

Curriculum vitae

PERSONAL INFORMATION

Pier Luigi Martelli



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Sex Male | Date of birth 07/01/1972 | Nationality Italian

EDUCATION AND TRAINING

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|-----------|---|-------------|
| 1998–2001 | PhD in Physics
University of Bologna, Bologna (Italy)
Thesis title: Hybrid systems of HMMs and Neural Networks for protein structure prediction. | EQF level 8 |
| 1991–1997 | Master Degree in Physics
University of Bologna, Bologna (Italy)
Thesis title: Prediction of Foldons in proteins | EQF level 7 |

WORK EXPERIENCE

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|--------------------|---|
| 31/03/2017–Present | Licensed for Full Professorship in Biochemistry (BIO/10) from the ASN national committee |
| 23/05/2016–Present | Director of the International 2-year Master (Laurea Magistrale Internazionale) in Bioinformatics
University of Bologna (Italy) |
| 01/02/2015–Present | Associate Professor in Biochemistry (BIO/10)
University of Bologna (Italy)
Research activity in Computational Biology and Bioinformatics at the Biocomputing Group of the University of Bologna. |

ADDITIONAL INFORMATION

Insitutional appointments

ELIXIR-IIB

Italian Node of the ELIXIR European Infrastructure for Life Science Information

- Since 2017: National contact person for the "Interoperability" Platform
- April 2018-January 2019: Local technical coordinator for the University of Bologna node

SIB

Italian Society of Biochemistry and Molecular Biology

- Since 2015: Elected coordinator of the group "Computational and Systems Biology" .

UNIVERSITY OF BOLOGNA

- Since 2018: Member of the Third-Mission commission (in representation of the Biological area).
- Since 2018: Member of the Research commission of the Department FaBIT.
- 2014-2017: Member of the panel "Biological sciences" of the Commission for the evaluation of the

research activity (VRA).

- 2014-2017: Member of the Research commission of the Department BiGeA.

Previous experiences

- 01/10/2006–31/01/2015: Assistant professor in Biochemistry (BIO/10) University of Bologna, Bologna (Italy)
- 01/10/2005–30/09/2006: Contract Researcher (Young Researcher contract) for the FIRB2003 Project “LIBI: International Laboratory of Bioinformatics”. University of Bologna, Bologna (Italy)
- 01/08/2003–31/07/2006: Contract Researcher (Assegno di Ricerca) for the FIRB2001 Project “Bioinformatics for Genomics and Proteomics”, University of Bologna, Bologna (Italy)
- 02/05/2002–30/04/2006: Fellow Researcher. Fellowship from the CNR Target Project on Molecular Genetics National Council for Research (CNR), Roma (Italy)
- 01/03/2001–28/02/2002: Fellow Researcher INBB Consortium- Istituto Nazionale di Biostrutture e Biosistemi, Roma (Italy)

Research Activity

Protein folding and theoretical molecular Biophysics

Since 1996, PLM has been involved in theoretical investigations on problems related to the protein folding by means of computational tools, mainly based on neural networks and genetic algorithms. In particular, the analysis of the predictive properties of feed-forward neural networks enabled the definition of an entropic criterion for selecting segment in alpha-helical structure that are likely to be the nucleation sites for the protein folding.

Development of tools for the prediction of protein structure and function

Since 1997 PLM is involved in the design and development of tools based on machine learning techniques for the prediction of structural and functional features of proteins ,starting from their residue sequences. In particular, PLM designed and implemented hybrid systems of neural networks (NN) and hidden Markov models (HMM) able also to elaborate the information contained in sequence profiles out of multiple sequence alignments. These tools have been adopted for developing predictors for -) the topology of membrane proteins, both with alpha-helical and beta-barrel structures; -) the bonding state of cysteine residues in proteins; -) the presence and localization of GPI-anchors; -) the presence and localization of target peptides and signal peptides.

He contributed to the development of the Bologna Annotation Resource (BAR)

Prediction of the relationship between SNPs and diseases

PLM collaborated in the implementation of SNPs&GO , a tool based on SVM for predicting whether a residue mutation is conducive to human disease. For the first time, this tool exploits the information contained in functional annotations encoded with the Gene Ontology terms. Several independent evaluations assessed that SNPs&GO is one of the best performing tools, among those available for the specific task at hand.

Prediction of the subcellular localization of eukaryotic proteins

PLM collaborated in the implementation of BaCellLo, a decision tree of support vector machines (SVM) able to discriminate up to four different localization in animals and fungi and up to five localizations in plants. BaCellLo represents the state of the art in the prediction of subcellular localization of eukaryotic proteins.

NGS data analysis in a Systems Biology context

PLM participated in different projects involving the analysis of NGS data on DNA and RNA of different species (human, *Triticum aestivum*, pig). In particular, he applied his expertise in structural and functional annotation of gene products and in characterization of the effect of variations.

He also participated to the development of NET-GE, a tool for functional enrichment, useful to target pathways shared by groups of genes (carrying variations or differentially expressed)

Protein modeling and investigations on the structure-function relationship

PLM studies the structure-function relationship using tools for protein modelling, molecular dynamics simulations, and molecular docking. In collaboration with experimental groups PLM achieved the following results: -) the computation of the three-dimensional models of proteins from thermophilic

organisms, in order to elucidate the features conducive to thermostability; -) the modelling and dynamic simulations of enzymes immobilized in membranes in bioreactors, in order to study the effects of immobilization on the structural stability; -) the simulation of the destabilizing effect of the double mutation at positions 7 and 14 on the sperm whale myoglobin; -) the simulation of the mobility of tryptophan residues in the beta-galactosidase from *Sulfolobus solfataricus* and the correlation with its fluorescence emission properties; -) the discovery and characterization of a fusogenic peptide in the glycoprotein H of *Herpes simplex virus*; -) the modelling of the C-terminal segment of the subunit B of the glyceraldehyde-3-phosphate dehydrogenase from *Spinacea olearia*; this peptide is particularly important for the regulation of the enzyme in relation to dark/light metabolisms.

Teaching activities

- 2006-current: Teaching activity at the International Master Degree in Bioinformatics of the University of Bologna (courses: Bio-medical databases, Elements of Computational Biology, Models of Biological Systems, Systems and In Silico Biology, Laboratory of Bioinformatics, Programming for Bioinformatics)
- June 2013: Lectures on "NGS Data Analysis" at the training school of PON project "Applicazione di biotecnologie molecolari e microrganismi protecnologici per la caratterizzazione e valorizzazione delle filiere lattiero-casearia e prodotti da forno di produzioni tipiche." (S. Margherita al Belice, AG)
- October 2012: Lectures on "Programming in Perl for NGS data analysis". RGB NET (Cost Action) Training School on "Rabbit and Pig Genome analysis" (Norwich, UK)
- January 2012: Special course in "Basic and Avdanced Bioinformatics" at Sultan Qabus University (Muscat, Oman)
- Academic Years 2004-2008: Special Course on "Probabilistic models for biological sequences" at Complutense University in Madrid (Spain), Master in Bioinformatics.
- Academic Years 2002-2006: Course on "Fisica Computazionale Applicata alle Macromolecole" at University of Trento, Degree in Biomedical Physics and Technology
- April 2006: Assistant to the course "Pills of Bioinformatics". Universidad Tecnica Particular de Loja (Ecuador)
- April 2003: Special Course on "HMMs, Basics and applications to molecular biology" at Bioinformatics Group of Sanofi-Synthélabo (Labège, Toulouse, Francia)
- Academic Year 2000-2001: Course module "Modellistica Molecolare" at University of Ferrara, Degree in Biology.

Editorial activity

Since 2017: member of the Editorial Board of "Computation"
 Since 2019: Associate Editor of "BMC Bioinformatics"

Reviewer for many Journals, among which: Bioinformatics, PLoS Computational Biology, PLoS One, Nuclaic Acids Research, Journal of Molecular Biology, Human Mutation, BMC Bioinformatics, BMC Genomics, BMC Systems Biology, Amino acids, Proteins, BioSystems, Journal of Genetics

Present and Past Collaborations

- University of Copenhagen (Denmark): Prof. Anders Krogh
- BIOSAPIENS EU Consortium
- Sabanci University and Acibadem University (Turkey): Prof. Ugur Sezerman
- CAS-MPG Partner Institute for Computational Biology in Shanghai (China): Dr. Christine Nardini
- CHIRON Vaccines SpA: Dr. Giulio Ratti
- CNR Institute for Protein Biochemistry and Enzimology in Naples: Prof. Mosè Rossi
- CNR Insitute for Biomembranes and Bioenergetics in Bari: Prof. Graziano Pesole
- Università di Padova: Prof. Piero Fariselli
- Second University of Napoli: Prof. Gustavo Damiano Mita, Prof. Gaetano Irace
- University of Milano-Bicocca: Prof. Paolo Tortora
- University of Rome "La Sapienza": Prof. Anna Tramontano
- University of Ferrara: Prof. Carlo Bergamini

- Quilmes University (Argentina): prof. Gustavo Parisi

Honours and awards

The paper: **Martelli PL, Fariselli P, Krogh A and Casadio R (2002) A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins- *Bioinformatics* 18: S46-S53** presented at the 10th International Conference on "Intelligent Systems for Molecular Biology" (ISMB02), Edmonton Canada, 3-7/8/2002 won the SGI best paper award

Main Grants and Projects

- Since Nov 2018: Coordinator of a WP of the H2020 project "CIRCLES: Controlling mlcRobiomes CircuLations for bEttEr food Systems".
- 2018-2021: Responsible of the PhD project "Metodi innovativi per l'analisi di Big Data Omici" funded by the Emilia-Romagna Region (POR FSE 2014-20)
- 2011-2015: coordinator of the Bologna University Unit for the PRIN Project "Integration of experimental and computational approaches for the study of human pathologies".

Organization activities

- Workshop of the Group "Computational and Systems Biology", Italian Society of Biochemistry and Molecular Biology: Bologna, Italy- 9 July 2019. Chair
- Short course on "Protein-protein interaction", Groups "Proteine" and "Computational and Systems Biology", Italian Society of Biochemistry and Molecular Biology: Bologna, Italy- 8 July 2019. Chair
- FEBS Workshop 2018 - The molecular basis of diseases: Can we infer phenotypes from protein variant analysis? Bologna 23-25 May 2018- Co-chair
- Bologna Winter Schools in Bioinformatics: from 1999 to 2018 (19 editions: <http://biocomp.unibo.it/bws.html>). Organizing committee-
- Workshop of the Group "Computational and Systems Biology", Italian Society of Biochemistry and Molecular Biology: Accademia delle Scienze, Bologna, Italy- 28 June 2017. Chair
- Workshop (Italian Society of Biochemistry-Group of Computational and Systems Biology/SYSBIO): "Dalle molecole alle funzioni biologiche complesse: Il metodo computazionale". Accademia delle Scienze, Bologna, Italy- 12 July 2016. Chair
- Proteine 2016 Congress. Dissecting Biological Complexity at the Molecular Level. Bologna, Italy- 30 March - 1 April 2016. Organizing Committee

Bibliometry

SCOPUS (July 2019):

Documents: 115, Total number of citations: 3084, h-index: 31

Publications

* Corresponding author

- Zhang J, Kinch LN, Cong Q, Katsonis P, Lichtarge O, Savojardo C, Babbi G, Martelli PL, Capriotti E, Casadio R, Garg A, Pal D, Weile J, Sun S, Verby M, Roth F.P, Grishin N.V. Assessing predictions on fitness effects of missense variants in calmodulin. (2019) Human Mutation. In press
- Monzon AM, Carraro M, Chiricosta L, Reggiani F, Han J, Ozturk K, Wang Y, Miller M, Bromberg Y, Capriotti E, Savojardo C, Babbi G, Martelli PL, Casadio R, Katsonis P, Lichtarge O, Carter H, Kousi M, Katsanis N, Andreoletti G, Mout J, Brenner SE, Ferrari C, Leonardi E, Tosatto SCE. Performance of computational methods for the evaluation of Pericentriolar Material 1 missense variants in CAGI-5 (2019) Human Mutation. In press
- Voskanian A, Katsonis P, Lichtarge O, Pejaver V, Radivojac P, Mooney SD, Capriotti E, Bromberg Y, Wang Y, Miller M, Martelli PL, Savojardo C, Babbi G, Casadio R, Cao Y, Sun Y, Shen Y, Garg A, Pal D, Yu Y, Huff CD, Tavtigian SV, Young E, Neuhausen SL, Ziv E, Pal LR, Andreoletti G, Brenner S, Kann MG. Assessing the performance of in-silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer (2019) Human Mutation. In press
- Savojardo C, Bruciaferri N, Tartari G, Martelli PL*, Casadio R. DeepMito: accurate prediction of protein submitochondrial localization using convolutional neural networks (2019) Bioinformatics. In press
- Savojardo C, Petrosino M, Babbi G, Bovo S, Corbi-Verge C, Casadio R, Fariselli P, Folkman L,

- Garg A, Karimi M, Katsonis P, Kim P.M, Lichtarge O, Martelli PL, Pasquo A, Pal D, Shen Y, Strokach A.V, Turina P, Zhou Y, Andreoletti G, Brenner S, Chiaraluce R, Consalvi V, Capriotti E. Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge (2019) *Human Mutation*. In press
- Pejaver V, Babbi G, Casadio R, Folkman L, Katsonis P, Kundu K, Lichtarge O, Martelli PL, Miller M, Moulton J, Pal LR, Savojardo C, Yin Y, Zhou Y, Radivojac P, Bromberg Y. Assessment of methods for predicting the effects of PTEN and TPMT protein variants (2019) *Human Mutation*. In press
 - McInnes G, Daneshjou R, Katsonis P, Lichtarge O, Srinivasan RG, Rana S, Radivojac P, Mooney SD, Pagel KA, Stamboulian M, Jiang Y, Capriotti E, Wang Y, Bromberg Y, Bovo S, Savojardo C, Martelli PL, Casadio R, Pal LR, Moulton J, Brenner S, Altman R. Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges (2019) *Human Mutation*. In press
 - Savojardo C, Babbi G, Bovo S, Capriotti E, Martelli PL*, Casadio R. Are machine learning based methods suited to address complex biological problems? Lessons from CAGI-5 challenges (2019) *Human Mutation*. In press
 - Vendramin V, Ormanbekova D, Scalabrin S, Scaglione D, Maccaferri M, Martelli P, Salvi S, Jurman I, Casadio R, Cattonaro F, Tuberosa R, Massi A, Morgante M. Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm (2019) *BMC Genomics* 20(1):278.
 - Savojardo C, Babbi G, Martelli PL*, Casadio R. Functional and Structural Features of Disease-Related Protein Variants (2019) *International Journal of Molecular Sciences* 20(7). pii: E1530
 - Nannini M, Tarantino G, Indio V, Ravegnini G, Astolfi A, Urbini M, De Leo A, Santini D, Ceccarelli C, Gruppioni E, Altimari A, Castellucci P, Fanti S, Di Scioscio V, Saponara M, Gatto L, Pession A, Martelli PL, Casadio R, Pantaleo MA. Molecular modelling evaluation of exon 18 His845_Asn848delinsPro PDGFR α mutation in a metastatic GIST patient responding to imatinib. (2019) *Scientific Reports* 9(1):2172.
 - Montanucci L, Savojardo C, Martelli PL, Casadio R, Fariselli P. On the biases in predictions of protein stability changes upon variations: the INPS test case (2019) *Bioinformatics*. In press
 - Montanucci L, Martelli PL, Ben-Tal N, Fariselli P. A natural upper bound to the accuracy of predicting protein stability changes upon mutations (2019) *Bioinformatics* 35(9):1513-1517.
 - 14: Savojardo C, Luchetti A, Martelli PL, Casadio R, Mantovani B. Draft genomes and genomic divergence of two *Lepidurus* tadpole shrimp species (Crustacea, Branchiopoda, Notostraca) (2019) *Molecular Ecology Resources* 19(1):235-244.
 - Savojardo C, Martelli PL*, Fariselli P, Profiti G, Casadio R. BUSCA: an integrative web server to predict subcellular localization of proteins. (2018) *Nucleic Acids Res* 46(W1):W459-W466.
 - Savojardo C, Martelli PL*, Fariselli P, Casadio R. DeepSig: deep learning improves signal peptide detection in proteins. (2018) *Bioinformatics* 34:1690-1696.
 - Babbi G, Martelli PL*, Profiti G, Bovo S, Savojardo C, Casadio R. eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes (2017) *BMC Genomics* 18(Suppl 5):554.
 - Profiti G, Martelli PL*, Casadio R. The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation (2017) *Nucleic Acids Res.* 45(W1):W285-W290.
 - Carraro M, Minervini G, Giollo M, Bromberg Y, Capriotti E, Casadio R, Dunbrack R, Elefanti L, Fariselli P, Ferrari C, Gough J, Katsonis P, Leonardi E, Lichtarge O, Menin C, Martelli PL, Niroula A, Pal LR, Repo S, Scaini MC, Vihinen M, Wei Q, Xu Q, Yang Y, Yin Y, Zaucha J, Zhao H, Zhou Y, Brenner SE, Moulton J, Tosatto SCE. Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI (2017) *Hum Mutat.* 38:1042-1050.
 - Xu Q, Tang Q, Katsonis P, Lichtarge O, Jones D, Bovo S, Babbi G, Martelli PL, Casadio R, Lee GR, Seok C, Fenton AW, Dunbrack RL Jr. Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4 (2017) *Hum Mutat.* 38:1123-1131.
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 - Savojardo C, Martelli PL*, Fariselli P, Casadio R. SChloro: directing Viridiplantae proteins to six chloroplastic sub-compartments (2017). *Bioinformatics* 33:347-353.
 - Savojardo C, Fariselli P, Martelli PL*, Casadio R. ISPREd4: interaction sites PREdiction in protein structures with a refining grammar model (2017) *Bioinformatics* 33:1656-1663.

- Capiotti E, Martelli PL, Fariselli P, Casadio R. Blind prediction of deleterious amino acid variations with SNPs&GO (2017) *Hum Mutat.* 38:1064-1071.
- Jiang Y, Oron, TR, et al. An expanded evaluation of protein function prediction methods shows an improvement in accuracy (2016) *Genome Biology*, 17 (1), art. no. 184, .
- Savojardo C, Fariselli P, Martelli PL*, Casadio R. INPS-MD: A web server to predict stability of protein variants from sequence and structure (2016) *Bioinformatics*, 32 (16), pp. 2542-2544.
- Martelli PL, Fariselli P, Savojardo C, Babbi G, Aggazio F, Casadio R. Large scale analysis of protein stability in OMIM disease related human protein variants (2016) *BMC Genomics*, 17, art. no. 397.
- Sazzini M, De Fanti S, Cherubini A, Quagliariello A, Profiti G, Martelli PL, Casadio R, Ricci C, Campieri M, Lanzini A, Volta U, Caio G, Franceschi C, Spisni E, Luiselli D. Ancient pathogen-driven adaptation triggers increased susceptibility to nonceliac wheat sensitivity in present-day European populations (2016) *Genes and Nutrition*, 11 (1), 11 p.
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- Martelli PL, Savojardo C, Fariselli P, Tasco G, Casadio R. Computer-based prediction of mitochondria-targeting peptides (2015) *Mitochondrial Medicine*, 1, pp. 305-320.
- Fariselli P, Martelli PL, Savojardo C, Casadio R. INPS: Predicting the impact of non-synonymous variations on protein stability from sequence (2015) *Bioinformatics*, 31 (17), pp. 2816-2821.
- Savojardo C, Martelli PL*, Fariselli P, Casadio R. TPpred3 detects and discriminates mitochondrial and chloroplastic targeting peptides in eukaryotic proteins (2015) *Bioinformatics*, 31 (20), pp. 3269-3275.
- Profiti, G, Piovesan, D, Martelli, PL, Fariselli, P, Casadio, R. Protein sequence annotation by means of community detection (2015) *Current Bioinformatics*, 10 (2), pp. 139-143.
- Akcapinar GB, Venturini A, Martelli PL, Casadio R, Sezerman UO. Modulating the thermostability of Endoglucanase I from *trichoderma reesei* using computational approaches (2015) *Protein Engineering, Design and Selection*, 28 (5), pp. 127-135.
- Martelli PL, Savojardo C, Fariselli P, Tasco G, Casadio, R. Computer-based prediction of mitochondria-targeting peptides (2015) *Methods in Molecular Biology*, 1264, pp. 305-320.
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- Savojardo, C, Martelli, PL*, Fariselli, P, Casadio, R. TPpred2: improving the prediction of mitochondrial targeting peptide cleavage sites by exploiting sequence motifs (2014) *Bioinformatics (Oxford, England)*, 30 (20), pp. 2973-2974.
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- Martelli PL, Fontanesi L, Piovesan D, Fariselli P, Casadio R. Mapping and annotating obesity-related genes in pig and human genomes (2014) *Protein and Peptide Letters*, 21 (8), pp. 840-846.
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- Savojardo C, Fariselli P, Martelli PL, Casadio R. BCov: A method for predicting β -sheet topology using sparse inverse covariance estimation and integer programming (2013) *Bioinformatics*, 29 (24), pp. 3151-3157.
- Piovesan D, Profiti G, Martelli PL, Fariselli P, Fontanesi L, Casadio R. SUS-BAR: A database of pig proteins with statistically validated structural and functional annotation (2013) *Database*, 2013, art. no. bat065, .
- Capiotti E, Calabrese R, Fariselli P, Martelli PL, Altman R.B, Casadio R. WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation (2013) *BMC genomics*, 14 Suppl 3, art. no. S6, .
- Di Lena D, Wu G, Martelli PL, Casadio R, Nardini C. MIMO: An efficient tool for molecular interaction maps overlap (2013) *BMC Bioinformatics*, 14, art. no. 159, .

- Indio V, Martelli PL*, Savojardo C, Fariselli P, Casadio R. The prediction of organelle-targeting peptides in eukaryotic proteins with Grammatical-Restrained Hidden Conditional Random Fields (2013) *Bioinformatics*, 29 (8), pp. 981-988.
- Porcellini E, Carbone I, Martelli PL, Ianni M, Casadio R, Pession A, Licastro F. Haplotype of single nucleotide polymorphisms in exon 6 of the MZF-1 gene and Alzheimer's disease (2013) *Journal of Alzheimer's Disease*, 34 (2), pp. 439-447.
- Piovesan, D, Martelli, PL, Fariselli, P, Profiti, G, Zauli, A, Rossi, I, Casadio, R. How to inherit statistically validated annotation within BAR+ protein clusters (2013) *BMC Bioinformatics*, 14 (SUPPL.3), art. no. S4, .
- Savojardo C, Fariselli P, Martelli PL, Casadio R. Prediction of disulfide connectivity in proteins with machine-learning methods and correlated mutations (2013) *BMC Bioinformatics*, 14 (SUPPL.1), art. no. S10, .
- Savojardo C, Fariselli P, Piovesan D, Martelli PL, Casadio R. Machine-learning methods to predict protein interaction sites in folded proteins (2012) *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 7548 LNBI, pp. 127-135.
- Fontanesi L, Schiavo G, Galimberti G, Calò DG, Scotti E, Martelli PL, Buttazzoni L, Casadio R, Russo V. A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes (2012) *BMC Genomics*, 13 (1), art. no. 583, .
- Martelli PL, Fariselli P, Balzani E, Casadio R. Predicting cancer-associated germline variations in proteins. (2012) *BMC genomics*, 13 Suppl 4, pp. S8.
- Juritz E, Fomasari MS, Martelli PL, Fariselli P, Casadio R, Parisi G. On the effect of protein conformation diversity in discriminating among neutral and disease related single amino acid substitutions. (2012) *BMC genomics*, 13 Suppl 4, pp. S5.
- Fontanesi L, Martelli PL, Scotti E, Russo V, Rogel-Gaillard C, Casadio R, Vernesi C. Exploring copy number variation in the rabbit (*Oryctolagus cuniculus*) genome by array comparative genome hybridization (2012) *Genomics*, 100 (4), pp. 245-251.
- Piovesan D, Profiti G, Martelli PL, Casadio R. The human "magnesome": Detecting magnesium binding sites on human proteins (2012) *BMC Bioinformatics*, 13 (SUPPL 1), art. no. S10, .
- Fontanesi L, Galimberti G, Calò DG, Fronza R, Martelli PL, Scotti E, Colombo M, Schiavo G, Casadio R, Buttazzoni L, Russo V. 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 (2012) *Journal of Animal Science*, 90 (8), pp. 2450-2464.
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- Pippucci T, Benelli M, Magi A, Martelli PL, Magini P, Torricelli F, Casadio R, Seri M, Romeo G. EX-HOM (EXome HOMozygosity): A proof of principle (2011) *Human Heredity*, 72 (1), pp. 45-53.
- Savojardo C, Fariselli P, Martelli PL, Shukla P, Casadio R. Prediction of the bonding state of cysteine residues in proteins with machine-learning methods (2011) *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 6685 LNBI, pp. 98-111.
- Savojardo C, Fariselli P, Alhamdoosh M, Martelli PL, Pierleoni A, Casadio R. Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization (2011) *Bioinformatics*, 27 (16), art. no. btr387, pp. 2224-2230.
- Piovesan D, Martelli PL, Fariselli P, Zauli A, Rossi I, Casadio R. BAR-PLUS: The Bologna Annotation Resource Plus for functional and structural annotation of protein sequences (2011) *Nucleic Acids Research*, 39 (SUPPL. 2), pp. W197-W202.
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- Pantaleo MA, Astolfi A, Indio V, Moore R, Thiessen N, Heinrich MC, Gnocchi C, Santini D, Catena F, Formica S, Martelli PL, Casadio R, Pession A, Biasco G. SDHA loss-of-function mutations in KIT-PDGFR α wild-type gastrointestinal stromal tumors identified by massively parallel sequencing (2011) *Journal of the National Cancer Institute*, 103 (12), pp. 983-987.
- Pierleoni A, Martelli PL, Casadio R. MemLoc: Predicting subcellular localization of membrane

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