


PERSONAL INFORMATION

Rita Casadio

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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

2017-ongoing. Elected Vice Chair of the ELIXIR Europe Board, which includes scientific representatives of 23 European countries.

2008-2010. Coordinator of the Project Bioinformatics and Computational Biology at the Life Science Department of the Italian Centro Nazionale delle Ricerche, 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 Osnabrueck (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

Foreign 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 integrates herself with her own research group and teaching classes, acting as a group leader and a professor (during her working life)

Organisational / managerial skills RC organised and organises the activities of her working group, acting as a group leader, for fund raising and steering research. 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; Multiscale Modelling; Machine Learning.
 RC is Full Professor of Biochemistry

Digital skills RC is Principal investigator of a lab with a computer network comprising several servers (some 250 cores, 20 TB disk space and up to 750 GB of RAM memory). The main activity is the development of algorithms for problem solving in Computational Biology/Bioinformatics. Interests include: Genome and Proteome Annotation, Single Nucleotide Polymorphism Annotation, Protein Structure and Function prediction, Protein Stability Prediction upon Variations, Multiscale Modelling. The lab is responsible of several public servers (www.biocomp.unibo.it) and several platforms for genome annotation. Tools are freely available, mainly based on machine and deep learning and compliant with the standards required by ELIXIR Europe (<https://www.elixireurope.org/>), the largest distributed european bioinformatic infrastructure.

ADDITIONAL INFORMATION

Recent scientific appointments

- 2019-ongoing- Appointed Editor of Journal of Molecular Biology
- 2019-ongoing- Appointed Editor of NAR Bioinformatics and Genomics
- 2019-ongoing- Appointed member of the FEBS (Federation of the European Biochemical Societies) Fellowship Committee
- 2018-2019-Appointed member of PRIN 2017 evaluation panel LS2
- 2018-ongoing-Appointed Research Associate of the CNR-IBIOM (Istituto di Biomembrane, Bioenergetica e Biotecnologie Molecolari)
- 2018-2019- Appointed member of ERC (European Research Council) evaluation panel LS2 (Genomics and Bioinformatics)
- 2017-ongoing- Representative of the Italian Ministry of Education, University and Research in the European ELIXIR Board (www.Elixir-Europe.org), the largest European Bioinformatics infrastructure, coordinated by the European Bioinformatics Institute, including 23 European Countries.
- 2016-2017. Invited member of HFSP (Human Frontiers Science Program) review committee for Fellowships
- 2015-ongoing. Italian representative in the NGP-Net (BMBS COST Action BM1405)
- 2014 (8/5)- 2018. Appointed Vice-chair (2014-2016) and Chair (2016-2018) of the Gordon Conference

on Human Single Nucleotide Polymorphisms & Disease

2013 - on going. Representative of the University of Bologna in ELIXIR IIB (Istituto Italiano di Bioinformatica), node of the European Bioinformatics infrastructure, ELIXIR Europe

2013 - 2017. 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

2017-ongoing. Appointed Vice Chair of the ELIXIR Europe Scientific Board

2017-ongoing. Appointed Vicedirector of the Giorgio Prodi Cancer Research center at the University of Bologna

2015-2018. Elected member of the Executive Board of the Italian Society of Biochemistry and Italian representative at the Federation of European Biochemical Societies (FEBS) Board

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.

2003-20013- Member of the board of directors of I.N.B.B, the Italian InterUniversity Consortium for Researches in Biostructures and Biosystems, acting also as a representative of the Italian Minister of Education, University and Research.

Research Activities

RC worked mainly in the field of membrane and protein Biophysics (particularly with bacteriorhodopsin from Halobacterium Halobium and F1F0 ATPases from mesophilic organisms), both experimentally and theoretically, and was particularly active in elucidating mechanisms of energy conservation in bacteria and mitochondria. She is presently interested in Bioinformatics and Computational Biology, developing computer modelling of relevant biological processes, such as protein folding, protein-protein and protein-DNA/RNA interactions. Her researches are devoted mainly to the application of Artificial Intelligence methods to different aspects of protein modelling, including prediction of structure to function relationship with deep and neural networks, hidden Markov models and labeling techniques, suited to analyse large volumes of data. One activity is the functional annotation of biosequences and their variants, also related to human diseases. Drug Design and molecular docking are among her interests (for details see <http://www.biocomp.unibo.it>). One major field of research has been/is 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 for problem solving of relevant biomedical and biotechnological problems and for large scale analysis of genomic, proteomic and interactomic data (for details see <http://lipid.biocomp.unibo.it>). The focus, among other topics, is on the implementation and developments of tools for the prediction of subcellular localisation of protein sequences, particularly of membrane proteins, for genome and variant annotation, for the prediction of variation effect on protein stability and interaction, and for multiscale modelling of data derived from Next Generation Sequencing. Projects aim to the analysis of interactomes, their functional relation with protein-protein interaction at the molecular level and modelling of the biological complexity.

As to RC qualifications: RC is the author of over 300 publications in the field of Computational Biology/Bioinformatics/Biophysics and presented (invited, oral, selected oral) the work of her group at more than 300 international and national meetings. On several occasions RC gave invited lectures and/or seminars in Europe, Cina, Turkey, Oman, Ecuador, and USA.

RC total IF is 909, with some 10246 total citations, a h-index of 46 according to SCOPUS for some 255 publications and g-index equal to 96). For details: <http://www.biocomp.unibo.it>

The list of her recent publications is available at www.biocomp.unibo.it and a selection (last six years) 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 Foundation, DFG, ERC) 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 international meetings such as ISMB, WABI (co-chaired in 2005), BIRD, BBIM all devoted to different computational aspects of Bioinformatics and Computational Biology.

Presently she is a member of the Editorial Board of JMB, 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 to the Special Section on Computational Biology and Bioinformatics (WABI) – Part 1 and 2 on Lecture Notes in Bioinformatics (Lecture Notes in Computer Science).

Recently RC acted as a reviewer for the research activities of CRG (Centre for Genomic Regulation), Barcelona-Spain and participates/ed to selection panels both in Europe and Italy.

Teaching and Assessment Activities

RC has been promoter, co-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.

RC has been involved in several PhD programs of the Bologna University, all related to Computational Biology and Bioinformatics and tutored some 40 theses of graduate and undergraduate students, through the years. She is now a faculty member of the PhD program in Data Science and Computation. She is teaching and routinely involved in other PhD programs in Europe, participating to the final exams of PhD Evaluation. She participated into final PhD evaluation sections in different occasions, including a joint doctorate program between LMU Munich, Technische Universität München and Moscow State University (2011); Stockholm University (2011); CNIO, Madrid (2012)

RC organised and gave one week courses on Bioinformatics at:

- Shanghai Jiao Tong University-Department of Automation, China (April 16-26, 2012; October 25-November 1, 2014)
- Sultan Quaboos University-College of Medicine and Health (Oman, January 12-26 20012)
- Loja University (Ecuador, April 2006)

She is often acting as a remote assessor for competing positions in EU and extra EU countries. She is/has been participating to several national selection committees, including the evaluation committee of a CNR call for a research position in Genetics/Bioinformatics (2017)

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

Memberships

RC is member of:

- the Academy of Science of the Bologna Institute (elected full honorary member since 2009 and Vice President, President of the Physical Classes for a three year term, since 1-11-2018)
- the Italian Society of Biochemistry (where she has been coordinating the group of Bioinformatics/Computational Biology (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

Since 1995 Rita Casadio is the group leader of the Biocomputing Unit of the University of Bologna. 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 of machine and deep learning. The results of these works have been selected several times for presentation at the International Forum of Bioinformatics "Intelligent Systems for Molecular Biology (ISMB)", with special recognitions (see below)

More recently the group has been/is active in International Competitions to assess the validity of its computational tools (all available for end users at www.biocomp.unibo.it) for annotation of disease related variants (CAGI, Critical Assessment of Genome Interpretation, since 2011-ongoing) and annotation of functions from protein sequences (CAFA, Critical Assessment of Function Annotation, since 2010-ongoing). The results of the group scored among the highest and were/are reported in co-authored publications with other emerging groups known at international level.

The group is member of the European Bioinformatics Community (ECBB), and is active in organizing international training courses since 1999 (Bologna Winter Schools) on Bioinformatics (www.biocomp.unibo.it), focusing on different aspects of the analysis of biological data.

In 2006 the Group organized in Bologna BITS, the Annual Conference of the Italian Society of Bioinformatics and more recently, workshops on Computational Biology (2016, 2017, 2018) with the sponsorship of the Italian Society of Biochemistry. Occasionally, the group hosted training activities of ELIXIR Europe (2017), and special workshops on Bioschemas, sponsored by ELIXIR Italy and Europe (2018).

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). It was involved in two European Cost Action activities for the Rabbit Genome (2011-2016) 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.

The Group presently offers and maintains some 30 tools and three specific data bases, all free for remote access and compliant with the standards required by ELIXIR Europe (<https://www.elixir-europe.org/>), integrated in the largest distributed european bioinformatic infrastructure.

The Group through the years hosted several foreign Professors (two of them ISA Fellows) and foreign PhD students for collaborations (<https://www.biocomp.unibo.it>)

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
 Stren 2nd Floor, Arlington, VA, 22202 per Brevetto Nazionale (United States of America) in United
 States of America

Selected Publications (last six years from www.biocomp.unibo.it)

1. 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, DiScioscio 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. *Sci Rep.* 2019 Feb 18;9(1):2172. doi: 10.1038/s41598-018-38028-x. PubMed PMID: 30778083; PubMed Central PMCID: PMC6379366.
2. 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. *Bioinformatics.* 2018 Nov 29. doi: 10.1093/bioinformatics/bty979. [Epub ahead of print] PubMed PMID: 30496382.
3. Ermini G, Tosetti C, Zocchi D, Mandreoli M, Caletti MT, Marchesini G; Bologna Section of the Italian College of General Practitioners and Primary Care. Type 2 diabetes treatment and progression of chronic kidney disease in Italian familypractice. *J Endocrinol Invest.* 2018 Nov 21. doi: 10.1007/s40618-018-0983-0. [Epub ahead of print] PubMed PMID: 30465248.
4. Savojardo C, Luchetti A, Martelli PL, Casadio R, Mantovani B. Draft genomes and genomic divergence of two *Lepidurus* tadpole shrimp species (Crustacea, Branchiopoda, Notostraca). *Mol Ecol Resour.* 2019 Jan;19(1):235-244. doi:10.1111/1755-0998.12952. Epub 2018 Oct 19. PubMed PMID: 30288922.
5. Savojardo C, Martelli PL, Fariselli P, Profiti G, Casadio R. BUSCA: an integrative web server to predict subcellular localization of proteins. *Nucleic Acids Res.* 2018 Jul 2;46(W1):W459-W466. doi: 10.1093/nar/gky320. PubMed PMID:29718411; PubMed Central PMCID: PMC6031068.
6. Diquigiovanni C, Bergamini C, Evangelisti C, Isidori F, Vettori A, Tiso N, Argenton F, Costanzini A, Iommarini L, Anbunathan H, Pagotto U, Repaci A, Babbi G, Casadio R, Lenaz G, Rhoden KJ, Porcelli AM, Fato R, Bowcock A, Seri M, Romeo G, Bonora E. Mutant MYO1F alters the mitochondrial network and induces tumor proliferation in thyroid cancer. *Int J Cancer.* 2018 Apr 19. doi:10.1002/ijc.31548. [Epub ahead of print] PubMed PMID: 29672841.
7. Savojardo C, Martelli PL, Fariselli P, Casadio R. DeepSig: deep learning improves signal peptide detection in proteins. *Bioinformatics.* 2018 May 15;34(10):1690-1696. doi: 10.1093/bioinformatics/btx818. PubMed PMID: 29280997; PubMed Central PMCID: PMC5946842.
8. Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C, Casadio R. eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. *BMC Genomics.* 2017 Aug 11;18(Suppl 5):554. doi: 10.1186/s12864-017-3911-3. PubMed PMID: 28812536; PubMed Central PMCID: PMC5558190.
9. Daneshjou R, Wang Y, Bromberg Y, Bovo S, Martelli PL, Babbi G, Lena PD, Casadio R, Edwards M, Gifford D, Jones DT, Sundaram L, Bhat RR, Li X, Pal LR, Kundu K, Yin Y, Moulton J, Jiang Y, Pejaver V, Pagel KA, Li B, Mooney SD, Radivojac P, Shah S, Carraro M, Gasparini A, Leonardi E, Giollo M, Ferrari C, Tosatto SCE, Bachar E, Azaria JR, Ofran Y, Unger R, Niroula A, Vihinen M, Chang B, Wang MH, Franke A, Petersen BS, Pirooznia M, Zandi P, McCombie R, Potash JB, Altman RB, Klein TE, Hoskins RA, Repo S, Brenner SE, Morgan AA. Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Hum Mutat.* 2017 Sep;38(9):1182-1192. doi:10.1002/humu.23280. Epub 2017 Jul 7. PubMed PMID: 28634997; PubMed Central PMCID: PMC5600620.
10. 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. *Hum Mutat.* 2017 Sep;38(9):1042-1050. doi: 10.1002/humu.23235. Epub 2017 May 16. PubMed PMID: 28440912; PubMed Central PMCID: PMC5561474.
11. Profiti G, Martelli PL, Casadio R. The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation. *Nucleic Acids Res.* 2017 Apr 27. doi:10.1093/nar/gkx330. [Epub ahead of print] PubMed PMID: 28453653; PubMed Central PMCID: PMC5570247.
12. 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 CAG14. *Hum Mutat.* 2017 Sep;38(9):1123-1131. doi: 10.1002/humu.23222. Epub 2017 May 2. PubMed PMID: 28370845; PubMed Central PMCID: PMC5561472.
13. Zuntini R, Cortesi L, Calistri D, Pippucci T, Martelli PL, 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 Apr 4;8(14):22640-22648. doi: 10.18632/oncotarget.15151. PubMed PMID: 28186987; PubMed Central PMCID: PMC5410251.
14. 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; PubMed Central PMCID: PMC5408801.
15. Savojardo C, Fariselli P, Martelli PL, Casadio R. ISPRED4: interaction sites PREDiction in protein structures with a refining grammar model. *Bioinformatics.* 2017 Jun 1;33(11):1656-1663. doi: 10.1093/bioinformatics/btx044. PubMed PMID:28130235.
16. Capriotti E, Martelli PL, Fariselli P, Casadio R. Blind prediction of deleterious amino acid variations with SNPs&GO. *Hum Mutat.* 2017 Sep;38(9):1064-1071. doi: 10.1002/humu.23179. Epub 2017 May 2. PubMed PMID: 28102005; PubMed Central PMCID: PMC5522651.
17. Linguiti G, Antonacci R, Tasco G, Grande F, Casadio R, Massari S, Castelli V, Consiglio A, Lefranc MP, Ciccarese 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.
18. 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, Skunna 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, Minneci 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.
19. 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 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.
20. 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.
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1.Coordinatore scientifico ESPRIT FP4-1998-DRUG: Supercomputing Drug Design for Industrial and

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2.Responsabile Unità PRIN 1997: Biocatalisi e Bioconversioni dal 15-02-1998 al 14-02-2000

3.Responsabile Unità PRIN 1999: Proprietà Strutturali e Funzionali, Aspetti Applicativi di Proteine Isolate da Termofili dal 26-11-1999 al 25-11-2001

4.Responsabile Unità FP5-IST BLOWULF: Speeding-up Biocomputing applications using a commodity-based parallel computer dal 01-12-2000 al 31-03-2002

5.Responsabile Unità PRIN 2001: Idrolasi da Microrganismi Termofili: Aspetti Strutturali, Funzionali ed Espressione Omologa ed Eterologa dal 12-12-2001 al 11-12-2003

6.Responsabile Unità PRIN 2002: Strumenti basati su apprendimento automatico per la genomica strutturale e funzionale dal 16-12-2002 al 15-12-2004

7.Responsabile Unità FIRB Progetti Negoziati 2001: Bioinformatica per la Genomica e la Proteomica dal 10-01-2003 al 10-07-2007

8.Responsabile Unità PRIN 2003: Idrolasi Termostabili e Termoattive da Archaea: Aspetti Strutturali e Funzionali dal 20-11-2003 al 19-11-2005

9.Responsabile unità locale FP6-2002-LIFESCIHEALTH: A European Network for Integrated Genome Annotation (BioSapiens) dal 01-01-2004 al 30-06-2009

10.Responsabile Unità FIRB Laboratori 2003: LIBI: Laboratorio Internazionale di BioInformatica dal 12-09-2005 al 12-09-2011

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