Yana Bromberg

List of Publications by Year
in descending order

84	4,755	159585 30	110387 64
papers	citations	h-index	g-index

98	98	98	8652
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	SNAP: predict effect of non-synonymous polymorphisms on function. Nucleic Acids Research, 2007, 35, 3823-3835.	14.5	728
2	PredictProteinâ€”an open resource for online prediction of protein structural and functional features. Nucleic Acids Research, 2014, 42, W337-W343.	14.5	589
3	Better prediction of functional effects for sequence variants. BMC Genomics, 2015, 16, S1.	2.8	478
4	SNAP predicts effect of mutations on protein function. Bioinformatics, 2008, 24, 2397-2398.	4.1	225
5	Collective judgment predicts disease-associated single nucleotide variants. BMC Genomics, 2013, 14, S2.	2.8	213
6	Comparative genomic and physiological analysis provides insights into the role ofAcidobacteriain organic carbon utilization in Arctic tundra soils. FEMS Microbiology Ecology, 2012, 82, 341-355.	2.7	170
7	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. Neuron, 2017, 94, 486-499.e9.	8.1	155
8	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	1.3	149
9	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
10	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
11	Functional analyses of variants reveal a significant role for dominant negative and common alleles in oligogenic Bardetâ€“Biedl syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10602-10607.	7.1	110
12	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. Cell Reports, 2018, 24, 3441-3454.e12.	6.4	91
13	Correlating protein function and stability through the analysis of single amino acid substitutions. BMC Bioinformatics, 2009, 10, S8.	2.6	76
14	News from the Protein Mutability Landscape. Journal of Molecular Biology, 2013, 425, 3937-3948.	4.2	72
15	Predicting Functional Effects of Synonymous Variants: A Systematic Review and Perspectives. Frontiers in Genetics, 2019, 10, 914.	2.3	67
16	Chapter 15: Disease Gene Prioritization. PLoS Computational Biology, 2013, 9, e1002902.	3.2	65
17	Bioinformatics for personal genome interpretation. Briefings in Bioinformatics, 2012, 13, 495-512.	6.5	62
18	Positional Cloning of â€œLisch-likeâ€, a Candidate Modifier of Susceptibility to Type 2 Diabetes in Mice. PLoS Genetics, 2008, 4, e1000137.	3.5	58

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19	Evolutionary history of redox metal-binding domains across the tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7042-7047.	7.1	56
20	Amino acid encoding for deep learning applications. BMC Bioinformatics, 2020, 21, 235.	2.6	53
21	Comprehensive in silico mutagenesis highlights functionally important residues in proteins. Bioinformatics, 2008, 24, i207-i212.	4.1	47
22	Computational predictors fail to identify amino acid substitution effects at rheostat positions. Scientific Reports, 2017, 7, 41329.	3.3	47
23	SNPdbe: constructing an nsSNP functional impacts database. Bioinformatics, 2012, 28, 601-602.	4.1	44
24	Protein function in precision medicine: deep understanding with machine learning. FEBS Letters, 2016, 590, 2327-2341.	2.8	43
25	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
26	In silico mutagenesis: a case study of the melanocortin 4 receptor. FASEB Journal, 2009, 23, 3059-3069.	0.5	37
27	Functional Basis of Microorganism Classification. PLoS Computational Biology, 2015, 11, e1004472.	3.2	37
28	Computational prediction shines light on type III secretion origins. Scientific Reports, 2016, 6, 34516.	3.3	37
29	Neutral and weakly nonneutral sequence variants may define individuality. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14255-14260.	7.1	36
30	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
31	Functional sequencing read annotation for high precision microbiome analysis. Nucleic Acids Research, 2018, 46, e23-e23.	14.5	33
32	Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. Journal of Molecular Biology, 2013, 425, 3993-4005.	4.2	31
33	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. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1054-1080.	2.6	31
34	Whole exome sequencing identifies novel candidate genes that modify chronic obstructive pulmonary disease susceptibility. Human Genomics, 2016, 10, 1.	2.9	29
35	funtrp: identifying protein positions for variation driven functional tuning. Nucleic Acids Research, 2019, 47, e142-e142.	14.5	29
36	Quantifying structural relationships of metal-binding sites suggests origins of biological electron transfer. Science Advances, 2022, 8, eabj3984.	10.3	24

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37	HFSP: high speed homology-driven function annotation of proteins. Bioinformatics, 2018, 34, i304-i312.	4.1	22
38	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
39	SNP-SIG Meeting 2011: Identification and annotation of SNPs in the context of structure, function, and disease. BMC Genomics, 2012, 13, S1.	2.8	21
40	fusionDB: assessing microbial diversity and environmental preferences via functional similarity networks. Nucleic Acids Research, 2018, 46, D535-D541.	14.5	21
41	Identifying Crohnâ€™s disease signal from variome analysis. Genome Medicine, 2019, 11, 59.	8.2	21
42	Deep learning of a bacterial and archaeal universal language of life enables transfer learning and illuminates microbial dark matter. Nature Communications, 2022, 13, 2606.	12.8	21
43	Common sequence variants affect molecular function more than rare variants?. Scientific Reports, 2017, 7, 1608.	3.3	20
44	Disease-related mutations predicted to impact protein function. BMC Genomics, 2012, 13, S11.	2.8	19
45	Ten simple rules for drawing scientific comics. PLoS Computational Biology, 2018, 14, e1005845.	3.2	19
46	Novel reductive dehalogenases from the marine sponge associated bacterium Desulfoluna spongiiphila. Environmental Microbiology Reports, 2017, 9, 537-549.	2.4	18
47	Decoding the effects of synonymous variants. Nucleic Acids Research, 2021, 49, 12673-12691.	14.5	17
48	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
49	mebipred: identifying metal-binding potential in protein sequence. Bioinformatics, 2022, 38, 3532-3540.	4.1	15
50	Mapping of Mcs30, a New Mammary Carcinoma Susceptibility Quantitative Trait Locus (QTL30) on Rat Chromosome 12: Identification of Fry as a Candidate Mcs Gene. PLoS ONE, 2013, 8, e70930.	2.5	14
51	Functionâ€based assessment of structural similarity measurements using metal coâ€factor orientation. Proteins: Structure, Function and Bioinformatics, 2014, 82, 648-656.	2.6	14
52	Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. PLoS Computational Biology, 2016, 12, e1005047.	3.2	14
53	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
54	Impact of vitamin A transport and storage on intestinal retinoid homeostasis and functions. Journal of Lipid Research, 2021, 62, 100046.	4.2	13

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55	Fingerprinting cities: differentiating subway microbiome functionality. Biology Direct, 2019, 14, 19.	4.6	11
56	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
57	Deep Carbon through Deep Time. , 2019, , 620-652.		10
58	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
59	TrAnsFuSE refines the search for protein function: oxidoreductases. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.3	9
60	Predicting embryonic aneuploidy rate in IVF patients using whole-exome sequencing. Human Genetics, 2022, 141, 1615-1627.	3.8	9
61	What went wrong with variant effect predictor performance for the PCM1 challenge. Human Mutation, 2019, 40, 1486-1494.	2.5	8
62	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	2.5	8
63	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. Human Mutation, 2019, 40, 1612-1622.	2.5	8
64	Snow microbiome functional analyses reveal novel aspects of microbial metabolism of complex organic compounds. MicrobiologyOpen, 2020, 9, e1100.	3.0	8
65	COMPUTATIONAL APPROACHES TO STUDY MICROBES AND MICROBIOMES. , 2016, , .		7
66	clubber: removing the bioinformatics bottleneck in big data analyses. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	7
67	Identifying mutationâ€driven changes in gene functionality that lead to venous thromboembolism. Human Mutation, 2019, 40, 1321-1329.	2.5	7
68	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
69	Virtual Boot Camp: <scp>COVID</scp>â€19 evolution and structural biology. Biochemistry and Molecular Biology Education, 2020, 48, 511-513.	1.2	5
70	Computational Approaches for Unraveling the Effects of Variation in the Human Genome and Microbiome. Annual Review of Biomedical Data Science, 2020, 3, 411-432.	6.5	5
71	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
72	Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. BMC Genomics, 2013, 14, S1.	2.8	4

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73	ISMB/ECCB 2017 proceedings. Bioinformatics, 2017, 33, i1-i2.	4.1	4
74	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	3.2	2
75	VarI-SIG 2015: methods for personalized medicine â€“ the role of variant interpretation in research and diagnostics. BMC Genomics, 2016, 17, 425.	2.8	2
76	Low Diversity of Human Variation Despite Mostly Mild Functional Impact of De Novo Variants. Frontiers in Molecular Biosciences, 2021, 8, 635382.	3.5	2
77	SNP-SIG 2013: the state of the art of genomic variant interpretation. Bioinformatics, 2015, 31, 449-450.	4.1	1
78	ISMB/ECCB 2019 Proceedings. Bioinformatics, 2019, 35, i1-i2.	4.1	1
79	Inferring Potential Cancer Driving Synonymous Variants. Genes, 2022, 13, 778.	2.4	1
80	COMPUTATIONAL APPROACHES TO UNDERSTANDING THE EVOLUTION OF MOLECULAR FUNCTION. , 2017, 22, 1-2.		0
81	ISMB 2018 proceedings. Bioinformatics, 2018, 34, i2-i3.	4.1	0
82	Abstract 2118: Phenotypic diversity of disease-associated transforming growth factor-Î² (TGF-Î²) type I receptor gene (TGFBR1) mutants. , 2011, , .		0
83	Interaction between dietary vitamin A, gut microbes, and host vitamin A status. FASEB Journal, 2019, 33, .	0.5	0
84	Tightening the (neural) net for protein structure prediction. Nature Reviews Genetics, 2022, , .	16.3	0