Emidio Capriotti

List of Publications by Year
in descending order

69	6,192	159585 30	91884 69
papers	citations	h-index	g-index

90	90	90	7311
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Predicting protein stability changes upon single-point mutation: a thorough comparison of the available tools on a new dataset. Briefings in Bioinformatics, 2022, 23, .	6.5	57
2	Evaluating the relevance of sequence conservation in the prediction of pathogenic missense variants. Human Genetics, 2022, 141, 1649-1658.	3.8	3
3	Turning Failures into Applications: The Problem of Protein Î”Î”G Prediction. Methods in Molecular Biology, 2022, 2449, 169-185.	0.9	5
4	DDGun: an untrained predictor of protein stability changes upon amino acid variants. Nucleic Acids Research, 2022, 50, W222-W227.	14.5	28
5	Network-based strategies for protein characterization. Advances in Protein Chemistry and Structural Biology, 2021, 127, 217-248.	2.3	0
6	Protein Stability Perturbation Contributes to the Loss of Function in Haploinsufficient Genes. Frontiers in Molecular Biosciences, 2021, 8, 620793.	3.5	20
7	ThermoScan: Semi-automatic Identification of Protein Stability Data From PubMed. Frontiers in Molecular Biosciences, 2021, 8, 620475.	3.5	6
8	Analysis and Interpretation of the Impact of Missense Variants in Cancer. International Journal of Molecular Sciences, 2021, 22, 5416.	4.1	28
9	A Deep-Learning Sequence-Based Method to Predict Protein Stability Changes Upon Genetic Variations. Genes, 2021, 12, 911.	2.4	20
10	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	19.0	105
11	Calibrating variant-scoring methods for clinical decision making. Bioinformatics, 2021, 36, 5709-5711.	4.1	10
12	Limitations and challenges in protein stability prediction upon genome variations: towards future applications in precision medicine. Computational and Structural Biotechnology Journal, 2020, 18, 1968-1979.	4.1	88
13	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
14	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
15	DDGun: an untrained method for the prediction of protein stability changes upon single and multiple point variations. BMC Bioinformatics, 2019, 20, 335.	2.6	81
16	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
17	Predicting gene expression level in E. coli from mRNA sequence information. , 2019, , .		1
18	Fido-SNP: the first webserver for scoring the impact of single nucleotide variants in the dog genome. Nucleic Acids Research, 2019, 47, W136-W141.	14.5	3

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19	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	2.5	16
20	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
21	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
22	Are machine learning based methods suited to address complex biological problems? Lessons from CAGIâ€5 challenges. Human Mutation, 2019, 40, 1455-1462.	2.5	6
23	Characterization of human frataxin missense variants in cancer tissues. Human Mutation, 2019, 40, 1400-1413.	2.5	16
24	Integrating molecular networks with genetic variant interpretation for precision medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2019, 11, e1443.	6.6	34
25	Blind prediction of deleterious amino acid variations with SNPs&GO. Human Mutation, 2017, 38, 1064-1071.	2.5	24
26	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
27	PhD-SNPg: a webserver and lightweight tool for scoring single nucleotide variants. Nucleic Acids Research, 2017, 45, W247-W252.	14.5	132
28	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
29	VpreB serves as an invariant surrogate antigen for selecting immunoglobulin antigen-binding sites. Science Immunology, 2016, 1, .	11.9	29
30	Computational methods and resources for the interpretation of genomic variants in cancer. BMC Genomics, 2015, 16, S7.	2.8	18
31	WALTZ-DB: a benchmark database of amyloidogenic hexapeptides. Bioinformatics, 2015, 31, 1698-1700.	4.1	61
32	ContrastRank: a new method for ranking putative cancer driver genes and classification of tumor samples. Bioinformatics, 2014, 30, i572-i578.	4.1	22
33	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. Nucleic Acids Research, 2014, 42, W356-W360.	14.5	3
34	In silico comparative characterization of pharmacogenomic missense variants. BMC Genomics, 2014, 15, S4.	2.8	11
35	Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. BMC Genomics, 2013, 14, S1.	2.8	4
36	Collective judgment predicts disease-associated single nucleotide variants. BMC Genomics, 2013, 14, S2.	2.8	213

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37	WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. BMC Genomics, 2013, 14, S6.	2.8	248
38	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. Bioinformatics, 2013, 29, 1112-1119.	4.1	20
39	Computational and Theoretical Methods for Protein Folding. Biochemistry, 2013, 52, 8601-8624.	2.5	63
40	WebRASP: a server for computing energy scores to assess the accuracy and stability of RNA 3D structures. Bioinformatics, 2013, 29, 2649-2650.	4.1	7
41	Bioinformatics and variability in drug response: a protein structural perspective. Journal of the Royal Society Interface, 2012, 9, 1409-1437.	3.4	66
42	Bioinformatics for personal genome interpretation. Briefings in Bioinformatics, 2012, 13, 495-512.	6.5	62
43	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
44	Bioinformatics challenges for personalized medicine. Bioinformatics, 2011, 27, 1741-1748.	4.1	223
45	A new disease-specific machine learning approach for the prediction of cancer-causing missense variants. Genomics, 2011, 98, 310-317.	2.9	68
46	The three-dimensional folding of the Î±-globin gene domain reveals formation of chromatin globules. Nature Structural and Molecular Biology, 2011, 18, 107-114.	8.2	274
47	Improving the prediction of disease-related variants using protein three-dimensional structure. BMC Bioinformatics, 2011, 12, S3.	2.6	94
48	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	3.5	137
49	All-atom knowledge-based potential for RNA structure prediction and assessment. Bioinformatics, 2011, 27, 1086-1093.	4.1	71
50	Comparative Modeling: The State of the Art and Protein Drug Target Structure Prediction. Combinatorial Chemistry and High Throughput Screening, 2011, 14, 532-547.	1.1	42
51	Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. BMC Bioinformatics, 2010, 11, 322.	2.6	38
52	SARA: a server for function annotation of RNA structures. Nucleic Acids Research, 2009, 37, W260-W265.	14.5	33
53	Functional annotations improve the predictive score of human disease-related mutations in proteins. Human Mutation, 2009, 30, 1237-1244.	2.5	552
54	Use of estimated evolutionary strength at the codon level improves the prediction of disease-related protein mutations in humans. Human Mutation, 2008, 29, 198-204.	2.5	37

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55	A three-state prediction of single point mutations on protein stability changes. BMC Bioinformatics, 2008, 9, S6.	2.6	267
56	RNA structure alignment by a unit-vector approach. Bioinformatics, 2008, 24, i112-i118.	4.1	46
57	Computational RNA Structure Prediction. Current Bioinformatics, 2008, 3, 32-45.	1.5	37
58	K-Fold: a tool for the prediction of the protein folding kinetic order and rate. Bioinformatics, 2007, 23, 385-386.	4.1	63
59	Machine learning and the prediction of protein structure: the state of the art. , 2006, , 359-370.		0
60	Diffusionâ€collision of foldons elucidates the kinetic effects of point mutations and suggests control strategies of the folding process of helical proteins. Proteins: Structure, Function and Bioinformatics, 2006, 64, 198-209.	2.6	2
61	Hierarchical Mechanochemical Switches in Angiostatin. ChemBioChem, 2006, 7, 1774-1782.	2.6	14
62	Predicting the insurgence of human genetic diseases associated to single point protein mutations with support vector machines and evolutionary information. Bioinformatics, 2006, 22, 2729-2734.	4.1	737
63	The WWWH of remote homolog detection: The state of the art. Briefings in Bioinformatics, 2006, 8, 78-87.	6.5	33
64	Predicting protein stability changes from sequences using support vector machines. Bioinformatics, 2005, 21, ii54-ii58.	4.1	142
65	I-Mutant2.0: predicting stability changes upon mutation from the protein sequence or structure. Nucleic Acids Research, 2005, 33, W306-W310.	14.5	1,502
66	A Minimal Model of Three-State Folding Dynamics of Helical Proteins. Journal of Physical Chemistry B, 2005, 109, 4215-4226.	2.6	3
67	Dynamics of the minimally frustrated helices determine the hierarchical folding of small helical proteins. Physical Review E, 2004, 69, 051905.	2.1	8
68	A neural-network-based method for predicting protein stability changes upon single point mutations. Bioinformatics, 2004, 20, i63-i68.	4.1	161
69	A Shannon entropy-based filter detects high- quality profile-profile alignments in searches for remote homologues. Proteins: Structure, Function and Bioinformatics, 2003, 54, 351-360.	2.6	12