

## PERSONAL INFORMATION

## Rita Casadio

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🌐 <http://www.biocomp.unibo.it>

Nationality Italian

## WORK EXPERIENCE

## Research Group leader and full professor

University of Bologna, Bologna (Italy)

**Academical Positions**

2011- on going. Joint Professor of the Shanghai Jiao Tong University, Shanghai China

2005- 2015 (1/29). President of the International Bologna Master in Bioinformatics. University of Bologna, Italy

2001(10/1)- on-going. Full Professor of Biochemistry. University of Bologna, Italy

1987 -2001 Associate Professor of Biophysics. University of Bologna, Italy

1981 - 1987 Permanent Researcher, Physics of Matter. University of Bologna, Italy

1978 - 1979 Assistant Research Biochemistry I, Cardiovascular Research Institute, University of California, San Francisco

1974 - 1981 Assegnista Ministeriale, University of Bologna, Italy.

**Consulting Activity**

2008-2010 Coordinator of the Project Bioinformatics and Computational Biology at the Life Science Department of the Italian CNR

## EDUCATION AND TRAINING

EQF level 8

1) Certificato di Studiosita' in Biofisica (Universita' degli Studi di Bologna)

2) Perfezionamento in Teoria e Applicazione delle Macchine Calcolatrici

3) Degree in Physics (Universita' degli Studi di Bologna)

4) Maturità classica

**Special courses and Fellowships**

1983- Introduzione alla Scienza della Complessita': Processi Stocastici e Autoorganizzazione nei Sistemi Complessi (Istituto di Aggiornamento e formazione dell'ENI-TEMA, Castelgandolfo)

1982- International School on Biothermokinetics (Biozentrum, Basel)

1981- Short Term Embo Fellowship at the Department of Biophysics, University of Osnabruck (Germany)

1980- Corso Avanzato di NMR applicata in Chimica Organica e Biologia (Universita' della Calabria, Rende)

1980- International Course on Bacteriorhodopsin (Science Academy, Szeged, Ungheria)

1978- Human Biology (Medical Center, University of California, San Francisco)

1977- 2nd International Course on the Bioenergetics of Biological Membranes (Gruppo Italiano di Bioenergetica ed Accademia dei Lincei, Roma)

1976- FEBS Advanced Course n.41 on the Biochemistry of Cellular Membranes (Politecnico Federale Svizzero, Zurigo)

1973- Advanced Course on Computer Science (Universita' degli Studi di Bologna)

PERSONAL SKILLS

Mother tongue(s) Italian

Other language(s)

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	C1	C1	C1	C1	C1

Levels: A1 and A2: Basic user - B1 and B2: Independent user - C1 and C2: Proficient user  
Common European Framework of Reference for Languages

Communication skills RC is able to integrate herself with her own research group and her classes, acting as a group leader and a professor (during her working life)

Organisational / managerial skills RC is able to organise the group work, to do fund raising and get results (RC acquired this experience during her working life)

Job-related skills **Life Science; Biotechnology; Information Technology**  
More specifically Bioinformatics; Computational Biology; Genomics; Proteomics; Interomics; Metabolomics; NGS data analysis  
Full Professor of Biochemistry

Digital competence In the lab we have a computer network comprising several servers and we routinely develop algorithms for problem solving in Computational Biology/Bioinformatics. Our activities include: Genome and proteome annotation, Single Nucleotide Polymorphism Annotation, Protein Structure and Function prediction, Protein Stability Prediction upon mutations. We run several public servers ([www.biocomp.unibo.it](http://www.biocomp.unibo.it)) and several platforms for genome annotation.

ADDITIONAL INFORMATION

**Recent scientific appointments**

- 2015-2019- Italian representative in the NGP-Net (BMBS COST Action BM1405)
- 2014 (8/5)- on going. Vice-chair (Elected) of the Gordon Conference Human Single Nucleotide Polymorphisms & Disease
- 2013 - on going. Representative of the University of Bologna in ELIXIR ITALIA, part of the largest European Bioinformatics infrastructure coordinated by the European Bioinformatics Institute.
- 2013 - on going. Member of the Steering Committee of the IRT Alma-Seq of the University of Bologna.
- 2011-2015. Italian representative in the RGB-Net (COST Action TD1101)

**Other recent appointments**

- 2015-on going. Elected member of the Executive Board of the Italian Society of Biochemistry
- 2012-2016. Elected member of the Coordinating Board of the Italian full Professors of Biochemistry.
- 2012-2013- Evaluating Expert (GEV 05) for the Italian Agency evaluating Universities and Researches (ANVUR) on the behalf of the Italian Ministry for Education, University and Research.
- RC has been member of the board of directors of I.N.B.B, an Italian InterUniversity Consortium for Researches in Biostructures and Biosystems, acting also as a representative of the Italian Minister of Education, University and Research (2002-2013).

**Research Activities and Acknowledgments**

RC has been working mainly in the fields of membrane and protein Biophysics (particularly with

bacteriorhodopsin from Halobacterium Halobium and F1F0 ATPases from mesophilic organisms), both experimentally and theoretically, including mechanisms of energy conservation in bacteria.

She is interested in Bioinformatics and Computational Biology, developing computer modelling of relevant biological processes, such as protein folding, protein-protein and protein-DNA interactions. Her researches have been devoted to different aspects of protein modelling, including prediction of secondary and tertiary structures with neural networks, hidden Markov models and genetic algorithms, molecular docking and drug design (for details see <http://www.biocomp.unibo.it>). One major field of research has been the implementation and developments of tools out of machine-learning approaches for the prediction of secondary and tertiary structure of proteins from their aminoacid residue sequences, particularly of membrane proteins and their transmembrane topology. Projects focused on the prediction of contact maps, of protein-protein and protein-DNA interaction, of the bonding state of cysteines and their topology. Presently her researches are mainly devoted to the specific development of tools out of machine learning based approaches for problem solving of relevant biomedical and biotechnological problems for large scale analysis of genomic, proteomic and interactomic data (for details see <http://lipid.biocomp.unibo.it>), focusing also on the implementation and developments of tools for the prediction subcellular localisation of proteins, particularly of membrane proteins, for the genome and SNPs annotation and the prediction of mutation effect on protein stability and interaction. Projects are devoted to the analysis of interactomes and their relation with protein-protein interaction at the molecular levels. RC is the author of over 200 scientific papers, one international patent of a peptidomimetic molecule, and presented her work at several (over 300) national and international meetings (for some details see <http://www.biocomp.unibo.it>).

**As to RC qualifications:** RC is the author of over 300 publications in the field of Computational Biology/Bioinformatics/Biophysics and has presented the work of her group at more than 300 international and national meetings (RC I:F is over 700, with 8449 total citations, and h index is 43 according to SCOPUS)

The list of her recent publications is available at [www.biocomp.unibo.it](http://www.biocomp.unibo.it) and a selection is also appended

#### Reviewing Activities

RC is currently acting as a reviewer and also included in the Associate Editor board of several Journals in the field of Bioinformatics, Computational Biology, Genomics and Information Technology. RC acted/acts as reviewer for several Italian, EU and extraEU funding agencies (such as FSRI, European Commission, NIH, Israeli Science Fundation, DFG) and is often contacted for writing evaluation letters during promotion selection procedures by foreign universities.

RC acted/acts as a referee for scientific journals such as Proteins, Protein Science, Bioinformatics, FEBS Lett, Proteomics, European Journal Biochemistry, EMBO J, NAR, and for PRIN, NIH and EC research projects. She is also regularly included in the reviewing committee of several international meeting such as ISMB, WABI (co-chaired in 2005), BIRD, all devoted to different computational aspects of Bioinformatics and Computational Biology. Presently she is a member of the Editorial Board of BMC Bioinformatics; BioDataMining; Advances in Bioinformatics; BMC Research Notes; Journal of Biomedicine and Biotechnology, Advanced Studies in Biology, The Open Chemical and Biomedical Methods Journal; she has been guest editor Guest Editor to the Special Section on Computational Biology and Bioinformatics (WABI) – Part 1 and 2 on Lecture Notes in Bioinformatics (Lecture Notes in Computer Science).

#### Teaching Activities

RC has been founder and coordinator (2005-2015) of the International Bologna Master in Bioinformatics, a two year 2nd level course at the Bologna University. She has been giving and gives courses of Molecular Theoretical Biophysics, Bioinformatics, Systems and Computational Biology.

She is routinely invited to give lectures to undergraduate and graduate students in different Master and PHD courses in Italy, Europe and Extra EU countries.

Recently RC organised and gave one week courses on Bioinformatics at:

- Sultan Quaboos University-College of Medicine and Health (Oman, January 12-26 20012).
- Shanghai Jiao Tong University-Department of Automation, China (April 16-26 2012; October 25-November 1, 2014)

She participated into final PHD evaluation sections in different occasions, recently including a joint doctorate program between LMU Munich, Technische Universität München and Moscow State University (2011); Stockholm University (2011); CNIO, Madrid (2012)

RC with the Biocomputing Unit of Bologna is active in organizing International Schools on Bioinformatics ([www.biocomp.unibo.it](http://www.biocomp.unibo.it)) and the Bologna Master in Bioinformatics.

### Memberships

RC is presently member of:

- the Academy of Science of the Bologna Institute (elected full honorary member since 2009)
- the Italian Society of Biochemistry (where she has been coordinating the group Bioinformatics (2011-2014)),
- the International Society of Computational Biology (ISCB, since 1999)\*,
- the Italian Society of Bioinformatics (since 2003, founder member)

\*RC has been a member of the board of directors of ISCB, the International Society of Computational Biology, comprising over 800 researchers, in the period 2003-2009.

RC has been also member of the American Biophysical Society, of the Protein Society, and of the Italian Society of Biophysics.

### The Biocomputing group of the Bologna University

About the Biocomputing Unit of the University of Bologna (group leader Rita Casadio). Since 1995 Rita Casadio is the group leader of the Biocomputing Unit of the University of Bologna, in the Department of Biology. The group became officially active in 1995, when the Interdepartmental Center for the Biotechnological Research of the University of Bologna (CIRB) supported the establishment of a Biocomputing Center. Since then research interests focus on different aspects of protein sequence analysis, mainly the development and implementation of predictive algorithms based on methods out of machine learning approaches. The results of these works have been selected several times for presentation at the International Forum of Bioinformatics "Intelligent Systems for Molecular Biology (ismb)". A method (CORNET) developed in the lab for the prediction of contact maps of proteins (a relevant step for the ab initio prediction of protein 3D structure) has been scored the best of its category in the Critical Assessment of Techniques for Protein Structure Prediction (CASP) No 4 and No 5 (Asimolar, California, 2000 and 2002). A method for predicting the topography of outer membrane proteins based on HMM and sequence profile has been acknowledged with the SGI best award at ismb02 (Edmonton, Canada, August 3-7, 2002). The unit is member of the European bioinformatics Community (ECBB), and is also active in organizing international training courses since 1999 (Bologna Winter Schools) on Bioinformatics ([www.biocomp.unibo.it](http://www.biocomp.unibo.it)). In 2006 the Group organized BITS, the Annual Conference of the Italian Society of Bioinformatics.

The Biocomputing group has been a node of a network of excellence (BIOSAPIENS) within the VIth European Community framework (2004-2009) and a node of the National platform LIBI for Bioinformatics (2003-2011). Presently it is involved in two European Cost Action activities for the Rabbit Genome (2011-ongoing) and NGP-NET in Biomedicine (2015-ongoing) and two Italian National projects for operative research in animal genetics. RC and the Biocomputing group had/have contacts and collaborations with some of the major research groups working in Bioinformatics and Computational Biology in Europe.

### Special recognitions to the Biocomputing Group work are listed below:

- 1) SGI Best Paper Award at the International Conference on Intelligent Systems for Molecular Biology 2002, (ISMB2002) Edmonton (Canada) August 3-7, 2002: Martelli PL, Fariselli P, Krogh A, Casadio R – A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins- Bioinformatics 18: S46-S53 (2002)
- 2) Selection for the Human Mutation Virtual Issue "Evaluating Mutation Patogenicity"; Tavtigian SV and Greenblatt MS, eds; May 2010: Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R – Functional annotations improve the predictive score of human disease-related mutations in proteins- Hum Mutat 30:1237-1244 (2009) (Selected for the Human Mutation Virtual Issue "Evaluating Mutation Patogenicity"; Tavtigian SV and Greenblatt MS, eds; May 2010)
- 3) Evaluated as Recommended by Faculty of 1000, Biology reports: Fariselli P, Finelli M, Marchignoli D, Martelli PL, Rossi I, Casadio R -MaxSubSeq: an algorithm for segment-length optimization. The case study of the transmembrane spanning segments- Bioinformatics 19:500-505 (2003)
- 4) Evaluated as Recommended by Faculty of 1000, Biology reports: Martelli PL, Fariselli P, Krogh A, Casadio R - A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins- Bioinformatics 18: S46-S53 (2002)

### Patents:

- 1) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio

"Molecole non peptidiche analoghe al peptide RGD con effetto inibitorio sulla adesione, la migrazione

e la

proliferazione cellulare" Domanda n. RM2001A000089 depositata il 21.02.2001 a ROMA per Brevetto Nazionale (Italy)

2) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio

"RGD-analog non-peptidic molecules having anti-adhesive, Anti-migration anti-proliferative effects"

Domanda n. WO 02/066421A1 depositata il 29.08.2002 a Agente: SARPI Maurizio, Studio Ferrario, Via

Collina 36 00187 ROMA ITALIA per Brevetto "Europeo" in ARIPO PATENT, EUASIAN PATENT, EUROPEAN PATENT, OAP PATENT (European Patent) Assegnatari: Istituto Dermatologico dell'Immacolata, Roma

3) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio

"RGD-analog non-peptidic molecules having anti-adhesive, anti-migration anti-proliferative effects"

Domanda n. US20020119932A1 depositata il 29.08.2002 a YOUNG & THOMPSON, 745 South 23rd Street 2nd Floor, Arlington, VA, 22202 per Brevetto Nazionale (United States of America) in United States of America

### Selected Publications (from [www.biocomp.unibo.it](http://www.biocomp.unibo.it))

(Last five years)

1. Zuntini R, Cortesi L, Calistri D, Pippucci T, Luigi Martelli P, Casadio R, Capizzi E, Santini D, Miccoli S, Medici V, Danesi R, Marchi I, Zampiga V, Fiorentino M, Ferrari S, Turchetti D. BRCA1 p.His1673del is a pathogenic mutation associated with a predominant ovarian cancer phenotype. *Oncotarget*. 2017 Feb 7. doi: 10.18632/oncotarget.15151. [Epub ahead of print] PubMed PMID: 28186987.
2. Savojardo C, Martelli PL, Fariselli P, Casadio R. SChloro: directing Viridiplantae proteins to six chloroplastic sub-compartments. *Bioinformatics*. 2017 Feb 1;33(3):347-353. doi: 10.1093/bioinformatics/btw656. PubMed PMID:28172591.
3. Savojardo C, Fariselli P, Luigi Martelli P, Casadio R. ISPREd4: Interaction Sites PREDiction in protein structures with a refining grammar model. *Bioinformatics*. 2017 Jan 27. pii: btx044. doi: 10.1093/bioinformatics/btx044. [Epub ahead of print] PubMed PMID: 28130235.
4. Capriotti E, Martelli PL, Fariselli P, Casadio R. Blind Prediction of Deleterious Amino Acid Variations with SNPs&GO. *Hum Mutat*. 2017 Jan 19. doi:10.1002/humu.23179. [Epub ahead of print] PubMed PMID: 28102005.
5. Savojardo C, Martelli PL, Fariselli P, Casadio R. SChloro: directing Viridiplantae proteins to six chloroplastic sub-compartments. *Bioinformatics*. 2016 Oct 22. pii: btw656. [Epub ahead of print] PubMed PMID: 27797765.
6. Linguiti G, Antonacci R, Tasco G, Grande F, Casadio R, Massari S, Castelli V, Consiglio A, Lefranc MP, Ciccicarese S. Genomic and expression analyses of *Tursiops truncatus* T cell receptor gamma (TRG) and alpha/delta (TRA/TRD) loci reveal a similar basic public  $\gamma\delta$  repertoire in dolphin and human. *BMC Genomics*. 2016 Aug 15;17(1):634. doi: 10.1186/s12864-016-2841-9. Erratum in: *BMC Genomics*. 2016 Oct 5;17(1):778. PubMed PMID: 27528257; PubMed Central PMCID: PMC4986337.
7. Jiang Y, Oron TR, Clark WT, Bankapur AR, D'Andrea D, Lepore R, Funk CS, Kahanda I, Verspoor KM, Ben-Hur A, Koo da CE, Penfold-Brown D, Shasha D, Youngs N, Bonneau R, Lin A, Sahraeian SM, Martelli PL, Profiti G, Casadio R, Cao R, Zhong Z, Cheng J, Altenhoff A, Skunca N, Dessimoz C, Dogan T, Hakala K, Kaewphan S, Mehryary F, Salakoski T, Ginter F, Fang H, Smithers B, Oates M, Gough J, Törönen P, Koskinen P, Holm L, Chen CT, Hsu WL, Bryson K, Cozzetto D, Minnici F, Jones DT, Chapman S, Bkc D, Khan IK, Kihara D, Ofer D, Rappoport N, Stern A, Cibrian-Uhalte E, Denny P, Foulger RE, Hietä R, Legge D, Lovering RC, Magrane M, Melidoni AN, Mutowo-Meullenet P, Pichler K, Shypitsyna A, Li B, Zakeri P, ElShal S, Tranchevent LC, Das S, Dawson NL, Lee D, Lees JG, Sillitoe I, Bhat P, Nepusz T, Romero AE, Sasidharan R, Yang H, Paccanaro A, Gillis J, Sedeño-Cortés AE, Pavlidis P, Feng S, Cejuela JM, Goldberg T, Hamp T, Richter L, Salamov A, Gabaldon T, Marcet-Houben M, Supek F, Gong Q, Ning W, Zhou Y, Tian W, Falda M, Fontana P, Lavezzo E, Toppo S, Ferrari C, Giollo M, Piovesan D, Tosatto SC, Del Pozo A, Fernández JM, Maietta P, Valencia A, Tress ML, Benso A, Di Carlo S, Politano G, Savino A, Rehman HU, Re M, Mesiti M, Valentini G, Bargsten JW, van Dijk AD, Gemovic B, Glisic S, Perovic V, Veljkovic V, Veljkovic N, Almeida-E-Silva DC, Vencio RZ, Sharan M, Vogel J, Kansakar L, Zhang S, Vucetic S, Wang Z, Sternberg MJ, Wass MN, Huntley

- RP, Martin MJ, O'Donovan C, Robinson PN, Moreau Y, Tramontano A, Babbitt PC, Brenner SE, Linial M, Orengo CA, Rost B, Greene CS, Mooney SD, Friedberg I, Radivojac P. An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biol.* 2016 Sep 7;17(1):184. doi: 10.1186/s13059-016-1037-6. PubMed PMID: 27604469; PubMed Central PMCID: PMC5015320.
8. Sazzini M, De Fanti S, Cherubini A, Quagliarello 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 non-celiac wheat sensitivity in present-day European populations. *Genes Nutr.* 2016 May 23;11:15. doi: 10.1186/s12263-016-0532-4. PubMed PMID: 27551316; PubMed Central PMCID: PMC4968434.
9. Bovo S, Di Lena P, Martelli PL, Fariselli P, Casadio R. NET-GE: a web-server for NETWORK-based human gene enrichment. *Bioinformatics.* 2016 Nov 15;32(22):3489-3491. PubMed PMID: 27485441.
10. 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. *BMC Genomics.* 2016 Jun 23;17 Suppl 2:397. doi:10.1186/s12864-016-2726-y. PubMed PMID: 27356511; PubMed Central PMCID: PMC4928156.
11. Savojardo C, Fariselli P, Martelli PL, Casadio R. INPS-MD: a web server to predict stability of protein variants from sequence and structure. *Bioinformatics.* 2016 Aug 15;32(16):2542-4. doi: 10.1093/bioinformatics/btw192. PubMed PMID: 27153629.
12. Ison J, Rapacki K, Ménager H, Kalaš M, Rydza E, Chmura P, Anthon C, Beard N, Berka K, Bolser D, Booth T, Bretaudeau A, Brezovsky J, Casadio R, Cesareni G, Coppens F, Cornell M, Cuccuru G, Davidsen K, Vedova GD, Dogan T, Doppelt-Azeroual O, Emery L, Gasteiger E, Gatter T, Goldberg T, Grosjean M, Grüning B, Helmer-Citterich M, Ienasescu H, Ioannidis V, Jespersen MC, Jimenez R, Juty N, Juvan P, Koch M, Laibe C, Li JW, Licata L, Mareuil F, Mičetić I, Friberg RM, Moretti S, Morris C, Möller S, Nenadic A, Peterson H, Profiti G, Rice P, Romano P, Roncaglia P, Saidi R, Schafferhans A, Schwämmle V, Smith C, Sperotto MM, Stockinger H, Vařeková RS, Tosatto SC, de la Torre V, Uva P, Via A, Yachdav G, Zambelli F, Vriend G, Rost B, Parkinson H, Løngreen P, Brunak S. Tools and data services registry: a community effort to document bioinformatics resources. *Nucleic Acids Res.* 2016 Jan 4;44(D1):D38-47. doi: 10.1093/nar/gkv1116. PubMed PMID: 26538599; PubMed Central PMCID: PMC4702812.
13. Profiti G, Fariselli P, Casadio R. AlignBucket: a tool to speed up 'all-against-all' protein sequence alignments optimizing length constraints. *Bioinformatics.* 2015 Dec 1;31(23):3841-3. doi: 10.1093/bioinformatics/btv451. PubMed PMID: 26231432.
14. Di Lena P, Martelli PL, Fariselli P, Casadio R. NET-GE: a novel NETWORK-based Gene Enrichment for detecting biological processes associated to Mendelian diseases. *BMC Genomics.* 2015;16 Suppl 8:S6. doi: 10.1186/1471-2164-16-S8-S6. PubMed PMID: 26110971; PubMed Central PMCID: PMC4480278.
15. Savojardo C, Martelli PL, Fariselli P, Casadio R. TPpred3 detects and discriminates mitochondrial and chloroplastic targeting peptides in eukaryotic proteins. *Bioinformatics.* 2015 Oct 15;31(20):3269-75. doi:10.1093/bioinformatics/btv367. PubMed PMID: 26079349.
16. Fariselli P, Martelli PL, Savojardo C, Casadio R. INPS: predicting the impact of non-synonymous variations on protein stability from sequence. *Bioinformatics.* 2015 Sep 1;31(17):2816-21. doi: 10.1093/bioinformatics/btv291. PubMed PMID:25957347.
17. Bayram Akcapinar G, Venturini A, Martelli PL, Casadio R, Sezerman UO. Modulating the thermostability of Endoglucanase I from *Trichoderma reesei* using computational approaches. *Protein Eng Des Sel.* 2015 May;28(5):127-35. doi: 10.1093/protein/gzv012. PubMed PMID: 25784767.
18. Martelli PL, Savojardo C, Fariselli P, Tasco G, Casadio R. Computer-based prediction of mitochondria-targeting peptides. *Methods Mol Biol.* 2015;1264:305-20. doi: 10.1007/978-1-4939-2257-4\_27. PubMed PMID: 25631024.
19. Maccaferri M, Ricci A, Salvi S, Milner SG, Noli E, Martelli PL, Casadio R, Akhunov E, Scalabrin S, Vendramin V, Ammar K, Blanco A, Desiderio F, Distelfeld A, Dubcovsky J, Fahima T, Faris J, Korol A, Massi A, Mastrangelo AM, Morgante M, Pozniak C, N'Diaye A, Xu S, Tuberosa R. A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. *Plant Biotechnol J.* 2015 Jun;13(5):648-63. doi: 10.1111/pbi.12288. PubMed PMID: 25424506.
20. Savojardo C, Martelli PL, Fariselli P, Casadio R. TPpred2: improving the prediction of mitochondrial targeting peptide cleavage sites by exploiting sequence motifs. *Bioinformatics.* 2014 Oct 15;30(20):2973-4. doi: 10.1093/bioinformatics/btu411. PubMed PMID: 24974200.
21. Ciccarese S, Vaccarelli G, Lefranc MP, Tasco G, Consiglio A, Casadio R, Linguiti G, Antonacci R. Characteristics of the somatic hypermutation in the *Camelus dromedarius* T cell receptor gamma (TRG) and delta (TRD) variable domains. *Dev Comp Immunol.* 2014 Oct;46(2):300-13. doi: 10.1016/j.dci.2014.05.001. PubMed PMID: 24836674.
22. Sazzini M, Schiavo G, De Fanti S, Martelli PL, Casadio R, Luiselli D. Searching for signatures of cold adaptations in modern and archaic humans: hints from the brown adipose tissue genes. *Heredity (Edinb).* 2014 Sep;113(3):259-67. doi: 10.1038/hdy.2014.24. PubMed PMID: 24667833; PubMed Central PMCID: PMC4815638.

23. Bertolini F, Schiavo G, Scotti E, Ribani A, Martelli PL, Casadio R, Fontanesi L. High-throughput SNP discovery in the rabbit (*Oryctolagus cuniculus*) genome by next-generation semiconductor-based sequencing. *Anim Genet*. 2014 Apr;45(2):304-7. doi: 10.1111/age.12121. PubMed PMID: 24444082.
24. Abruzzo PM, Marini M, Bolotta A, Malisardi G, Manfredini S, Ghezzi A, Pini A, Tasco G, Casadio R. Frataxin mRNA isoforms in FRDA patients and normal subjects: effect of tocotrienol supplementation. *Biomed Res Int*. 2013;2013:276808. doi:10.1155/2013/276808. PubMed PMID: 24175286; PubMed Central PMCID: PMC3794619.
25. 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. *Database (Oxford)*. 2013 Sep 23;2013:bat065. doi:10.1093/database/bat065. PubMed PMID: 24065691; PubMed Central PMCID: PMC3781388.
26. Savojardo C, Fariselli P, Martelli PL, Casadio R. BCov: a method for predicting  $\beta$ -sheet topology using sparse inverse covariance estimation and integer programming. *Bioinformatics*. 2013 Dec 15;29(24):3151-7. doi:10.1093/bioinformatics/btt555. PubMed PMID: 24064422.
27. Martelli PL, Fontanesi L, Piovesan D, Fariselli P, Casadio R. Mapping and annotating obesity-related genes in pig and human genomes. *Protein Pept Lett*. 2014;21(8):840-6. PubMed PMID: 23855670.
28. Capriotti E, Calabrese R, Fariselli P, Martelli PL, Altman RB, Casadio R. WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. *BMC Genomics*. 2013;14 Suppl 3:S6. doi:10.1186/1471-2164-14-S3-S6. PubMed PMID: 23819482; PubMed Central PMCID: PMC3665478.
29. Di Lena P, Wu G, Martelli PL, Casadio R, Nardini C. MIMO: an efficient tool for molecular interaction maps overlap. *BMC Bioinformatics*. 2013 May 15;14:159. doi: 10.1186/1471-2105-14-159. PubMed PMID: 23672344; PubMed Central PMCID: PMC3680968.
30. Pantaleo MA, Astolfi A, Urbini M, Nannini M, Paterini P, Indio V, Saponara M, Formica S, Ceccarelli C, Casadio R, Rossi G, Bertolini F, Santini D, Pirini MG, Fiorentino M, Basso U, Biasco G; GIST Study Group. Analysis of all subunits, SDHA, SDHB, SDHC, SDHD, of the succinate dehydrogenase complex in KIT/PDGFR wild-type GIST. *Eur J Hum Genet*. 2014 Jan;22(1):32-9. doi: 10.1038/ejhg.2013.80. PubMed PMID: 23612575; PubMed Central PMCID: PMC3865408.
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