

# Yana Bromberg

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6391632/publications.pdf>

Version: 2024-02-01

84  
papers

4,755  
citations

159585

30  
h-index

110387

64  
g-index

98  
all docs

98  
docs citations

98  
times ranked

8652  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of the <scp>SARSâ€CoV</scp>â€2 proteome in three dimensions (3D) during the first 6 months of the <scp>COVID</scp>â€19 pandemic. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1054-1080.	2.6	31
2	Quantifying structural relationships of metal-binding sites suggests origins of biological electron transfer. <i>Science Advances</i> , 2022, 8, eabj3984.	10.3	24
3	Tightening the (neural) net for protein structure prediction. <i>Nature Reviews Genetics</i> , 2022, , .	16.3	0
4	Predicting embryonic aneuploidy rate in IVF patients using whole-exome sequencing. <i>Human Genetics</i> , 2022, 141, 1615-1627.	3.8	9
5	Inferring Potential Cancer Driving Synonymous Variants. <i>Genes</i> , 2022, 13, 778.	2.4	1
6	Deep learning of a bacterial and archaeal universal language of life enables transfer learning and illuminates microbial dark matter. <i>Nature Communications</i> , 2022, 13, 2606.	12.8	21
7	<i>mebipred</i>: identifying metal-binding potential in protein sequence. <i>Bioinformatics</i> , 2022, 38, 3532-3540.	4.1	15
8	Impact of vitamin A transport and storage on intestinal retinoid homeostasis and functions. <i>Journal of Lipid Research</i> , 2021, 62, 100046.	4.2	13
9	Low Diversity of Human Variation Despite Mostly Mild Functional Impact of De Novo Variants. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 635382.	3.5	2
10	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	14.5	135
11	Decoding the effects of synonymous variants. <i>Nucleic Acids Research</i> , 2021, 49, 12673-12691.	14.5	17
12	Snow microbiome functional analyses reveal novel aspects of microbial metabolism of complex organic compounds. <i>MicrobiologyOpen</i> , 2020, 9, e1100.	3.0	8
13	Virtual Boot Camp: <scp>COVID</scp>â€19 evolution and structural biology. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 511-513.	1.2	5
14	Computational Approaches for Unraveling the Effects of Variation in the Human Genome and Microbiome. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 411-432.	6.5	5
15	Amino acid encoding for deep learning applications. <i>BMC Bioinformatics</i> , 2020, 21, 235.	2.6	53
16	ISMB/ECCB 2019 Proceedings. <i>Bioinformatics</i> , 2019, 35, i1-i2.	4.1	1
17	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	2.5	5
18	What went wrong with variant effect predictor performance for the PCM1 challenge. <i>Human Mutation</i> , 2019, 40, 1486-1494.	2.5	8

#	ARTICLE	IF	CITATIONS
19	Assessment of predicted enzymatic activity of <i>N</i> -acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	2.5	10
20	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI 5. <i>Human Mutation</i> , 2019, 40, 1474-1485.	2.5	8
21	Predicting Functional Effects of Synonymous Variants: A Systematic Review and Perspectives. <i>Frontiers in Genetics</i> , 2019, 10, 914.	2.3	67
22	Identifying Crohn's disease signal from variome analysis. <i>Genome Medicine</i> , 2019, 11, 59.	8.2	21
23	Deep Carbon through Deep Time. , 2019, , 620-652.		10
24	funtrp: identifying protein positions for variation driven functional tuning. <i>Nucleic Acids Research</i> , 2019, 47, e142-e142.	14.5	29
25	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. <i>Human Mutation</i> , 2019, 40, 1612-1622.	2.5	8
26	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. <i>Human Mutation</i> , 2019, 40, 1495-1506.	2.5	16
27	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019, 40, 1314-1320.	2.5	10
28	Identifying mutation-driven changes in gene functionality that lead to venous thromboembolism. <i>Human Mutation</i> , 2019, 40, 1321-1329.	2.5	7
29	Fingerprinting cities: differentiating subway microbiome functionality. <i>Biology Direct</i> , 2019, 14, 19.	4.6	11
30	Interaction between dietary vitamin A, gut microbes, and host vitamin A status. <i>FASEB Journal</i> , 2019, 33, .	0.5	0
31	Functional sequencing read annotation for high precision microbiome analysis. <i>Nucleic Acids Research</i> , 2018, 46, e23-e23.	14.5	33
32	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. <i>Cell Reports</i> , 2018, 24, 3441-3454.e12.	6.4	91
33	fusionDB: assessing microbial diversity and environmental preferences via functional similarity networks. <i>Nucleic Acids Research</i> , 2018, 46, D535-D541.	14.5	21
34	HFSP: high speed homology-driven function annotation of proteins. <i>Bioinformatics</i> , 2018, 34, i304-i312.	4.1	22
35	ISMB 2018 proceedings. <i>Bioinformatics</i> , 2018, 34, i2-i3.	4.1	0
36	Ten simple rules for drawing scientific comics. <i>PLoS Computational Biology</i> , 2018, 14, e1005845.	3.2	19

#	ARTICLE	IF	CITATIONS
37	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. <i>Neuron</i> , 2017, 94, 486-499.e9.	8.1	155
38	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	2.5	13
39	clubber: removing the bioinformatics bottleneck in big data analyses. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	7
40	Common sequence variants affect molecular function more than rare variants?. <i>Scientific Reports</i> , 2017, 7, 1608.	3.3	20
41	Novel reductive dehalogenases from the marine sponge associated bacterium <i>Desulfoluna spongiphila</i> . <i>Environmental Microbiology Reports</i> , 2017, 9, 537-549.	2.4	18
42	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
43	Computational predictors fail to identify amino acid substitution effects at rheostat positions. <i>Scientific Reports</i> , 2017, 7, 41329.	3.3	47
44	ISMB/ECCB 2017 proceedings. <i>Bioinformatics</i> , 2017, 33, i1-i2.	4.1	4
45	COMPUTATIONAL APPROACHES TO UNDERSTANDING THE EVOLUTION OF MOLECULAR FUNCTION. , 2017, 22, 1-2.		0
46	Computational prediction shines light on type III secretion origins. <i>Scientific Reports</i> , 2016, 6, 34516.	3.3	37
47	COMPUTATIONAL APPROACHES TO STUDY MICROBES AND MICROBIOMES. , 2016, , .		7
48	Protein function in precision medicine: deep understanding with machine learning. <i>FEBS Letters</i> , 2016, 590, 2327-2341.	2.8	43
49	VarI-SIG 2015: methods for personalized medicine – the role of variant interpretation in research and diagnostics. <i>BMC Genomics</i> , 2016, 17, 425.	2.8	2
50	Whole exome sequencing identifies novel candidate genes that modify chronic obstructive pulmonary disease susceptibility. <i>Human Genomics</i> , 2016, 10, 1.	2.9	29
51	Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. <i>PLoS Computational Biology</i> , 2016, 12, e1005047.	3.2	14
52	Better prediction of functional effects for sequence variants. <i>BMC Genomics</i> , 2015, 16, S1.	2.8	478
53	Functional Basis of Microorganism Classification. <i>PLoS Computational Biology</i> , 2015, 11, e1004472.	3.2	37
54	SNP-SIG 2013: the state of the art of genomic variant interpretation. <i>Bioinformatics</i> , 2015, 31, 449-450.	4.1	1

#	ARTICLE	IF	CITATIONS
55	PredictProteinâ€”an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	14.5	589
56	Functionâ€”based assessment of structural similarity measurements using metal coâ€”factor orientation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 648-656.	2.6	14
57	Evolutionary history of redox metal-binding domains across the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7042-7047.	7.1	56
58	Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. <i>BMC Genomics</i> , 2013, 14, S1.	2.8	4
59	Collective judgment predicts disease-associated single nucleotide variants. <i>BMC Genomics</i> , 2013, 14, S2.	2.8	213
60	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. <i>Gastroenterology</i> , 2013, 145, 339-347.	1.3	149
61	News from the Protein Mutability Landscape. <i>Journal of Molecular Biology</i> , 2013, 425, 3937-3948.	4.2	72
62	Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. <i>Journal of Molecular Biology</i> , 2013, 425, 3993-4005.	4.2	31
63	Chapter 15: Disease Gene Prioritization. <i>PLoS Computational Biology</i> , 2013, 9, e1002902.	3.2	65
64	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. <i>PLoS Computational Biology</i> , 2013, 9, e1003350.	3.2	2
65	Neutral and weakly nonneutral sequence variants may define individuality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14255-14260.	7.1	36
66	Mapping of Mcs30, a New Mammary Carcinoma Susceptibility Quantitative Trait Locus (QTL30) on Rat Chromosome 12: Identification of Fry as a Candidate Mcs Gene. <i>PLoS ONE</i> , 2013, 8, e70930.	2.5	14
67	SNPdbe: constructing an nsNP functional impacts database. <i>Bioinformatics</i> , 2012, 28, 601-602.	4.1	44
68	TrAnsFuSE refines the search for protein function: oxidoreductases. <i>Integrative Biology (United Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 22)</i> , 2012, 13, 1-13.	1.3	0
69	Bioinformatics for personal genome interpretation. <i>Briefings in Bioinformatics</i> , 2012, 13, 495-512.	6.5	62
70	Comparative genomic and physiological analysis provides insights into the role of <i>Acidobacteria</i> in organic carbon utilization in Arctic tundra soils. <i>FEMS Microbiology Ecology</i> , 2012, 82, 341-355.	2.7	170
71	SNP-SIG Meeting 2011: Identification and annotation of SNPs in the context of structure, function, and disease. <i>BMC Genomics</i> , 2012, 13, S1.	2.8	21
72	Disease-related mutations predicted to impact protein function. <i>BMC Genomics</i> , 2012, 13, S11.	2.8	19

#	ARTICLE	IF	CITATIONS
73	Abstract 2118: Phenotypic diversity of disease-associated transforming growth factor- $\beta^2$ (TGF- $\beta^2$ ) type I receptor gene (TGFBRI) mutants. , 2011, , .		0
74	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. Nucleic Acids Research, 2010, 38, W523-W528.	14.5	34
75	Functional analyses of variants reveal a significant role for dominant negative and common alleles in oligogenic Bardet-Biedl syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10602-10607.	7.1	110
76	Conserved Amino Acids within the Adenovirus 2 E3/19K Protein Differentially Affect Downregulation of MHC Class I and MICA/B Proteins. Journal of Immunology, 2010, 184, 255-267.	0.8	21
77	<i>In silico</i> mutagenesis: a case study of the melanocortin 4 receptor. FASEB Journal, 2009, 23, 3059-3069.	0.5	37
78	Association of functionally significant Melanocortin-4 but not Melanocortin-3 receptor mutations with severe adult obesity in a large North American case-control study. Human Molecular Genetics, 2009, 18, 1140-1147.	2.9	112
79	Correlating protein function and stability through the analysis of single amino acid substitutions. BMC Bioinformatics, 2009, 10, S8.	2.6	76
80	New in protein structure and function annotation: hotspots, single nucleotide polymorphisms and the 'Deep Web'. Current Opinion in Drug Discovery & Development, 2009, 12, 408-19.	1.9	5
81	Comprehensive <i>in silico</i> mutagenesis highlights functionally important residues in proteins. Bioinformatics, 2008, 24, i207-i212.	4.1	47
82	Positional Cloning of 'Lisch-like', a Candidate Modifier of Susceptibility to Type 2 Diabetes in Mice. PLoS Genetics, 2008, 4, e1000137.	3.5	58
83	SNAP predicts effect of mutations on protein function. Bioinformatics, 2008, 24, 2397-2398.	4.1	225
84	SNAP: predict effect of non-synonymous polymorphisms on function. Nucleic Acids Research, 2007, 35, 3823-3835.	14.5	728