

# Castrense Savojardo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5917192/publications.pdf>

Version: 2024-02-01

56  
papers

1,836  
citations

394421

19  
h-index

302126

39  
g-index

58  
all docs

58  
docs citations

58  
times ranked

2467  
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine learning solutions for predicting protein-protein interactions. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	14.6	19
2	Cloning the barley necrotic disease lesion mimic mutant using complementation by sequencing. <i>Plant Genome</i> , 2022, , e20187.	2.8	0
3	A Glance into MTHFR Deficiency at a Molecular Level. <i>International Journal of Molecular Sciences</i> , 2022, 23, 167.	4.1	2
4	Turning Failures into Applications: The Problem of Protein $\beta$ -G Prediction. <i>Methods in Molecular Biology</i> , 2022, 2449, 169-185.	0.9	5
5	Molecular Effects of Mutations in Human Genetic Diseases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6408.	4.1	0
6	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.	6.5	13
7	Computer-Aided Prediction of Protein Mitochondrial Localization. <i>Methods in Molecular Biology</i> , 2021, 2275, 433-452.	0.9	2
8	Huntingtin: A Protein with a Peculiar Solvent Accessible Surface. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2878.	4.1	3
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.	4.2	13
10	BENZ WS: the Bologna ENZYme Web Server for four-level EC number annotation. <i>Nucleic Acids Research</i> , 2021, 49, W60-W66.	14.5	7
11	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.	3.5	5
12	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021, 18, 1122-1127.	19.0	105
13	DeepREx-WS: A web server for characterising protein-solvent interaction starting from sequence. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5791-5799.	4.1	4
14	Comparative genomics of tadpole shrimps (Crustacea, Branchiopoda, Notostraca): Dynamic genome evolution against the backdrop of morphological stasis. <i>Genomics</i> , 2021, 113, 4163-4172.	2.9	7
15	DeepMito: accurate prediction of protein sub-mitochondrial localization using convolutional neural networks. <i>Bioinformatics</i> , 2020, 36, 56-64.	4.1	61
16	Protein-Protein Interaction Methods and Protein Phase Separation. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 89-112.	6.5	18
17	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.	3.2	3
18	Large-scale prediction and analysis of protein sub-mitochondrial localization with DeepMito. <i>BMC Bioinformatics</i> , 2020, 21, 266.	2.6	6

#	ARTICLE	IF	CITATIONS
19	Solvent Accessibility of Residues Undergoing Pathogenic Variations in Humans: From Protein Structures to Protein Sequences. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 626363.	3.5	58
20	Transmembrane Domain Prediction. , 2019, , 46-52.		0
21	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019, 40, 1463-1473.	2.5	8
22	Assessing predictions of the impact of variants on splicing in CAGI5. <i>Human Mutation</i> , 2019, 40, 1215-1224.	2.5	18
23	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. <i>Human Mutation</i> , 2019, 40, 1546-1556.	2.5	19
24	Assessing computational predictions of the phenotypic effect of cystathionine- $\beta$ -synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	2.5	5
25	Assessment of predicted enzymatic activity of $\pm$ N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	2.5	10
26	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
27	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. <i>Human Mutation</i> , 2019, 40, 1392-1399.	2.5	16
28	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
29	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. <i>Human Mutation</i> , 2019, 40, 1495-1506.	2.5	16
30	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
31	Are machine learning based methods suited to address complex biological problems? Lessons from CAGI-5 challenges. <i>Human Mutation</i> , 2019, 40, 1455-1462.	2.5	6
32	Functional and Structural Features of Disease-Related Protein Variants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1530.	4.1	15
33	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.	8.8	261
34	On the biases in predictions of protein stability changes upon variations: the INPS test case. <i>Bioinformatics</i> , 2019, 35, 2525-2527.	4.1	32
35	Draft genomes and genomic divergence of two <i>Lepidurus</i> tadpole shrimp species (Crustacea, Tj ETQq1 1 0.784314 rgBT /Over to	4.8	14
36	DeepSig: deep learning improves signal peptide detection in proteins. <i>Bioinformatics</i> , 2018, 34, 1690-1696.	4.1	92

#	ARTICLE	IF	CITATIONS
37	BUSCA: an integrative web server to predict subcellular localization of proteins. <i>Nucleic Acids Research</i> , 2018, 46, W459-W466.	14.5	270
38	SChloro: directing <i>Viridiplantae</i> proteins to six chloroplastic sub-compartments. <i>Bioinformatics</i> , 2017, 33, 347-353.	4.1	21
39	ISPRED4: interaction sites PREDiction in protein structures with a refining grammar model. <i>Bioinformatics</i> , 2017, 33, 1656-1663.	4.1	28
40	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. <i>BMC Genomics</i> , 2017, 18, 554.	2.8	52
41	INPS-MD: a web server to predict stability of protein variants from sequence and structure. <i>Bioinformatics</i> , 2016, 32, 2542-2544.	4.1	170
42	Large scale analysis of protein stability in OMIM disease related human protein variants. <i>BMC Genomics</i> , 2016, 17, 397.	2.8	37
43	TPpred3 detects and discriminates mitochondrial and chloroplastic targeting peptides in eukaryotic proteins. <i>Bioinformatics</i> , 2015, 31, 3269-3275.	4.1	46
44	INPS: predicting the impact of non-synonymous variations on protein stability from sequence. <i>Bioinformatics</i> , 2015, 31, 2816-2821.	4.1	109
45	Computer-Based Prediction of Mitochondria-Targeting Peptides. <i>Methods in Molecular Biology</i> , 2015, 1264, 305-320.	0.9	6
46	TPpred2: improving the prediction of mitochondrial targeting peptide cleavage sites by exploiting sequence motifs. <i>Bioinformatics</i> , 2014, 30, 2973-2974.	4.1	34
47	Prediction of disulfide connectivity in proteins with machine-learning methods and correlated mutations. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	10
48	BCov: a method for predicting $\beta$ -sheet topology using sparse inverse covariance estimation and integer programming. <i>Bioinformatics</i> , 2013, 29, 3151-3157.	4.1	17
49	The prediction of organelle-targeting peptides in eukaryotic proteins with Grammatical-Restrained Hidden Conditional Random Fields. <i>Bioinformatics</i> , 2013, 29, 981-988.	4.1	17
50	BETAWARE: a machine-learning tool to detect and predict transmembrane beta-barrel proteins in prokaryotes. <i>Bioinformatics</i> , 2013, 29, 504-505.	4.1	41
51	Machine-Learning Methods to Predict Protein Interaction Sites in Folded Proteins. <i>Lecture Notes in Computer Science</i> , 2012, , 127-135.	1.3	2
52	Improving the detection of transmembrane $\beta$ -barrel chains with N-to-1 extreme learning machines. <i>Bioinformatics</i> , 2011, 27, 3123-3128.	4.1	21
53	Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization. <i>Bioinformatics</i> , 2011, 27, 2224-2230.	4.1	37
54	MemPype: a pipeline for the annotation of eukaryotic membrane proteins. <i>Nucleic Acids Research</i> , 2011, 39, W375-W380.	14.5	28

#	ARTICLE	IF	CITATIONS
55	Prediction of the Bonding State of Cysteine Residues in Proteins with Machine-Learning Methods. Lecture Notes in Computer Science, 2011, , 98-111.	1.3	3
56	Grammatical-Restrained Hidden Conditional Random Fields for Bioinformatics applications. Algorithms for Molecular Biology, 2009, 4, 13.	1.2	17