

# Rita Casadio

## List of Publications by Year in descending order

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250  
papers

15,982  
citations

36691

53  
h-index

22488

117  
g-index

271  
all docs

271  
docs citations

271  
times ranked

20908  
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine learning solutions for predicting protein-protein interactions. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	6.2	19
2	A Glance into MTHFR Deficiency at a Molecular Level. <i>International Journal of Molecular Sciences</i> , 2022, 23, 167.	1.8	2
3	Turning Failures into Applications: The Problem of Protein $\beta$ -G Prediction. <i>Methods in Molecular Biology</i> , 2022, 2449, 169-185.	0.4	5
4	On the critical review of five machine learning-based algorithms for predicting protein stability changes upon mutation. <i>Briefings in Bioinformatics</i> , 2021, 22, 601-603.	3.2	13
5	Computer-Aided Prediction of Protein Mitochondrial Localization. <i>Methods in Molecular Biology</i> , 2021, 2275, 433-452.	0.4	2
6	Whole Genome Sequence Analysis of <i>Brucella abortus</i> Isolates from Various Regions of South Africa. <i>Microorganisms</i> , 2021, 9, 570.	1.6	6
7	Huntingtin: A Protein with a Peculiar Solvent Accessible Surface. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2878.	1.8	3
8	Biallelic variants in <i>LIG3</i> cause a novel mitochondrial neurogastrointestinal encephalomyopathy. <i>Brain</i> , 2021, 144, 1451-1466.	3.7	28
9	BetAware-Deep: An Accurate Web Server for Discrimination and Topology Prediction of Prokaryotic Transmembrane $\beta$ -barrel Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 166729.	2.0	13
10	Computational Resources for Molecular Biology 2021. <i>Journal of Molecular Biology</i> , 2021, 433, 166962.	2.0	0
11	BENZ WS: the Bologna ENZYme Web Server for four-level EC number annotation. <i>Nucleic Acids Research</i> , 2021, 49, W60-W66.	6.5	7
12	Mapping OMIM Disease-Related Variations on Protein Domains Reveals an Association Among Variation Type, Pfam Models, and Disease Classes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 617016.	1.6	5
13	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021, 18, 1122-1127.	9.0	105
14	DeepREx-WS: A web server for characterising protein-solvent interaction starting from sequence. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5791-5799.	1.9	4
15	Comparative genomics of tadpole shrimps (Crustacea, Branchiopoda, Notostraca): Dynamic genome evolution against the backdrop of morphological stasis. <i>Genomics</i> , 2021, 113, 4163-4172.	1.3	7
16	DeepMito: accurate prediction of protein sub-mitochondrial localization using convolutional neural networks. <i>Bioinformatics</i> , 2020, 36, 56-64.	1.8	61
17	Protein-Protein Interaction Methods and Protein Phase Separation. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 89-112.	2.8	18
18	Highlighting Human Enzymes Active in Different Metabolic Pathways and Diseases: The Case Study of EC 1.2.3.1 and EC 2.3.1.9. <i>Biomedicines</i> , 2020, 8, 250.	1.4	3

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19	Large-scale prediction and analysis of protein sub-mitochondrial localization with DeepMito. BMC Bioinformatics, 2020, 21, 266.	1.2	6
20	NETGE-PLUS: Standard and Network-Based Gene Enrichment Analysis in Human and Model Organisms. Journal of Proteome Research, 2020, 19, 2873-2878.	1.8	3
21	Cauliflower Mosaic Virus TAV, a Plant Virus Protein That Functions like Ribonuclease H1 and is Cytotoxic to Glioma Cells. BioMed Research International, 2020, 2020, 1-10.	0.9	2
22	Solvent Accessibility of Residues Undergoing Pathogenic Variations in Humans: From Protein Structures to Protein Sequences. Frontiers in Molecular Biosciences, 2020, 7, 626363.	1.6	58
23	Transmembrane Domain Prediction. , 2019, , 46-52.		0
24	Protein Functional Annotation. , 2019, , 8-14.		0
25	PhenPath: a tool for characterizing biological functions underlying different phenotypes. BMC Genomics, 2019, 20, 548.	1.2	8
26	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	1.1	8
27	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	1.1	18
28	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	1.1	10
29	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. Human Mutation, 2019, 40, 1546-1556.	1.1	19
30	Assessing computational predictions of the phenotypic effect of cystathionine- $\beta$ -synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
31	Assessment of predicted enzymatic activity of $\pm$ N-acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
32	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. Human Mutation, 2019, 40, 1474-1485.	1.1	8
33	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	1.1	16
34	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.	1.1	8
35	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	1.1	16
36	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	1.1	10

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37	Are machine learning based methods suited to address complex biological problems? Lessons from CAGI challenges. <i>Human Mutation</i> , 2019, 40, 1455-1462.	1.1	6
38	Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. <i>BMC Genomics</i> , 2019, 20, 278.	1.2	7
39	Functional and Structural Features of Disease-Related Protein Variants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1530.	1.8	15
40	Molecular modelling evaluation of exon 18 His845_Asn848delinsPro PDGFR $\beta$ mutation in a metastatic GIST patient responding to imatinib. <i>Scientific Reports</i> , 2019, 9, 2172.	1.6	5
41	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
42	On the biases in predictions of protein stability changes upon variations: the INPS test case. <i>Bioinformatics</i> , 2019, 35, 2525-2527.	1.8	32
43	Draft genomes and genomic divergence of two <i>Lepidurus</i> tadpole shrimp species (Crustacea, Tj ETQq1 1 0.784314 rgBT /Overlo	2.2	14
44	Mutant MYO1F alters the mitochondrial network and induces tumor proliferation in thyroid cancer. <i>International Journal of Cancer</i> , 2018, 143, 1706-1719.	2.3	35
45	DeepSig: deep learning improves signal peptide detection in proteins. <i>Bioinformatics</i> , 2018, 34, 1690-1696.	1.8	92
46	BUSCA: an integrative web server to predict subcellular localization of proteins. <i>Nucleic Acids Research</i> , 2018, 46, W459-W466.	6.5	270
47	SChloro: directing <i>Viridiplantae</i> proteins to six chloroplastic sub-compartments. <i>Bioinformatics</i> , 2017, 33, 347-353.	1.8	21
48	Blind prediction of deleterious amino acid variations with SNPs&GO. <i>Human Mutation</i> , 2017, 38, 1064-1071.	1.1	24
49	The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation. <i>Nucleic Acids Research</i> , 2017, 45, W285-W290.	6.5	18
50	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. <i>Human Mutation</i> , 2017, 38, 1123-1131.	1.1	17
51	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	1.1	13
52	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.	1.1	39
53	ISPRED4: interaction sites PREDiction in protein structures with a refining grammar model. <i>Bioinformatics</i> , 2017, 33, 1656-1663.	1.8	28
54	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. <i>BMC Genomics</i> , 2017, 18, 554.	1.2	52

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55	BRCA1 p.His1673del is a pathogenic mutation associated with a predominant ovarian cancer phenotype. <i>Oncotarget</i> , 2017, 8, 22640-22648.	0.8	10
56	Function Prediction of Proteins from their Sequences with BAR 3.0. , 2017, 1, 001-005.		0
57	Genomic and expression analyses of <i>Tursiops truncatus</i> T cell receptor gamma (TRG) and alpha/delta (TRA/TRD) loci reveal a similar basic public I <sup>3</sup> I repertoire in dolphin and human. <i>BMC Genomics</i> , 2016, 17, 634.	1.2	32
58	INPS-MD: a web server to predict stability of protein variants from sequence and structure. <i>Bioinformatics</i> , 2016, 32, 2542-2544.	1.8	170
59	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
60	NET-GE: a web-server for NETwork-based human gene enrichment. <i>Bioinformatics</i> , 2016, 32, 3489-3491.	1.8	14
61	Large scale analysis of protein stability in OMIM disease related human protein variants. <i>BMC Genomics</i> , 2016, 17, 397.	1.2	37
62	Ancient pathogen-driven adaptation triggers increased susceptibility to non-celiac wheat sensitivity in present-day European populations. <i>Genes and Nutrition</i> , 2016, 11, 15.	1.2	5
63	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	6.5	113
64	NET-GE: a novel NETwork-based Gene Enrichment for detecting biological processes associated to Mendelian diseases. <i>BMC Genomics</i> , 2015, 16, S6.	1.2	15
65	AlignBucket: a tool to speed up "all-against-all" protein sequence alignments optimizing length constraints. <i>Bioinformatics</i> , 2015, 31, 3841-3843.	1.8	3
66	TPpred3 detects and discriminates mitochondrial and chloroplastic targeting peptides in eukaryotic proteins. <i>Bioinformatics</i> , 2015, 31, 3269-3275.	1.8	46
67	INPS: predicting the impact of non-synonymous variations on protein stability from sequence. <i>Bioinformatics</i> , 2015, 31, 2816-2821.	1.8	109
68	Modulating the thermostability of Endoglucanase I from <i>Trichoderma reesei</i> using computational approaches. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 127-135.	1.0	40
69	A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. <i>Plant Biotechnology Journal</i> , 2015, 13, 648-663.	4.1	386
70	Computer-Based Prediction of Mitochondria-Targeting Peptides. <i>Methods in Molecular Biology</i> , 2015, 1264, 305-320.	0.4	6
71	Protein Sequence Annotation by Means of Community Detection. <i>Current Bioinformatics</i> , 2015, 10, 139-143.	0.7	0
72	Searching for signatures of cold adaptations in modern and archaic humans: hints from the brown adipose tissue genes. <i>Heredity</i> , 2014, 113, 259-267.	1.2	32

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73	High-throughput SNP discovery in the rabbit ( <i>Oryctolagus cuniculus</i> ) genome by next-generation semiconductor-based sequencing. <i>Animal Genetics</i> , 2014, 45, 304-307.	0.6	14
74	TPpred2: improving the prediction of mitochondrial targeting peptide cleavage sites by exploiting sequence motifs. <i>Bioinformatics</i> , 2014, 30, 2973-2974.	1.8	34
75	Characteristics of the somatic hypermutation in the <i>Camelus dromedarius</i> T cell receptor gamma (TRG) and delta (TRD) variable domains. <i>Developmental and Comparative Immunology</i> , 2014, 46, 300-313.	1.0	48
76	Analysis of all subunits, SDHA, SDHB, SDHC, SDHD, of the succinate dehydrogenase complex in KIT/PDGFR wild-type GIST. <i>European Journal of Human Genetics</i> , 2014, 22, 32-39.	1.4	90
77	How to inherit statistically validated annotation within BAR+ protein clusters. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	8
78	Prediction of disulfide connectivity in proteins with machine-learning methods and correlated mutations. <i>BMC Bioinformatics</i> , 2013, 14, S10.	1.2	10
79	WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. <i>BMC Genomics</i> , 2013, 14, S6.	1.2	248
80	The side chain of glutamine 13 is the acyl-donor amino acid modified by type 2 transglutaminase in subunit T of the native rabbit skeletal muscle troponin complex. <i>Amino Acids</i> , 2013, 44, 227-234.	1.2	1
81	Expression of different forms of transglutaminases by immature cells of <i>Helianthus tuberosus</i> sprout apices. <i>Amino Acids</i> , 2013, 44, 271-283.	1.2	14
82	BCov: a method for predicting $\beta$ -sheet topology using sparse inverse covariance estimation and integer programming. <i>Bioinformatics</i> , 2013, 29, 3151-3157.	1.8	17
83	Role of the C-terminus of <i>Pleurotus eryngii</i> Ery4 laccase in determining enzyme structure, catalytic properties and stability. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 1-13.	1.0	25
84	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
85	Expression of IGF-1 receptor in KIT/PDGF receptor wild-type gastrointestinal stromal tumors with succinate dehydrogenase complex dysfunction. <i>Future Oncology</i> , 2013, 9, 121-126.	1.1	30
86	Haplotype of Single Nucleotide Polymorphisms in Exon 6 of the MZF-1 Gene and Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2013, 34, 439-447.	1.2	5
87	The prediction of organelle-targeting peptides in eukaryotic proteins with Grammatical-Restrained Hidden Conditional Random Fields. <i>Bioinformatics</i> , 2013, 29, 981-988.	1.8	17
88	Extended and Robust Protein Sequence Annotation over Conservative Nonhierarchical Clusters. <i>ACM Journal on Emerging Technologies in Computing Systems</i> , 2013, 9, 1-8.	1.8	1
89	BETAWARE: a machine-learning tool to detect and predict transmembrane beta-barrel proteins in prokaryotes. <i>Bioinformatics</i> , 2013, 29, 504-505.	1.8	41
90	Frataxin mRNA Isoforms in FRDA Patients and Normal Subjects: Effect of Tocotrienol Supplementation. <i>BioMed Research International</i> , 2013, 2013, 1-9.	0.9	15

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91	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat065-bat065.	1.4	4
92	CBFA2T3-GLIS2 fusion transcript is a novel common feature in pediatric, cytogenetically normal AML, not restricted to FAB M7 subtype. Blood, 2013, 121, 3469-3472.	0.6	119
93	MIMO: an efficient tool for molecular interaction maps overlap. BMC Bioinformatics, 2013, 14, 159.	1.2	16
94	Mapping and Annotating Obesity-Related Genes in Pig And Human Genomes. Protein and Peptide Letters, 2013, 21, 840-846.	0.4	2
95	Generation of diversity by somatic mutation in the <i>Ctamelus dromedarius</i> T cell receptor gamma variable domains. European Journal of Immunology, 2012, 42, 3416-3428.	1.6	27
96	Exploring copy number variation in the rabbit ( <i>Oryctolagus cuniculus</i> ) genome by array comparative genome hybridization. Genomics, 2012, 100, 245-251.	1.3	19
97	A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. BMC Genomics, 2012, 13, 583.	1.2	80
98	The human "magnesome": detecting magnesium binding sites on human proteins. BMC Bioinformatics, 2012, 13, S10.	1.2	26
99	Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian Large White pigs using a selective genotyping approach. Journal of Animal Science, 2012, 90, 2450-2464.	0.2	65
100	On the effect of protein conformation diversity in discriminating among neutral and disease related single amino acid substitutions. BMC Genomics, 2012, 13, S5.	1.2	35
101	Predicting cancer-associated germline variations in proteins. BMC Genomics, 2012, 13, S8.	1.2	28
102	Machine-Learning Methods to Predict Protein Interaction Sites in Folded Proteins. Lecture Notes in Computer Science, 2012, , 127-135.	1.0	2
103	Is There an Optimal Substitution Matrix for Contact Prediction with Correlated Mutations?. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1017-1028.	1.9	7
104	SDHA Loss-of-Function Mutations in KIT-PDGFR Wild-Type Gastrointestinal Stromal Tumors Identified by Massively Parallel Sequencing. Journal of the National Cancer Institute, 2011, 103, 983-987.	3.0	137
105	EX-HOM (EXome HOMozygosity): A Proof of Principle. Human Heredity, 2011, 72, 45-53.	0.4	27
106	A novel subfamily of mitochondrial dicarboxylate carriers from <i>Drosophila melanogaster</i> : Biochemical and computational studies. Biochimica Et Biophysica Acta - Bioenergetics, 2011, 1807, 251-261.	0.5	18
107	Blurring contact maps of thousands of proteins: what we can learn by reconstructing 3D structure. BioData Mining, 2011, 4, 1.	2.2	46
108	Correlating disease-related mutations to their effect on protein stability: A large-scale analysis of the human proteome. Human Mutation, 2011, 32, 1161-1170.	1.1	89

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109	Improving the detection of transmembrane $\beta$ -barrel chains with N-to-1 extreme learning machines. <i>Bioinformatics</i> , 2011, 27, 3123-3128.	1.8	21
110	Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization. <i>Bioinformatics</i> , 2011, 27, 2224-2230.	1.8	37
111	MemLoc: predicting subcellular localization of membrane proteins in eukaryotes. <i>Bioinformatics</i> , 2011, 27, 1224-1230.	1.8	49
112	MemPype: a pipeline for the annotation of eukaryotic membrane proteins. <i>Nucleic Acids Research</i> , 2011, 39, W375-W380.	6.5	28
113	BAR-PLUS: the Bologna Annotation Resource Plus for functional and structural annotation of protein sequences. <i>Nucleic Acids Research</i> , 2011, 39, W197-W202.	6.5	22
114	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, D80-D85.	6.5	38
115	Divide and Conquer Strategies for Protein Structure Prediction. , 2011, , 23-46.		3
116	Prediction of the Bonding State of Cysteine Residues in Proteins with Machine-Learning Methods. <i>Lecture Notes in Computer Science</i> , 2011, , 98-111.	1.0	3
117	The Prediction of Protein-Protein Interacting Sites in Genome-Wide Protein Interaction Networks: The Test Case of the Human Cell Cycle. <i>Current Protein and Peptide Science</i> , 2010, 11, 601-608.	0.7	10
118	Thermodynamics of binding of regulatory ligands to tissue transglutaminase. <i>Amino Acids</i> , 2010, 39, 297-304.	1.2	16
119	An initial comparative map of copy number variations in the goat ( <i>Capra hircus</i> ) genome. <i>BMC Genomics</i> , 2010, 11, 639.	1.2	120
120	Allergenicity of different apple cultivars assessed by means of skin prick test and sensitisation to recombinant allergens Mal d 1 and Mal d 3 in a group of Italian apple-allergic patients. <i>International Journal of Food Science and Technology</i> , 2010, 45, 1517-1523.	1.3	12
121	Fast overlapping of protein contact maps by alignment of eigenvectors. <i>Bioinformatics</i> , 2010, 26, 2250-2258.	1.8	39
122	Topology prediction of membrane proteins: how distantly related homologs come into play. , 2010, , 61-82.		1
123	Improving Coiled-Coil Prediction with Evolutionary Information. <i>Lecture Notes in Computer Science</i> , 2010, , 20-32.	1.0	1
124	On the Reconstruction of Three-dimensional Protein Structures from Contact Maps. <i>Algorithms</i> , 2009, 2, 76-92.	1.2	4
125	CCHMM_PROF: a HMM-based coiled-coil predictor with evolutionary information. <i>Bioinformatics</i> , 2009, 25, 2757-2763.	1.8	46
126	A graph theoretic approach to protein structure selection. <i>Artificial Intelligence in Medicine</i> , 2009, 45, 229-237.	3.8	6



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127	Functional annotations improve the predictive score of human disease-related mutations in proteins. <i>Human Mutation</i> , 2009, 30, 1237-1244.	1.1	552
128	Plant and animal transglutaminases: do similar functions imply similar structures?. <i>Amino Acids</i> , 2009, 36, 643-657.	1.2	51
129	The Bologna Annotation Resource: a Non Hierarchical Method for the Functional and Structural Annotation of Protein Sequences Relying on a Comparative Large-Scale Genome Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 4362-4371.	1.8	9
130	Grammatical-Restrained Hidden Conditional Random Fields for Bioinformatics applications. <i>Algorithms for Molecular Biology</i> , 2009, 4, 13.	0.3	17
131	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206.	13.9	53
132	The FAGenomicH project: towards a whole candidate gene approach to identify markers associated with fatness and production traits in pigs and investigate the pig as a model for human obesity. <i>Italian Journal of Animal Science</i> , 2009, 8, 87-89.	0.8	0
133	Prediction of Protein-Protein Interacting Sites: How to Bridge Molecular Events to Large Scale Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2009, , 1-17.	1.0	2
134	On the Upper Bound of the Prediction Accuracy of Residue Contacts in Proteins with Correlated Mutations: The Case Study of the Similarity Matrices. <i>Lecture Notes in Computer Science</i> , 2009, , 62-72.	1.0	0
135	A New Protein Representation Based on Fragment Contacts: Towards an Improvement of Contact Maps Predictions. <i>Lecture Notes in Computer Science</i> , 2009, , 210-221.	1.0	1
136	A combined approach of mass spectrometry, molecular modeling, and site-directed mutagenesis highlights key structural features responsible for the thermostability of <i>Sulfolobus solfataricus</i> carboxypeptidase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1843-1852.	1.5	6
137	Use of estimated evolutionary strength at the codon level improves the prediction of disease-related protein mutations in humans. <i>Human Mutation</i> , 2008, 29, 198-204.	1.1	37
138	The Pros and Cons of Predicting Protein Contact Maps. , 2008, 413, 199-217.		18
139	Prediction of the disulfide-bonding state of cysteines in proteins at 88% accuracy. <i>Protein Science</i> , 2008, 11, 2735-2739.	3.1	30
140	PredGPI: a GPI-anchor predictor. <i>BMC Bioinformatics</i> , 2008, 9, 392.	1.2	553
141	A three-state prediction of single point mutations on protein stability changes. <i>BMC Bioinformatics</i> , 2008, 9, S6.	1.2	267
142	Reconstruction of 3D Structures From Protein Contact Maps. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 357-367.	1.9	69
143	FT-COMAR: fault tolerant three-dimensional structure reconstruction from protein contact maps. <i>Bioinformatics</i> , 2008, 24, 1313-1315.	1.8	52
144	Predicting protein thermostability changes from sequence upon multiple mutations. <i>Bioinformatics</i> , 2008, 24, i190-i195.	1.8	41

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145	Progress and challenges in predicting protein-protein interaction sites. <i>Briefings in Bioinformatics</i> , 2008, 10, 233-246.	3.2	145
146	The prediction of protein subcellular localization from sequence: a shortcut to functional genome annotation. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2008, 7, 63-73.	3.8	55
147	Thinking the Impossible: How to Solve the Protein Folding Problem With and Without Homologous Structures and More. , 2007, 350, 305-320.		9
148	eSLDB: eukaryotic subcellular localization database. <i>Nucleic Acids Research</i> , 2007, 35, D208-D212.	6.5	64
149	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	3.3	206
150	Molecular mechanism of thioredoxin regulation in photosynthetic A2B2-glyceraldehyde-3-phosphate dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11109-11114.	3.3	76
151	Guest Editor's Introduction to the Special Section on Computational Biology and Bioinformatics (WABI) – Part 2. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 3-3.	1.9	2
152	Cloning, functional identification and structural modelling of <i>Vitis vinifera</i> S-adenosylmethionine decarboxylase. <i>Journal of Plant Physiology</i> , 2007, 164, 1208-1219.	1.6	8
153	Robust Determinants of Thermostability Highlighted by a Codon Frequency Index Capable of Discriminating Thermophilic from Mesophilic Genomes. <i>Journal of Proteome Research</i> , 2007, 6, 2502-2508.	1.8	7
154	Bioinformatics in Italy: BITS2006, the third annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2007, 8, .	1.2	0
155	A computational approach for detecting peptidases and their specific inhibitors at the genome level. <i>BMC Bioinformatics</i> , 2007, 8, S3.	1.2	5
156	Prediction of Structurally-Determined Coiled-Coil Domains with Hidden Markov Models. , 2007, , 292-302.		13
157	Reconstruction of 3D Structures from Protein Contact Maps. <i>Lecture Notes in Computer Science</i> , 2007, , 578-589.	1.0	11
158	Fault Tolerance for Large Scale Protein 3D Reconstruction from Contact Maps. <i>Lecture Notes in Computer Science</i> , 2007, , 25-37.	1.0	6
159	High Throughput Protein Similarity Searches in the LIBI Grid Problem Solving Environment. <i>Lecture Notes in Computer Science</i> , 2007, , 414-423.	1.0	1
160	New <i>Escherichia coli</i> outer membrane proteins identified through prediction and experimental verification. <i>Protein Science</i> , 2006, 15, 884-889.	3.1	43
161	Machine learning and the prediction of protein structure: the state of the art. , 2006, , 359-370.		0
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