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	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
2	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
3	Functional annotations improve the predictive score of human disease-related mutations in proteins. Human Mutation, 2009, 30, 1237-1244.	2.5	552
4	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
5	A three-state prediction of single point mutations on protein stability changes. BMC Bioinformatics, 2008, 9, S6.	2.6	267
6	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
7	Bioinformatics challenges for personalized medicine. Bioinformatics, 2011, 27, 1741-1748.	4.1	223
8	Collective judgment predicts disease-associated single nucleotide variants. BMC Genomics, 2013, 14, S2.	2.8	213
9	A neural-network-based method for predicting protein stability changes upon single point mutations. Bioinformatics, 2004, 20, i63-i68.	4.1	161
10	Predicting protein stability changes from sequences using support vector machines. Bioinformatics, 2005, 21, ii54-ii58.	4.1	142
11	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	3.5	137
12	PhD-SNPg: a webserver and lightweight tool for scoring single nucleotide variants. Nucleic Acids Research, 2017, 45, W247-W252.	14.5	132
13	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	19.0	105
14	Improving the prediction of disease-related variants using protein three-dimensional structure. BMC Bioinformatics, 2011, 12, S3.	2.6	94
15	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
16	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
17	All-atom knowledge-based potential for RNA structure prediction and assessment. Bioinformatics, 2011, 27, 1086-1093.	4.1	71
18	A new disease-specific machine learning approach for the prediction of cancer-causing missense variants. Genomics, 2011, 98, 310-317.	2.9	68

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19	Bioinformatics and variability in drug response: a protein structural perspective. Journal of the Royal Society Interface, 2012, 9, 1409-1437.	3.4	66
20	K-Fold: a tool for the prediction of the protein folding kinetic order and rate. Bioinformatics, 2007, 23, 385-386.	4.1	63
21	Computational and Theoretical Methods for Protein Folding. Biochemistry, 2013, 52, 8601-8624.	2.5	63
22	Bioinformatics for personal genome interpretation. Briefings in Bioinformatics, 2012, 13, 495-512.	6.5	62
23	WALTZ-DB: a benchmark database of amyloidogenic hexapeptides. Bioinformatics, 2015, 31, 1698-1700.	4.1	61
24	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
25	RNA structure alignment by a unit-vector approach. Bioinformatics, 2008, 24, i112-i118.	4.1	46
26	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
27	Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. BMC Bioinformatics, 2010, 11, 322.	2.6	38
28	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
29	Computational RNA Structure Prediction. Current Bioinformatics, 2008, 3, 32-45.	1.5	37
30	Integrating molecular networks with genetic variant interpretation for precision medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2019, 11, e1443.	6.6	34
31	The WWWH of remote homolog detection: The state of the art. Briefings in Bioinformatics, 2006, 8, 78-87.	6.5	33
32	SARA: a server for function annotation of RNA structures. Nucleic Acids Research, 2009, 37, W260-W265.	14.5	33
33	VpreB serves as an invariant surrogate antigen for selecting immunoglobulin antigen-binding sites. Science Immunology, 2016, 1, .	11.9	29
34	Analysis and Interpretation of the Impact of Missense Variants in Cancer. International Journal of Molecular Sciences, 2021, 22, 5416.	4.1	28
35	DDGun: an untrained predictor of protein stability changes upon amino acid variants. Nucleic Acids Research, 2022, 50, W222-W227.	14.5	28
36	Blind prediction of deleterious amino acid variations with SNPs&GO. Human Mutation, 2017, 38, 1064-1071.	2.5	24

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37	ContrastRank: a new method for ranking putative cancer driver genes and classification of tumor samples. Bioinformatics, 2014, 30, i572-i578.	4.1	22
38	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
39	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
40	Protein Stability Perturbation Contributes to the Loss of Function in Haploinsufficient Genes. Frontiers in Molecular Biosciences, 2021, 8, 620793.	3.5	20
41	A Deep-Learning Sequence-Based Method to Predict Protein Stability Changes Upon Genetic Variations. Genes, 2021, 12, 911.	2.4	20
42	Computational methods and resources for the interpretation of genomic variants in cancer. BMC Genomics, 2015, 16, S7.	2.8	18
43	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
44	Characterization of human frataxin missense variants in cancer tissues. Human Mutation, 2019, 40, 1400-1413.	2.5	16
45	Hierarchical Mechanochemical Switches in Angiostatin. ChemBioChem, 2006, 7, 1774-1782.	2.6	14
46	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
47	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
48	In silico comparative characterization of pharmacogenomic missense variants. BMC Genomics, 2014, 15, S4.	2.8	11
49	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
50	Calibrating variant-scoring methods for clinical decision making. Bioinformatics, 2021, 36, 5709-5711.	4.1	10
51	Dynamics of the minimally frustrated helices determine the hierarchical folding of small helical proteins. Physical Review E, 2004, 69, 051905.	2.1	8
52	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
53	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
54	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

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55	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
56	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
57	ThermoScan: Semi-automatic Identification of Protein Stability Data From PubMed. Frontiers in Molecular Biosciences, 2021, 8, 620475.	3.5	6
58	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
59	Turning Failures into Applications: The Problem of Protein Î”Î”G Prediction. Methods in Molecular Biology, 2022, 2449, 169-185.	0.9	5
60	Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. BMC Genomics, 2013, 14, S1.	2.8	4
61	A Minimal Model of Three-State Folding Dynamics of Helical Proteins. Journal of Physical Chemistry B, 2005, 109, 4215-4226.	2.6	3
62	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
63	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
64	Evaluating the relevance of sequence conservation in the prediction of pathogenic missense variants. Human Genetics, 2022, 141, 1649-1658.	3.8	3
65	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
66	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
67	Predicting gene expression level in E. coli from mRNA sequence information. , 2019, , .		1
68	Machine learning and the prediction of protein structure: the state of the art. , 2006, , 359-370.		0
69	Network-based strategies for protein characterization. Advances in Protein Chemistry and Structural Biology, 2021, 127, 217-248.	2.3	0