
69	MicroRNA targets in Drosophila. Genome Biology, 2003, 5, R1.	13.9	3,023
70	The Small RNA Profile during Drosophila melanogaster Development. Developmental Cell, 2003, 5, 337-350.	3.1	866
71	Can sequencing shed light on cell cycling?. Nature, 2001, 409, 844-846.	13.7	97
72	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.	2.9	108

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73	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.	1.6	35
74	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.	2.0	10
75	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.	2.0	13