

## PERSONAL INFORMATION



## Rita Casadio

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🌐 <http://www.biocomp.unibo.it>

Nationality Italian

## WORK EXPERIENCE

**Senior Researcher and Honorary Group Leader Biocomputing Group, University of Bologna, Bologna (Italy)****Academical Positions**

2019 (11/1)-ongoing **Professor Alma Mater and Lecturer**, University of Bologna.

2011- 2019. 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)- 2019 (11/1). 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**

2017-2019. 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 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

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 integrate 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 the activities of her working group, acting as a group leader, doing fund raising and getting results. Presently she is working actively within the group.  
 (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 and Bioinformatics)

Digital skills The Biocomputing Group counts on a computer network, comprising several servers (some 500 cores, 300 TB disk space and up to 1000 GB of RAM memory) and routinely develops 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, Multiscale Modelling. We run several public servers ([www.biocomp.unibo.it](http://www.biocomp.unibo.it)) and several platforms for genome annotation. Our tools are mainly based on machine and deep learning.

ADDITIONAL INFORMATION

**Honor**

2020-Distinctive honor of **FELLOW** from The International Society for Computational Biology (ISCB Fellow) in recognition of significance contributions and service to the field of computational biology.

**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 Associate Professor 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](http://www.Elixir-Europe.org)), the largest European Bioinformatics infrastructure

2016-2017 Invited member of HFSP (Human Frontiers Science Program) review committee for Fellowships

2015-2019. 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 - 2019. Representative of the University of Bologna in ELIXIR ITALIA, node of the largest European Bioinformatics infrastructure coordinated by the European Bioinformatics Institute.

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 appointments

2020-ongoing. Cochair of the ISCB-ECCB 2021 conference, the largest and most high profile annual meeting of scientists working in computational biology.

2017-2019. Appointed Vice Chair of the Elixir Europe Scientific Board

2017-2019. Appointed Vice Director 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 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 started her career 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. After that, she became 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 have been/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 volume 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 based on machine and deep learning for problem solving of relevant biomedical and biotechnological problems for large scale analysis of genomic, proteomic and interactomic data (for details see <http://biocomp.unibo.it>) with specific focus among other topics on the implementation and developments of tools for the prediction subcellular localisation of proteins, particularly of membrane proteins, for genome and variant annotation, the prediction of variation effect on protein stability and interaction, and mutiscale modelling of data derived from Next Generation sequencing data. Tools developed by the group are compliant with the standards required by ELIXIR Europe (<https://www.elixir-europe.org/>) and integrated in the largest distributed european bioinformatic infrastructure. Projects are devoted to the analysis of interactomes, their relation with protein-protein interaction at the molecular levels 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, Equador, and USA.

RC total IF is > 1000, with some 12,400 total citations, h-index of 54 according to SCOPUS and g-index > 99). For details: <http://www.biocomp.unibo.it>, <https://www.scopus.com> <https://orcid.org/0000-0002-7462-7039>.

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

### Reviewing Activities

RC is currently acting as JMB editor, and 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, Israelian Science Fundation, DFG, ERC, CNR, MIUR, Regione Toscana) 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, BBIM 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 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 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 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)

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 and also member of the evaluation committee of a CNR call for a research position in Genetics/Bioinformatics.

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.

RC has been involved in several PHD programs of the Bologna University, all related to Computational Biology and Bioinformatics for about some 30 theses 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.

### Memberships

RC is presently 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

About the Biocomputing Unit of the University of Bologna.

Since 1995 Rita Casadio has been 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)". 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) was 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 was acknowledged with the SGI best award at ismb02 (Edmonton, Canada, August 3-7, 2002).

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](http://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 always 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](http://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 through the years hosted several Professors (two of them ISA Fellows) and 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 (in the last 3 years, [www.biocomp.unibo.it](http://www.biocomp.unibo.it))

1. Madeo G, Savojardo C, Martelli PL, **Casadio R**. BetAware-Deep: An Accurate Web Server for Discrimination and Topology Prediction of Prokaryotic Transmembrane  $\beta$ -barrel Proteins. *J Mol Biol.* 2021 (in press) doi: <https://doi.org/10.1016/j.jmb.2020.166729>
2. Babbi G, Savojardo C, Martelli PL, **Casadio R**. Huntingtin: A Protein with a Peculiar Solvent Accessible Surface. *Int. J. Mol. Sci.* 2021, 22(6), 2878; <https://doi.org/10.3390/ijms22062878>
3. Ledwaba MB, Glover BA, Matle I, Profiti G, Martelli PL, **Casadio R**, . . . van Heerden, H. Whole genome sequence analysis of brucella abortus isolates from various regions of South Africa. *Microorganisms* 2021. 9(3), 1-14. doi:10.3390/microorganisms9030570
4. Savojardo C, Martelli PL, **Casadio R**, Fariselli, P. On the critical review of five machine learning-based algorithms for predicting protein stability changes upon mutation. *Briefings in Bioinformatics* 2021. 22(1), 601-603. doi:10.1093/bib/bbz168
5. Savojardo C, Manfredi M, Martelli PL, **Casadio R**. Solvent Accessibility of Residues Undergoing Pathogenic Variations in Humans: From Protein Structures to Protein Sequences. *Front Mol Biosci.* 2021 Jan 7;7:626363. doi:10.3389/fmolb.2020.626363. PMID: 33490109; PMCID: PMC7817970.
6. Savojardo C, Martelli PL, Tartari G, **Casadio R**. Large-scale prediction and analysis of protein sub-mitochondrial localization with DeepMito. *BMC Bioinformatics.* 2020 Sep 16;21(Suppl 8):266. doi: 10.1186/s12859-020-03617-z. PMID: 32938368; PMCID: PMC7493403.
7. Babbi G, Baldazzi D, Savojardo C, Pier Luigi M, **Casadio R**. 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. *Biomedicines.* 2020 Jul 29;8(8):250. doi: 10.3390/biomedicines8080250. PMID: 32751059; PMCID: PMC7459455.
8. Turri V, Latinovic OS, Bonafè M, Toyang N, Parigi M, Calassanzio M, Martelli PL, Vagheggini A, Abbati G, Sarnelli A, **Casadio R**, Ratti C, Massi P, Schoelz JE, Salvato MS, Piccinini F, Martinelli G. Cauliflower Mosaic Virus TAV, a Plant Virus Protein That Functions like Ribonuclease H1 and is Cytotoxic to Glioma Cells. *Biomed Res Int.* 2020 Mar 16;2020:7465242. doi: 10.1155/2020/7465242. PMID: 32258141; PMCID: PMC7102451.
9. Bovo S, Martelli PL, Di Lena P, **Casadio R**. NETGE-PLUS: Standard and Network-Based Gene Enrichment Analysis in Human and Model Organisms. *J Proteome Res.* 2020 Jul 2;19(7):2873-2878. doi: 10.1021/acs.jproteome.9b00749. Epub 2020 Feb 4. PMID: 31971806.
10. Zhou N, Jiang Y, Bergquist TR, Lee AJ, Kacsoh BZ, Crocker AW, Lewis KA, Georghiu G, Nguyen HN, Hamid MN, Davis L, Dogan T, Atalay V, Rifaioğlu AS, Dalkıran A, Cetin Atalay R, Zhang C, Hurto RL, Freddolino PL, Zhang Y, Bhat P, Supek F, Fernández JM, Gemovic B, Perovic VR, Davidović RS, Sumonja N, Veljkovic N, Asgari E, Mofrad MRK, Profiti G, Savojardo C, Martelli PL, **Casadio R**, . . . and Radivojac P, Friedberg I. The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biol.* 2019 Nov 19;20(1):244. doi: 10.1186/s13059-019-1835-8. PMID: 31744546; PMCID: PMC6864930.
11. Clark WT, Kasak L, Bakolitsa C, Hu Z, Andreoletti G, Babbi G, Bromberg Y, **Casadio R**, Dunbrack R, Folkman L, Ford CT, Jones D, Katsonis P, Kundu K, Lichtarge O, Martelli PL, Mooney SD, Nodzak C, Pal LR, Radivojac P, Savojardo C, Shi X, Zhou Y, Uppal A, Xu Q, Yin Y, Pejaver V, Wang M, Wei L, Moulton J, Yu GK, Brenner SE, LeBowitz JH. Assessment of predicted enzymatic activity of  $\alpha$ -N-acetylglucosaminidase variants of unknown significance for CAGI 2016. *Hum Mutat.* 2019 Sep;40(9):1519-1529. doi: 10.1002/humu.23875. PMID: 31342580; PMCID: PMC7156275.
12. Kasak L, Hunter JM, Udani R, Bakolitsa C, Hu Z, Adhikari AN, Babbi G, **Casadio R**, Gough J, Guerrero RF, Jiang Y, Joseph T, Katsonis P, Kotte S, Kundu K, Lichtarge O, Martelli

PL, Mooney SD, Moulton J, Pal LR, Poitras J, Radivojac P, Rao A, Sivadasan N, Sunderam U, Saipradeep VG, Yin Y, Zaucha J, Brenner SE, Meyn MS. CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. *Hum Mutat.* 2019 Sep;40(9):1373-1391. doi: 10.1002/humu.23874. Epub 2019 Sep 3. PMID: 31322791; PMCID: PMC7318886.

13. Babbi G, Martelli PL, **Casadio R**. PhenPath: a tool for characterizing biological functions underlying different phenotypes. *BMC Genomics.* 2019 Jul 16;20(Suppl 8):548. doi: 10.1186/s12864-019-5868-x. PMID: 31307376; PMCID: PMC6631446.

14. Kasak L, Bakolitsa C, Hu Z, Yu C, Rine J, Dimster-Denk DF, Pandey G, De Baets G, Bromberg Y, Cao C, Capriotti E, **Casadio R**, Van Durme J, Giollo M, Karchin R, Katsonis P, Leonardi E, Lichtarge O, Martelli PL, Masica D, Mooney SD, Olatubosun A, Radivojac P, Rousseau F, Pal LR, Savojardo C, Schymkowitz J, Thusberg J, Tosatto SCE, Vihinen M, Väliho J, Repo S, Moulton J, Brenner SE, Friedberg I. Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. *Hum Mutat.* 2019 Sep;40(9):1530-1545. doi: 10.1002/humu.23868. Epub 2019 Sep 3. PMID: 31301157; PMCID: PMC7325732.

15. Mount SM, Avsec Ž, Carmel L, **Casadio R**, Çelik MH, Chen K, Cheng J, Cohen NE, Fairbrother WG, Fenesh T, Gagneur J, Gotea V, Holzer T, Lin CF, Martelli PL, Naito T, Nguyen TYD, Savojardo C, Unger R, Wang R, Yang Y, Zhao H. Assessing predictions of the impact of variants on splicing in CAGI5. *Hum Mutat.* 2019 Sep;40(9):1215-1224. doi: 10.1002/humu.23869. Epub 2019 Aug 19. PMID: 31301154; PMCID: PMC6744318.

16. Cline MS, Babbi G, Bonache S, Cao Y, **Casadio R**, de la Cruz X, Díez O, Gutiérrez-Enríquez S, Katsonis P, Lai C, Lichtarge O, Martelli PL, Mishne G, Moles-Fernández A, Montalban G, Mooney SD, O'Conner R, Ootes L, Özkan S, Padilla N, Pagel KA, Pejaver V, Radivojac P, Riera C, Savojardo C, Shen Y, Sun Y, Topper S, Parsons MT, Spurdle AB, Goldgar DE; ENIGMA Consortium. Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. *Hum Mutat.* 2019 Sep;40(9):1546-1556. doi: 10.1002/humu.23861. Epub 2019 Aug 23. PMID: 31294896; PMCID: PMC6744348.

17. 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 FP, Grishin NV. Assessing predictions on fitness effects of missense variants in calmodulin. *Hum Mutat.* 2019 Sep;40(9):1463-1473. doi: 10.1002/humu.23857. Epub 2019 Sep 3. PMID: 31283071; PMCID: PMC6744288.

18. 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, Moulton 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. *Hum Mutat.* 2019 Sep;40(9):1474-1485. doi: 10.1002/humu.23856. Epub 2019 Aug 17. PMID: 31260570; PMCID: PMC7354699.

19. 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 SE, 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. *Hum Mutat.* 2019 Sep;40(9):1612-1622. doi: 10.1002/humu.23849. Epub 2019 Aug 17. PMID: 31241222; PMCID: PMC6744287.

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