

# Emidio Capriotti PhD

## CURRICULUM VITÆ

**Name:** Emidio Capriotti  
**Nationality:** Italian  
**Date of birth:** February, 1973  
**Place of birth:** Roma, Italy  
**Languages:** Italian, English, Spanish

### Positions

- Oct 2019** Associate Professor: Department of Pharmacy and Biotechnology (FaBiT). University of Bologna, Bologna, Italy
- 2016-2019** Senior Assistant Professor (RTD type B): Department of Pharmacy and Biotechnology (FaBiT) and Department of Biological, Geological, and Environmental Sciences (BiGeA). University of Bologna, Bologna, Italy.
- 2015-2016** Junior Group Leader: Institute of Mathematical Modeling of Biological Systems, University of Düsseldorf, Düsseldorf, Germany
- 2012-2015** Assistant Professor: Division of Informatics, Department of Pathology, University of Alabama at Birmingham (UAB), Birmingham (AL), USA.
- 2011-2012** Marie-Curie IOF: Contracted Researcher at the Department of Mathematics and Computer Science, University of Balearic Islands (UIB), Palma de Mallorca, Spain.
- 2009-2011** Marie-Curie IOF: Postdoctoral Researcher at the Helix Group, Department of Bioengineering, Stanford University, Stanford (CA), USA.
- 2006-2009** Postdoctoral Researcher in the Structural Genomics Group at Department of Bioinformatics and Genetics, Prince Felipe Research Center (CIPF) Valencia, Spain.
- 2004-2006** Contract researcher at Department of Biology, University of Bologna, Bologna, Italy.
- 2001-2003** Ph.D student in Physical Sciences at University of Bologna, Bologna, Italy.

### Education

- Sep 2004** Master in Bioinformatics (first level)  
University of Bologna, Bologna (Italy).
- Jun 2004** Ph.D. in Physical Sciences  
University of Bologna, Bologna (Italy).
- Jul 1999** *Laurea* (B.S.) Degree in Physical Sciences, score 106/110  
University of Bologna, Bologna (Italy).

### Visiting

- Jun 2012 – Jul 2012** Prof. Frederic Rousseau and Prof. Joost Schymkowitz, VIB Switch Laboratory, KU Leuven, Leuven (Belgium)
- May 2009** Prof. Francisco Melo group. Department of Molecular Genetics and Microbiology. Pontificia Universidad Catolica de Chile, Santiago de Chile (Chile).

<b>Jul 2008 - Aug 2008</b>	Prof. Andrej Sali group, Departments of Biopharmaceutical Sciences and Pharmaceutical Chemistry, University of California at San Francisco (UCSF), San Francisco (CA).
<b>Aug 2005 - Nov 2005</b>	Prof. Jeffrey Skolnick group. Center of Excellence in Bioinformatics University of New York at Buffalo, Buffalo (NY)
<b>Awards and Grants</b>	
<b>Sep 2019 -</b>	Unit Coordinator: Research Projects of National Relevance (PRIN-201744NR8S) Ministry of Education, University and Research (MIUR). Integrative tools for defining the molecular basis of the diseases: Computational and Experimental methods for Protein Variant Interpretation.
<b>Sep 2017 – Sep 2018</b>	University of Bologna Cooperation Grant: International Cooperation Project UNIBO-UCSD. Study and development of computational methods for cancer genome interpretation.
<b>Dec 2017</b>	Ministry of Education, Universities and Research: Fondo per il finanziamento delle attività base di ricerca 2017.
<b>Jun 2012 – Jul 2012</b>	Short term EMBO Fellowship for “Computational methods to predict the functional impact of protein variations on alpha-galactosidase and the efficacy of pharmacological chaperone therapy” at KU Leuven, Leuven (Belgium)
<b>Sep 2011 – Aug 2012</b>	Marie-Curie IOF at the Department of Mathematics and Computer Sciences, University of Balearic Islands (UIB).
<b>Sep 2009 – Aug 2011</b>	Marie-Curie IOF at the Helix Group, Department of Bioengineering, Stanford University
<b>Oct 2006 – Aug 2009</b>	Postdoc Research Fellowship. in the Structural Genomics Group at Department of Bioinformatics and Genetics, Prince Felipe Research Center (CIPF) Valencia, Spain
<b>Jul 2008 – Aug 2008</b>	Short-term research fellowship from the Valencian Government (Spain) for the development of a method for RNA structure prediction using MODELLER program. Project supervised by Prof. Andrej Sali, Departments of Biopharmaceutical Sciences and Pharmaceutical Chemistry, University of California, San Francisco (UCSF).
<b>Sep 2004 - Sep 2006</b>	Postdoc Research Fellowship. <i>BioSapiens</i> Network of Excellence, funded by the European Union's VI Framework Programme.
<b>Aug 2005 - Dec 2005</b>	Marco Polo Research Fellowship for “Implementation of new software for protein structure prediction” developed in the Center of Excellence in Bioinformatics University at Buffalo under the supervision of Prof. Jeffrey Skolnick
<b>Jan 2003 - May 2004</b>	National Institute for Biophysics and Biomaterials (INBB) Research Fellowship. Partially supported by MURST (FISR 2002) project <i>Hydrolases from Thermophiles: Structure, Function and Homologous and Heterologous Expression</i> .
<b>Sep 2001 - Sep 2002</b>	SPINNER Consortium (Regione Emilia-Romagna) Research Fellowship for Technology Transfer through a grant to the BioDec project.

### Teaching activity

At the University of Bologna, I am member of the committee of the PhD program in Data Sciences and Computation. I am contributing to the training activity in the International Master in Bioinformatics as instructor for the second module of Laboratory of Bioinformatics 1.

From 2015 to 2016, at the University of Düsseldorf I gave 2 one-week modules as part of the master courses “Introduction to Systems Biotechnology” and “Biological Networks”.

From 2014 to 2015 at the University of Alabama at Birmingham, in collaboration with Dr. Malay Basu, I was course master in two courses in the Graduate Biomedical Science program at UAB and organizer of the CB2 (Computational Biology and Bioinformatics) Journal Club at UAB. The list of courses given during last few years is reported below.

<b>2017-2018</b>	Module 2: Laboratory of Bioinformatics 1 (66563), International Master in Bioinformatics (60 hours). University of Bologna.
------------------	--

<b>2016-2017</b>	Module 2: Laboratory of Bioinformatics 1 (66563), International Master in Bioinformatics (60 hours). University of Bologna.
<b>2015-2016</b>	Module: Introduction to Computational Biology and Bioinformatics. Introduction to Molecular Systems Biotechnology course (M4453). Molecular Systems Biotechnology Master (20 hours). University of Düsseldorf. Module: Introduction to Protein-Protein Interaction Network. Biological Networks course (M4424). Molecular Systems Biotechnology Master (20 hours). University of Düsseldorf
<b>2015-2016</b>	GBSC 703-01A - Introduction to Scientific Computing, Graduate Biomedical Science Program (48 hours). University of Alabama at Birmingham (USA).
<b>2014-2015</b>	GBSC 703-01E Computational Biology and Bioinformatics, Graduate Biomedical Science Program (40 hours). University of Alabama at Birmingham (USA).
<b>2014-2015</b>	GBSC 703-01A - Introduction to Scientific Computing, Graduate Biomedical Science Program (48 hours). University of Alabama at Birmingham (USA).
<b>2013-2014</b>	GBSC 703-01A - Introduction to Scientific Computing, Graduate Biomedical Science Program (30 hours). University of Alabama at Birmingham (USA).

I was also contracted professor for the following courses held by Prof. Rita Casadio at the University of Bologna (Italy):

<b>2004-2005</b>	Bioinformatics - Degree in Biotechnology (30 hours)
<b>2003-2004</b>	Laboratory of Biophysics II - Degree in Biotechnology Models for Biological Systems - Degree in Biotechnology (90 hours total)
<b>2002-2003</b>	Structural Biochemistry - Degree in Biotechnology (70 hours)
<b>2001-2002</b>	Laboratory of Biophysics II - Degree in Biotechnology (25 hours)

### Mentoring activity

Currently, I am co-mentoring the research activity Jaume Sastre Tomàs, PhD student at the Department of Mathematics and Informatics, University of Balearic Islands (Spain). In the past, I directed the thesis of:

Alessandro Vinceti	Title: Development of new tools for predicting the impact of genetic variants in the cancer genome. International Master in Bioinformatics at the University of Bologna (Italy). Bologna, 25 September 2019.
Emina Merdan	Title: Characterizing the impact of mutations at functional and network levels in Lung Adenocarcinoma. International Master in Bioinformatics at the University of Bologna (Italy). Bologna, 26 September 2018.
Oronzo Tassiello	Title: Computational methods for scoring genomes of Lung Adenocarcinoma International Master in Bioinformatics at the University of Bologna (Italy). Bologna, 9 March 2018.
Luigi Chiricosta	Title: Detecting cancer causing genes and variants in Colon Adenocarcinoma. International Master in Bioinformatics at the University of Bologna (Italy). Bologna, 26 September 2017.

At the University of Alabama at Birmingham, I was supervising the research activity of one postdoc (Dr. Rui Tian) and one master student (Shivani Viradia).

Previously, I collaborated with Prof. Rita Casadio, Dr Mario Compiani and Dr Marc A. Marti-Renom to mentor the research activity of the following students:

Alberto Stizza	BS thesis in Physical Sciences, Catholic University of Brescia (Italy)
Daniela Danesi	BS thesis in Physical Sciences, Catholic University of Brescia (Italy)
Maria Procopio	BS thesis in Physical Sciences, University of Bologna (Italy)
Remo Calabrese	PhD thesis in Biotechnology, University of Bologna (Italy)
Giulia Gentile	MS thesis in Bioinformatics, CRS4 Bioinformatics Laboratory Cagliari (Italy)
Stefania Bosi	PhD student, University La Sapienza, Roma (Italy)
Miquel Oltre Sastre	Master thesis, Open University of Catalonia (Spain)

## Reviewer activity

I am faculty member of the F1000 Biology in the section of Bioinformatics. I am reviewer for the following journals: Nature Communications, Bioinformatics, Briefings in Bioinformatics, Nucleic Acids Research, The American Journal of Human Genetics, PLOS Computational Biology, Scientific Reports, Cancer Research, Oncotarget, BMC Bioinformatics, PLOS ONE, BMC Genomics, Proteins, Human Mutation, Human Genetics, Human Genomics, Amino Acids, BMC Structural Biology, Database, Current Bioinformatics, Current Protein and Peptide Science, Journal of Bioinformatics and Computational Biology, Neurocomputing, Information Fusion, IEEE/ACM Transactions on Computational Biology and Bioinformatics. I was reviewer of projects for the Medical Research Council of the United Kingdom and for the Austrian Academy of Sciences.

## Other scientific activity

I am member of the International Society of Computational Biology (ISCB). I served as co-chair in the organization of the Personal Genomics session at the Pacific Symposium of Biocomputing (PSB) 2011. I was member of the Data Committee in the first edition of the Critical Assessment of Genome Interpretation (CAGI) 2010. From 2011, in collaboration with Yana Bromberg and Hannah Carter, I organized 6 editions of the VarI-SIG meeting (formerly SNP-SIG) in Vienna (Austria), Long Beach, (California), Berlin (Germany), Boston (Massachusetts), Dublin (Ireland) and Orlando (USA). With Yana Bromberg and Hannah Carter I am co-editor of 5 BMC Genomics special issues publishing selected works among those presented at the VarI-SIG meetings from 2011 to 2015. More information about the VarI-SIG meeting is available at <http://varisig.biofold.org>. In 2013, I was member of the Proceedings Papers Committee for the ISMB/ECCB Conference. In 2015 I was member of the Late Breaking Research Committee for the ISMB/ECCB Conference. In 2016 I was co-chair of the Disease track for the ISCB Latin American Conference in Buenos Aires (Argentina). I was co-chair of the VarI-COSI session at the ISMB/ECCB Conference in July 21-25, 2017 Prague (Czech Republic). In 2018 I was Area Chair and co-chair of the VarI-COSI session at the ISMB Conference held on July 6-10, Chicago (USA). The same year I was assessor for the Fratxin challenge at the V edition of the Critical Assessment of Genome Interpretation (CAGI) meeting, July 5-7, Chicago (USA).

## Personal research projects

- 2017-2018** Univeristy of Bologna Cooperation Grant: International Cooperation Project UNIBO-UCSD. Study and development of computational methods for cancer genome interpretation.
- 2017** Ministry of Education, Universities and Research: Fondo di Finanziamento per le Attività Base di Ricerca (FFABR).
- 2009-2012** Marie Curie International Outgoing Fellowships for Career Development, New methods to evaluate the impact of single point protein mutation on human health.
- 2012** EMBO Short Term Fellowship, Computational methods to predict the functional impact of protein variations on alpha-galactosidase and the efficacy of pharmacological chaperone therapy.
- 2008** Short-term research fellowship from the Valencian Government (Spain), Development of a method for RNA structure prediction using MODELLER program.
- 2005** Marco Polo Research Fellowship, Implementation of new software for protein structure protein structure prediction.

## Participation in research projects

- Sep 2019 -** Integrative tools for defining the molecular basis of the diseases: computational and experimental methods for protein variant interpretation (MIUR-PRIN-201744NR8S)  
PI: Piero Fariselli Role: Unit Coordinator
- 2018-2020** Role of VpreB in immunoglobulin antigen binding site selection (NIH 1R21AI134027-01A1)  
PI: Harry Schroeder. Role: Consultant.
- 2016-2018** Bioinformatics applications in phylogenetics, metagenomics, systems biology and cancer genomics. (MEC: DPI2015-67082-P)  
PI: Francesc Andreu Rossello'. Role: Investigator.
- 2015-2017** The pre-BCR CDR-H3 sensing site and H chain selection (NIH: 1R21AI117703-01A1).  
PI: Harry Schroeder. Role: Co-Investigator.
- 2014-2015** Mechanisms of glucose mediated cardiac mitochondrial dysfunction (NIH: 3R00HL111322-04S1).  
PI: Adam Wende. Role: Co-Investigator.
- 2006-2008** Marie Curie Reintegration Grant - European Union, PI: Marc A. Marti-Renom.  
RNA Comparative Modeling.
- 2004-2006** VI Framework Programme - European Union, PI: Janet Thornton.  
Biosapiens Network of Excellence, A European Virtual Institute for Genome Annotation.
- 2003-2004** FIS2002 - Italian Ministry of Education Research and University (MIUR), PI: Rita Casadio.  
Hydrolases from Thermophiles: Structure, Function and Homologous and Heterologous Expression.

## Research Interests

- Analysis and interpretation of cancer genome.
- Genome interpretation and prediction of disease-related protein mutations.
- Machine learning approaches in molecular biology.
- Protein-protein interactions.
- RNA structure comparison and prediction.
- Protein folding kinetics.
- Prediction of protein stability changes upon mutation.
- Protein structural prediction by threading methods and building by homology.
- Molecular dynamics of protein systems.

## Developed Web Servers, Tools and Databases

- **ContrastRank**: probabilistic method for cancer gene prioritization and cancer sample classification.  
WEB: <http://snps.biofold.org/contrastrank>
- **DrCancer**: predictor of cancer causing non-synonymous single nucleotide polymorphisms.  
WEB: <http://snps.biofold.org/drcancer>
- **Fido-SNP**: predicts the impact of genetic variants in coding and non-coding regions of the dog genome.  
WEB: <http://snps.biofold.org/fido-snp>
- **I-Mutant1.0**: Neural Network based method to predict the sign of free energy change of proteins upon single point mutation.  
WEB: <http://gpcr2.biocomp.unibo.it/cgi/predictors/I-Mutant/I-Mutant.cgi>
- **I-Mutant2.0**: Support Vector Machine based method to predict the sign and the value of free energy change of proteins upon single point mutation.  
WEB: <http://folding.biofold.org/i-mutant>
- **K-Fold**: Support Vector Machine based method to predict the mechanism and rate of protein folding kinetic.  
WEB: <http://folding.biofold.org/k-fold>
- **Meta-SNP**: Meta-predictor of disease causing variants that uses PANTHER, PhD-SNP, SIFT and SNAP.  
WEB: <http://snps.biofold.org/meta-snp>
- **Omidios**: Omidios, a database of pre-calculated likely impact of a Single Nucleotide Polymorphism in the human genome.  
WEB: <http://sgt.cnag.cat/services/Omidios/>
- **PhD-SNP**: Support Vector Machine based Method to discriminate between disease-related and neutral mutations in proteins.  
WEB: <http://snps.biofold.org/phd-snp>
- **PhD-SNP9**: A gradient boosting-based method for predicting the impact of genetic variants in coding and non-coding regions.  
WEB: <http://snps.biofold.org/phd-snp9>
- **SARA**: a tool for Structural Alignment of Ribonucleic Acids.  
WEB: <http://structure.biofold.org/sara>
- **SARA-Coffee**: tool for RNA multiple structural alignment obtained merging SARA and T-Coffee.  
WEB: <http://www.tcoffee.org/Projects/saracoffee/>
- **WebRASP**: statistical potential for scoring the quality of RNA three-dimensional structure.  
WEB: <http://melolab.org/webrasp>
- **WS-SNPs&GO**: predictor of human disease related mutations in proteins with functional annotation.  
WEB: <http://snps.biofold.org/snps-and-go>

## International conferences meetings and schools

- XXVI Intelligent Systems for Molecular Biology meeting (ISMB), Chicago, (USA), 6-10 July 2018.
- V Critical Assessment of Genome Interpretation (CAGI). Chicago, (USA), 5-7 July 2018.
- The molecular basis of diseases: Can we infer phenotypes from protein variant analysis? FEBS Advanced Course. 23-25 May 2018, Bologna, Italy
- Bologna Winter School 2018: *Big Data and Bioinformatics*. Bologna (Italy), 12-16 February 2018.
- XXV Intelligent Systems for Molecular Biology meeting (ISMB) and XVI European Conference on Computational Biology (ECCB), Prague, (Czech Republic), 21-25 July 2017
- Bologna Winter School 2017: *Revisiting Bioinformatics Foundations*. Bologna (Italy), 13-17 February 2017.
- XIV Intelligent Systems for Molecular Biology meeting (ISMB), Orlando, FL (USA), 8-12 July 2016
- Bologna Winter School 2016: *In Silico Markers for Precision Medicine*. Bologna (Italy) 22-26 February 2016.
- EMBL Conference on Cancer Genomics, Heidelberg (Germany), 1-4 November 2015.
- XXIII Intelligent Systems for Molecular Biology meeting (ISMB) and XIV European Conference on Computational Biology (ECCB), Dublin (Ireland), 12-14 July 2015
- UAB NHGRI IV Short Course on Next-Generation Sequencing; Technology and Statistical Methods. Birmingham

- (AL), 15-18 December 2014.
- XIII European Conference on Computational Biology (ECCB), Strasbourg (France), 7-10 September 2014.
- XXII Intelligent Systems for Molecular Biology meeting (ISMB), Boston, Massachusetts (USA), 13-15 July 2014.
- VarI-SIG meeting. Identification and annotation of genetic variants in the context of structure, function, and disease. Boston, Massachusetts (USA), 12 July 2014.
- XXI Intelligent Systems for Molecular Biology meeting (ISMB) and XII European Conference on Computational Biology (ECCB), Berlin (Germany), 21-23 July 2013
- SNP-SIG meeting. Identification and annotation of SNPs in the context of structure, function, and disease. Berlin (Germany), 19 July 2013
- Critical Assessment of Genome Interpretation (CAGI). Berlin (Germany), 17-18 July 2013.
- ESHG Course in Next Generation Sequencing, Bertinoro di Romagna (Italy), 17-20 May 2013
- Summit on Translational Bioinformatics (TBI), San Francisco, California (USA), 18-20 March 2013.
- XX Intelligent Systems for Molecular Biology meeting (ISMB), Long Beach, California (USA), 15-17 July 2012.
- SNP-SIG meeting. Identification and annotation of SNPs in the context of structure, function, and disease. Long Beach, California (USA), 14 July 2012.
- Bologna Winter School 2012 *Proteins and their variants: structure and function prediction*. Bologna (Italy) 13-17 February 2012.
- XIX Intelligent Systems for Molecular Biology meeting (ISMB) and X European Conference on Computational Biology (ECCB), Vienna (Austria), 17-19 July 2011.
- SNP-SIG meeting. Identification and annotation of SNPs in the context of structure, function, and disease. Vienna (Austria), 15 July 2011.
- EMBO Young Scientist Forum. International Institute of Molecular and Cell Biology (IIMCB), Warsaw (Poland), June 30<sup>th</sup> – July 1<sup>st</sup> 2011.
- Pacific Symposium on Biocomputing (PSB) 2011. Big Islands, Hawaii January 3-7 2011.
- Critical Assessment of Genome Interpretation (CAGI). University of California at Berkeley. Berkeley, California (USA), 10 December 2010.
- Biomedical Computation at Stanford (BCATS). Stanford University. Palo Alto, California (USA), 6 November 2010.
- Exploring the functional consequences of genomic variation (HGVS meeting), Washington DC (USA), 2 November 2010
- II Workshop on Annotation, Interpretation and Management of Mutations (AIMM) and IX European Conference on Computational Biology (ECCB), Ghent (Belgium), 26-29 September 2010.
- 4<sup>th</sup> Comprehensive Cancer Research Training Program (CCRTP) at Stanford University, Palo Alto California (USA), 13-17 September 2010.
- 9<sup>th</sup> International Conference on Computational Systems Bioinformatics (CSB). Stanford, Palo Alto, California (USA), 16-18 August 2010.
- XVIII Intelligent Systems for Molecular Biology meeting (ISMB), Boston (USA), 11-13 July 2010.
- Biomedical Computation at Stanford (BCATS). Stanford University. Palo Alto, California (USA), 7 November, 2009.
- Lipari International Summer School on Bioinformatics and Computational Biology. RNAs: structure, function and therapy. Lipari (ME) 13-20 June, 2009.
- VII European Conference on Computational Biology (ECCB), Cagliari (Italy), 22-26 September 2008.
- Workshop on Applications of Protein Models in Biomedical Research, University of California San Francisco (UCSF), San Francisco (CA) 11-12 July, 2008
- III Course on Molecular Evolution, Phylogenetics and Phylogenomics, Valencia (Spain) 12-16 May 2008.
- Non-Coding RNAs: Computational Challenges and Applications. Antalya (Turkey) 28-30 April 2008.
- XV Intelligent Systems for Molecular Biology meeting (ISMB) and VI European Conference on Computational Biology (ECCB), Vienna (Austria), 21-25 July 2007.
- ISMB 3DSig Satellite Meeting - Structural Bioinformatics and Computational Biophysics, Vienna (Austria), 19-20 July 2007.
- EMBO Workshop: Viral RNA: Structure Function and Targeting. EMBL Heidelberg (Germany) 5-7 March 2007.
- Bologna Winter School 2006. Applied Bioinformatics: The test case of Human Genome. Bologna (Italy), 13-17 February, 2006.
- Bologna Winter School 2005: *How Complex is Functional Genomics?* Bologna (Italy), 13-19 February 2005.
- XII Intelligent Systems for Molecular Biology (ISMB) and III European Conference on Computational Biology meeting (ECCB), Glasgow (Scotland) 31 July – 4 August 2004.
- Bologna Winter School 2004: *The State of the Art of Protein-Protein Interaction Networks. The role of the "in silico" approach*, Bologna (Italy) 8-14 February 2004.
- Meeting Galileo Project. Marseille (France) 27-28 June 2003.
- Bologna Winter School 2003: *Hot Topics in Structural Genomics* Bologna (Italy) 9-15 February 2003.
- Bologna Winter School 2002: *Predicting 3D Structure of Difficult Proteins*. Bologna (Italy) 3-9 February 2002.
- Bologna Winter School 2001: *In Silico Biomolecular Recognition*. Bologna (Italy) 4-10 February 2001.
- Bologna Summer School: *Biotechnology Protein Sequence Analysis in the Genomic Era*. Bologna (Italy) 10-16 October 1999.

## National conferences meetings and schools

- Computational and Translational Methods for Cancer Genomics, Bologna 29 May, 2018.
- German Conference on Bioinformatics (GCB) 2015, Dortmund (Germany), 27-30 September 2015.
- UAB Comprehensive Cancer Center, 15<sup>th</sup> Annual Research Retreat and Research Competition, Birmingham, Alabama (USA), October 29 2012.
- VIII Jornadas de Bioinformatica. Valencia (Spain), 13-15 February 2008.
- VI Meeting on Nucleic Acids and Nucleotides (RANN07), Valencia (Spain), 22-23 November 2007.
- VII Jornadas de Bioinformatica. Zaragoza (Spain), 20-22 November 2006.
- Bioinformatics Italian Society (BITS) Annual Meeting 2006. Bologna (Italy), 28-29 April 2006.
- Bioinformatics Italian Society (BITS) Annual Meeting 2004 Padova (Italy), 26-27 March 2004.
- Workshop Staminal Cells: *Properties and Perspectives*. Bressanone (Italy), 11-13 September 2003.
- XI National School of Biophysics: Biophysics of the Cell. Bressanone (Italy), 8-10 September 2003.
- IX National School of Biophysics: *Biophysics and Biomaterials*. Bressanone (Italy), 3-5 September 2001.
- XXXI National Congress of Physical Chemistry, Padova (Italy), 19-23 June 2001.

## Invited talks

- 07 Aug 2006** Centro de Investigacion Principe Felipe (CIPF), Valencia (Spain)  
**23 Oct 2007** Centro Nacional de Investigaciones Oncológicas (CNIO), Madrid (Spain)  
**06 May 2008** Département d'Informatique, Université Libre de Bruxelles (ULB), Bruxelles (Belgium)  
**23 Apr 2009** Departament de Ciències Matemàtiques i Informàtica, Universitat de les Illes Balears (UIB), Palma de Mallorca (Spain)  
**27 May 2010** Buck Institute, Novato (California, USA)  
**02 Jul 2010** Luxembourg Centre for System Biomedicine, Luxemburg University, Luxembourg  
**20 Sep 2010** Department of Genetics and Bioengineering, Yeditepe University, Istanbul (Turkey)  
**25 Jan 2011** Department of Medicinal Chemistry and Molecular Pharmacology, Purdue University, Lafayette (Indiana, USA).  
**18 Feb 2011** Lawrence Berkeley National Laboratory, Berkeley (California, USA).  
**21 Mar 2011** Department of Computer Sciences, Wayne State University, Detroit (Michigan, USA).  
**06 Apr 2011** J. Craig Venter Institute, San Diego (California, USA)  
**22 Apr 2011** Department of Bioengineering, University of Texas at Dallas (Texas, USA)  
**17 May 2011** Department of Pathology, University of Alabama at Birmingham (Alabama, USA)  
**26 May 2011** Department of Computer Science, Université Pierre et Marie Curie, Paris (France)  
**16 Jun 2011** Instituto Gulbenkian de Ciencia, Oeiras (Portugal)  
**29 Jun 2011** International Institute of Molecular and Cell Biology, Warsaw (Poland)  
**04 Oct 2011** Institut de Cancerologie Gustave Roussy, Villejuif (France)  
**06 Oct 2011** Karlsruhe Institute of Technology, Karlsruhe (Germany)  
**12 Jun 2012** Switch Lab, KU Leuven, Leuven (Belgium)  
**30 Apr 2013** Biomedical Informatics Day, Adelaide (SA, Australia)  
**16 Jul 2013** Institute for Medical and Human Genetics, Charité University, Berlin (Germany)  
**07 Oct 2013** CCNR, Northeastern University, Boston (Massachusetts, USA)  
**10 Dec 2013** Macromolecular Biochemistry Research Center (CRBM), CNRS, Montpellier (France)  
**14 Dec 2013** Computational Biology Institute (IBC), CNRS, Montpellier (France)  
**12 Feb 2014** Institute of Genetics and Molecular and Cell Biology (IGBMC), Strasbourg (France)  
**22 May 2014** Montpellier Cancer Research Institute, University of Montpellier, Montpellier (France)  
**06 Aug 2014** Izmir Biomedicine and Genome Center (IBG), Izmir (Turkey)  
**18 Sep 2014** Technical University of Munich (TUM), Munich (Germany)  
**26 Sep 2014** Pontificia Universidad Catolica de Chile, Santiago de Chile (Chile)  
**12 Sep 2016** Adam Mickiewicz University (AMU), Poznan (Poland)

## Invited lectures

- 01 Sep 2011** Statistics and Genomics Seminar, University of California, Berkeley (California, USA)  
**17 Feb 2012** Bologna Winter School 2012, Bologna (Italy)  
**08 Feb 2013** Anatomic Pathology Didactic Conference. University of Alabama at Birmingham (Alabama, USA)  
**15 Feb 2013** Genetics and Genomics Seminar Series. University of Alabama at Birmingham (Alabama, USA)  
**04 Mar 2013** GBM-722 Bioinformatics Course. University of Alabama at Birmingham (Alabama, USA)  
**07 Mar 2013** Biotechnology Professional Master. University of Alabama at Birmingham (Alabama, USA)  
**22 Apr 2013** GBS Structural Biology Course. University of Alabama at Birmingham (Alabama, USA)  
**14 May 2013** Laboratory Medicine Seminar. University of Alabama at Birmingham (Alabama, USA)  
**17 May 2013** European School of Genetic Medicine. European School of Genetic Medicine, Bertinoro (Forlì, Italy)  
**02 Feb 2014** GBM-722 Bioinformatics Course. University of Alabama at Birmingham (Alabama, USA)

**06 Mar 2014** Biotechnology Professional Master. University of Alabama at Birmingham (Alabama, USA)  
**03 Jul 2014** GBS-758 New Perspectives in Cardiovascular Biology. University of Alabama at Birmingham (Alabama, USA)  
**08 Oct 2014** Biotechnology Professional Master. University of Alabama at Birmingham (Alabama, USA)  
**18 Dec 2014** UAB NHGRI IV Short Course on Next-Generation Sequencing; Technology and Statistical Methods. University of Alabama at Birmingham (Alabama, USA)  
**25/26 Feb 2016** Bologna Winter School 2016, University of Bologna (Italy).  
**09 Jun 2017** PhD Program in Biochemistry, "La Sapienza" University, Roma (Italy)  
**06 Sep 2017** Special course on NGS data analysis. CRO National Cancer Institute, Aviano (Italy)  
**17 Jan 2019** Winter School University of Verona, Canazei (Italy)  
**17 Jul 2019** University of Lisboa, Lisboa (Portugal)

## Publications

I published 43 research articles and 9 reviews in international peer-reviewed journals with impact factor. I also published 17 between book chapters (9) and congress acts (8). Using Google Scholar my papers received more than 4,000 citations corresponding to an h-index of 27. According to Scopus, my papers received more than 3,000 citations corresponding to an h-index of 25. Using Web of Science my articles received more than 2,700 citations corresponding to h-index of 23.

Google Scholar: <https://goo.gl/Fyy8M4>

Scopus: <https://goo.gl/F6cMSy>

ORCID: <http://orcid.org/0000-0002-2323-0963>

ResearcherID: <http://www.researcherid.com/rid/D-9318-2011>

ResearchGate: <https://goo.gl/o7HmPo>

## Papers on international journals with impact factor

**Capriotti E, Fariselli P, Rossi I, Casadio R** (2004). A Shannon entropy-based filter detects high-quality profile-profile alignments in searches for remote homologues. **Proteins** 54:351-360. (IF: 2.627, Google Citations: 16)

**Compiani M, Capriotti E, Casadio R** (2004). The dynamics of the minimally frustrated helices determine the hierarchical folding of small helical proteins. **Phys Rev E**. 65:051905-8. (IF: 2.288 Google Citations: 9)

**Capriotti E, Fariselli P, Casadio R** (2004). A neural network-based method for predicting protein stability changes upon single point mutations. **Bioinformatics**. 20 (Suppl 1):I63-I68. (IF: 4.981, Google Citations: 158)

**Stizza A, Capriotti E, Compiani M** (2005). A minimal model of three-state folding dynamics of helical proteins. **Journal of Physical Chemistry B**, 109: 4215-4226. (IF: 3.302, Google Citations: 2)

**Capriotti E, Fariselli P, Casadio R** (2005). I-Mutant2.0: predicting stability changes upon mutation from the protein sequence or structure. **Nucleic Acids Research**, 33 Web Server Issue: W306-W310. (IF: 9.112, Google Citations: 622)

**Capriotti E, Fariselli P, Calabrese R, Casadio R** (2005). Predicting protein stability changes from sequences using support vector machines. **Bioinformatics**, 21 Suppl 2:ii54-ii58. (IF: 4.981, Google Citations: 122)

**Capriotti E, Compiani M** (2006). Diffusion-Collision of Foldons Elucidates the Kinetic Effects of Point Mutations and Suggests Control Strategies of the Folding Process of Helical Proteins. **Proteins**, 64: 198-209. (IF: 2.627, Google Citations: 2)

**Grandi F, Sandal M, Guarguaglini G, Capriotti E, Casadio R, Samori B** (2006). Hierarchical mechanochemical switches in Angiostatin. **ChemBiochem**, 7; 1774-1782. (IF: 3.082, Google Citations: 23)

**Capriotti E, Calabrese R, Casadio R.** (2006). Predicting the insurgence of human genetic diseases associated to single point protein mutations with Support Vector Machines and evolutionary information. **Bioinformatics**, 22; 2729-2734. (IF: 4.981, Google Citations: 377)

**Capriotti E\*, Casadio R** (2007). K-Fold: a tool for the prediction of the protein folding kinetic order and rate. **Bioinformatics**, 23; 385-386. (IF: 4.981, Google Citations: 52)

**Capriotti E, Arbiza L, Casadio R, Dopazo J, Dopazo H, Marti-Renom MA** (2008). The use of estimated evolutionary strength at the codon level improves the prediction of disease related protein mutations in human. **Human Mutation**, 29; 198-204. (IF: 5.144, Google Citations: 40)



**Capriotti E, Marti-Renom M.** (2008). RNA structure alignment by a unit-vector approach. **Bioinformatics**, 24; i112-i116. (IF: 4.981, Google Citations: 57)

**Capriotti E, Fariselli P, Rossi I, Casadio R.** (2008). A three-state prediction of single point mutations on protein stability changes. **BMC Bioinformatics**. 9 (Suppl 2); S6. (IF: 2.576, Google Citations: 157)

*Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R* (2009) Functional annotations improve the predictive score of human disease-related mutations in proteins. **Human Mutations**, 30; 1237-1244. (IF: 5144, Google Citations: 356)

**Capriotti E, Marti-Renom M** (2009) SARA: a server for function annotation of RNA structures. **Nucleic Acids Research**. 37 (Web Server issue); W260-W265. (IF: 9.112, Google Citations: 47)

**Capriotti E, Marti-Renom MA.** (2010). Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. **BMC Bioinformatics**. 11; 322. (IF: 2.576, Google Citation: 29)

*Baù D, Sanyal A, Lajoie BR, Capriotti E, Byron M, Lawrence JB, Dekker J, Marti-Renom MA* (2011). The three-dimensional folding of the  $\alpha$ -globin gene domain reveals formation of chromatin globules. **Nature Structure & Molecular Biology**. 18; 107-114. (IF: 13.309, Google Citation: 209)

**Capriotti E, Norambuena T, Marti-Renom MA, Melo F.** (2011). All atom knowledge-based potential for RNA structure prediction and assessment. **Bioinformatics**. 27; 1086-1093. (IF: 4.981, Google Citation: 27)

**Capriotti E\*, Altman RB.** (2011). Improving the prediction of disease-related variants using protein three-dimensional structure. **BMC Bioinformatics**. 12 (Suppl 4); S3. (IF: 2.67, Google Citation: 59)

**Capriotti E\*, Altman RB.** (2011). A new disease-specific machine learning approach for the prediction of cancer-causing missense variants. **Genomics**. 98; 310-317. (IF: 2.284, Google Citation: 38)

*Dewey FE, Chen R, Cordero SP, Ormond KE, Caeshu C, Karczewski KJ, Whirl-Carrillo M, Wheeler MT, Dudley JT, Byrnes JK, Cornejo OE, Knowles JW, Woon M, Sangkuhl K, Gong L, Thorn CF, Hebert JM, Capriotti E, David SP, Pavlovic A, West A, Thakuria JV, Ball MP, Zarnek AW, Rehm HL, Church GM, West JS, Bustamante CD, Snyder M, Altman RB, Klein TE, Butte AJ, Ashley EA.* (2011). Phased whole-genome genetic risk in a family quartet using a major allele reference sequence. **PLOS Genetics** 7; e1002280. (IF: 7.528, Google Citation: 95)

*Kemena C, Bussotti G, Capriotti E, Marti-Renom MA, Cedric Notredame C.* (2013). Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. **Bioinformatics**. 29:1112-1119. (IF: 4.981, Google Citation: 4)

**Capriotti E\*, Calabrese R, Fariselli P, Martelli PL, Altman RB, Casadio R\*.** (2013). WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variations using functional annotation. **BMC Genomics**. 14 (Suppl 3): S6. (IF: 3.986, Google Citation: 43)

**Capriotti E\*, Altman RB, Bromberg Y\*.** (2013) Collective judgment predicts disease-associated single nucleotide variants. **BMC Genomics**. 14 (Suppl 3): S2. (IF: 3.986, Google Citation: 70)

*Norambuena T, Cares JF, Capriotti E, Melo F* (2013). WebRASP: a server for computing energy scores to assess the accuracy and stability of RNA 3D structures. **Bioinformatics**. 29: 2649-2650. (IF: 4.981, Google Citation: 1)

*Li B, Seligman C, Thusberg J, Miller JL, Auer J, Whirl-Carrillo M, Capriotti E, Klein TE, Mooney SD.* (2014). In silico comparative characterization of pharmacogenomic missense variants. **BMC Genomics**. 15 (Suppl 4): S4. (IF: 3.986, Google Citation: 2)

*Di Tommaso P, Bussotti G, Kemena C, Capriotti E, Chatzou M, Prieto Barja P, Notredame C.* (2014). SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. **Nucleic Acids Research**. 42 (Web Server Issue): W356-W360. (IF: 9.112, Google Citations: 14)

*Tian R, Basu MK, Capriotti E\*.* (2014). ContrastRank: a new method for ranking putative cancer driver genes and classification of tumor samples. **Bioinformatics**. 30: i572-i578. (IF: 4.981, Google Citation: 3)

*Beerten J, Van Durme J, Gallardo R, Capriotti E, Serpell L, Schymkowitz J and Rousseau F* (2015). WALTZ-DB: a benchmark database of amyloidogenic hexapeptide-tides. **Bioinformatics**. 31:1698-1700. (IF: 4.981, Google Citation: 13)

*Khass M, Blackburn T, Burrows PD, Walter MR, Capriotti E, Schroeder HW Jr.* (2016). VpreB serves as an invariant surrogate antigen for selecting immunoglobulin antigen-binding sites. **Science Immunology**. 1: DOI: 10.1126/sciimmunol.aaf6628.

Capriotti E\*, Martelli PL, Fariselli P, Casadio R. (2017). Blind prediction of deleterious amino acid variations with SNPs&GO. **Human Mutation**. DOI:10.1002/humu.23179

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, Zauha J, Zhao H, Zhou Y, Brenner SE, Moulton J, Tosatto SCE. (2017). Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. **Human Mutation**. DOI:10.1002/humu.23235.

**Capriotti E\***, Fariselli P. (2017). PhD-SNP<sup>g</sup>: A webserver and lightweight tool for scoring single nucleotide variants. **Nucleic Acids Research**. DOI:10.1093/nar/gkx369.

**Capriotti E\***, Montanucci L, Profiti G, Rossi I, Giannuzzi D, Aresu L, Fariselli P\*. (2019). Fido-SNP: The first webserver for scoring the impact of single nucleotide variants in the dog genome. **Nucleic Acids Research**. DOI: 10.1093/nar/gkz420

Savojardo C, Babbi G, Bovo S, **Capriotti E**, Martelli PL, Casadio R. (2019). Are machine learning based methods suited to address complex biological problems? Lessons from CAGI-5 challenges. **Human Mutation**. DOI: 10.1002/humu.23784.

Petrosino M, Pasquo A, Novak L, Toto A, Gianni S, Mantuano E, Veneziano L, Minicozzi V, Pastore A, Puglisi R, **Capriotti E**, Chiaraluce R, Consalvi V. (2019). Characterization of human frataxin missense variants in cancer tissues. **Human Mutation**. DOI: 10.1002/humu.23789.

Montanucci L, **Capriotti E\***, Frank Y, Ben-Tal N, Fariselli P. (2019). DDGun: an untrained method for the prediction of protein stability changes upon single and multiple point variations. **BMC Bioinformatics**. 20 (Suppl 14): 335.

Savojardo C, Petrosino M, Babbi G, Bovo S, Corbi-Verge C, Casadio R, Piero Fariselli P, Folkman L, Garg A, Karimi M, Katsonis P, Kim PM, Lichtarge O, Martelli PL, Pasquo A, Pal D, Shen Y, Strokach AV, Turina P, Zhou Y, Andreoletti G, Brenner S, Chiaraluce R, Consalvi V, **Capriotti E\***. (2019). Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. **Human Mutation**. DOI: 10.1002/humu.23843.

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, Pal LR, Radivojac P, Rousseau F, Savojoardo C, Schymkowitz J, Thusberg J, Tosatto SCE, Vihinen M, Väliäho J, Repo S, Moulton J, Brenner SE, Friedberg I. (2019). Assessing Computational Predictions of the Phenotypic Effect of Cystathionine-beta-Synthase Variants. **Human Mutation**. DOI: 10.1002/humu.23868.

Zhang J, Kinch LN, Cong Q, Katsonis P, Lichtarge O, Savojoardo C, Babbi G, Martelli PL, **Capriotti E**, Casadio R, Garg A, Pal D, Weile J, Sun S, Verby M, Roth FP, Grishin NV. (2019) Assessing predictions on fitness effects of missense variants in calmodulin. **Human Mutation**. DOI: 10.1002/humu.23857.

Monzon AM, Carraro M, Chiricosta L, Reggian F, Han J, Ozturk K, Wang Y, Miller M, Bromberg Y, **Capriotti E**, Savojoardo 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. (2019). Performance of computational methods for the evaluation of Pericentriolar Material 1 missense variants in CAGI-5. **Human Mutation**. DOI: 10.1002/humu.23856.

Voskanian A, Katsonis P, Lichtarge O, Pejaver V, Radivojac P, Mooney SD, **Capriotti E**, Bromberg Y, Wang Y, Miller M, Martelli PL, Savojoardo 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, Moulton J, Kann MG. (2019). Assessing the performance of in-silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. **Human Mutation**. DOI: 10.1002/humu.23849.

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, Savojoardo C, Martelli PL, Casadio R, Pal LR, Moulton J, Brenner S, Altman R. (2019). Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. **Human Mutation**. DOI: 10.1002/humu.23825.

## Reviews on international journals with impact factor

Fariselli P, Rossi I, **Capriotti E**, Casadio R (2007). The WWWH of remote homolog detection: The state of the art. **Briefings in Bioinformatics**, 8; 78-87. (IF: 9.617, Google Citations: 36)

**Capriotti E**, Marti-Renom MA (2008). Computational RNA structure prediction. **Current Bioinformatics**, 3; 32-45. (IF: 0.912, Google Citations: 39)

Liu T, Tang GW, **Capriotti E\***. (2011). Comparative modeling: the state of the art and protein drug target structure prediction. **Combinatorial Chemistry & High Throughput Screening**. 14: 532-547. (IF: 1.222, Google Citation: 43)

Fernald GH, Capriotti E, Daneshjou R, Karczewski KJ, Altman RB. (2011). Bioinformatics challenges for personalized medicine. **Bioinformatics**. 27: 1741-1748. (IF: 4.981, Google Citation: 198)

Capriotti E\*, Nehrt NL, Kann MG\*, Bromberg Y\*. (2012). Bioinformatics for personal genome interpretation. **Briefings in Bioinformatics**. 13; 495-512. (IF: 9.112, Google Citation: 55)

Lahti JL, Tang GW, Capriotti E, Liu T, Altman RB. (2012) Bioinformatics and variability in drug response: a protein structural perspective. **Journal of Royal Society Interface**. 9: 1409-1437. (IF: 3.913, Google Citation: 53).

Compiani M\*, Capriotti E\*. (2013) Computational and theoretical methods for protein folding. **Biochemistry**. 52: 8601-8624. (IF: 3.015. Google Citation: 21)

Tian R, Basu MK, Capriotti E\*. (2015). Computational methods and resources for the interpretation of genomic variants in cancer. **BMC Genomics**. 16 (Suppl. 8): S7. (IF: 3.986, Google Citation: 1)

Capriotti E\*, Ozturk K, Carter H. (2018). Integrating molecular network with genetic variant interpretation for precision medicine. **WIREs Systems Biology and Medicine**. e1443.

#### Paper on international journals without impact factor

Capriotti E, Casadio R (2006). The Evaluation of Protein Folding Rate Constant is Improved by Predicting the Folding Kinetic Order with a SVM-based Method. **WSEAS Transactions on Biology and Biomedicine**. Issue 4, Volume 3, April 2006, pp 304-310. (ISSN 1109-9518)

#### Book chapters and congress acta

Casadio R, Capriotti E, Compiani M, Fariselli P, Jacoboni I, Martelli PL, Rossi I, Tasco G. Neural Networks and the Prediction of Protein Structure. In: Artificial Intelligence and Heuristic Methods for Bioinformatics (Frasconi P and Shamir R Editors) **NATO Series Books. IOS Press Amsterdam**, 2003, pag. 22-33.

Casadio R, Calabrese R, Capriotti E, Compiani M, Fariselli P, Marani P, Montanucci L, Martelli PL, Rossi I, Tasco G Machine learning and the prediction of protein structure: the state of the art. **X International Conference on Information Processing and Management of Uncertainty in Knowledge-Based Systems (IPMU 2004)**. July 4-9 2004, Perugia Italy, Publisher: La Sapienza, Roma, pag 933-940.

Compiani M, Capriotti E, Casadio R. A Stochastic and computational method for estimating the folding rates of wild type and mutant proteins. **II International Meeting on Complexity in the Living: a problem-oriented approach**. September 28-30 2004, Roma, Italy.

Capriotti E, Casadio R. A machine learning approach for predicting kinetic order and rate constant of protein folding. 2006 **WSEAS International Conference on Mathematical Biology and Ecology (MABE '06)** 18-20/01/2006 Miami, Florida, USA, pp. 123-127.

Bartoli L, Capriotti E, Fariselli P, Martelli PL, Casadio R. The pros and cons of predicting protein contact maps. **Protein Structure Prediction Series: Methods in Molecular Biology**. Springer, Humana Press, 2007 (Zaki M and Bystroff C Editors) 2nd ed., 2007, 413: pp. 199-218. (Google Citations: 28)

Capriotti E, Marti-Renom, MA. Assessment of protein structure predictions. **Computational Structural Biology: Methods and Applications**. World Scientific Publishing Company (Schwede T and Peitsch MC Editors) 2008, pp 89:109. (Google Citations: 5)

Marti-Renom MA, Capriotti E, Shindyalov I, Bourne P. **Structural Comparison and Alignment**. Structural Bioinformatics II Edition. John Wiley & Sons, Inc., 2009, pp 397:418. (Google Citations: 7)

Dufour D, Capriotti E, Marti-Renom MA. (2013). Computational methods for RNA structure prediction and analysis. **RNA Nanotechnology**. PanStanford Publishing, 2013, pp. 21-50.

Capriotti E. Comparative modeling and structure prediction: application to drug discovery. **In silico drug discovery and design**. Future Science Publishing, 2013, pp. 34-48.

## Meeting reports

Alkan C, Capriotti E, Eskin E, Hormozdiari F, Kann MG. **PERSONAL GENOMICS - Session Introduction**. World Scientific Publishing Company (Russ B Altman, Keith Dunker, Lawrence Hunter, Tiffany A. Jung and Teri E Klein) Pacific Symposium on Biocomputing. PSB2011, 3-7 January 2011, Big Island, Hawaii (USA). 2011, pp. 229-230.

Bromberg Y, Capriotti E. **SNP-SIG Meeting 2011: Identification and annotation of SNPs in the context of structure, function, and disease**. BMC Genomics. 2012, 13 (Suppl 4): S1. (Google Citations: 4)

Bromberg Y, Capriotti E. **Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations**. BMC Genomics. 2013, 14 (Suppl 3): S1.

Bromberg Y, Capriotti E. **SNP-SIG 2013: from coding to non-coding - new approaches for genomic variant interpretation**. BMC Genomics. 2014, 15 (Suppl 4): S1.

Bromberg Y, Capriotti E. **SNP-SIG 2013: the state of the art of genomic variant interpretation**. Bioinformatics. 2015, 31:449-450.

Bromberg Y, Capriotti E. **Varl-SIG 2014 - From SNPs to variants: interpreting different types of genetic variants**. BMC Genomics 2015, 16(Suppl 8): I1.

Bromberg Y, Capriotti E, Carter H. **Varl-SIG 2015: methods for personalized medicine - the role of variant interpretation in research and diagnostics**. BMC Genomics. 2016, 17 Suppl 2:425.

Bromberg Y, Capriotti E, Carter H. **Varl-COSI 2018: a forum for research advances in variant interpretation and diagnostics**. BMC Genomics. 2019 Jul 16;20(Suppl 8):550.

## Posters

Compiani M, Capriotti E, Casadio R (2000). The diffusion collision model as a tool to predict the folding times of proteins (oral presentation). **Molecular graphics and Modelling soc: XVIII Int. Meeting: Modelling Biomolecular Mechanism** York, April 5-8 2000.

Compiani M, Capriotti E, Casadio R (2000) Minimal frustration in native proteins allows reliable estimates of the helical content of peptides. **Computational Biophysics 2000**, Nice (France) June 13-15 2000, pag. 14.

Compiani M, Capriotti E, Casadio R (2001) Estimating the folding times of all-alpha proteins by means of a diffusion-collision model and a neural network. **XXXI Congresso Nazionale di Chimica Fisica**. Padova (Italy), June 19-23 2001, pag. 152.

Compiani M, Capriotti E, Casadio R (2001) A diffusion-collision model uses the thermodynamic information extracted by a neural network to predict the folding times of all-alpha proteins. **Europhysics Conference on Computational Physics**. Aachen (Germany), September 5-8 2001, pag. A65.

Compiani M\*, Capriotti E, Casadio R (2001) Stochastic models and neural networks to compute the folding times of all- $\alpha$  proteins (oral presentation). **International School of Liquid Crystal**, Erice (Italy), October 22-26 2001.

Martelli PL, Fariselli P, Tasco G, Capriotti E, Casadio R (2002) Fishing new outer membrane proteins with neural networks. **Gruppo di Cooperazione "Bioinformatica"**, Certosa di Pontignano, Siena (Italy), March 15-16 2002.

Capriotti E, Rossi I, Fariselli P, Casadio R (2002) Building on the BASICs: protein fold recognition/threading based on "generalized" profile alignments. **V Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction**, December 1-5 2002 Asilomar, California (USA).

Capriotti E, Rossi I, Fariselli P, Casadio R (2002) Detecting high quality profile-profile alignments using Shannon entropy. **V Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction**, December 1-5 2002 Asilomar, California (USA).

Capriotti E, Rossi I, Fariselli P, Casadio R (2003) Detecting high-quality profile-profile alignments using Shannon entropy. **Bologna Winter School: Hot Topics in Structural Genomics**, Bologna (Italy), February 9-15 2003.

Compiani M, Capriotti E, Casadio R (2003) The initiation sites of folding determine the mechanism and the kinetics of the folding process of helical proteins. **Lincei EMBO Symposium: Protein Folding and Misfolding**, Roma (Italy), April 3-5 2003.

Compiani M\*, Capriotti E, Casadio R (2003) Reconstruction of the protein folding in terms of a minimal set of critical aminoacids (oral presentation). **XXI Congresso nazionale della Società Chimica Italiana**. Torino (Italy), June 22-27 2003.

Capriotti E, Rossi I, Fariselli P, Casadio R. (2003) A Shannon entropy-based filter improves the detection of high quality profile-profile alignments in remote-homologous searching. **ISMB 2003 XI International Conference on Intelligent System for Molecular Biology**, Brisbane (Australia), June 29 – July 6 2003.

Capriotti E, Rossi I, Fariselli P, Casadio R. (2003) Improving the detection of protein remote homologues using Shannon Entropy Information. **Workshop Biologia delle Cellule Staminali: Proprieta' e Prospettive**. Bressanone, Bolzano (Italy), September 11-13 2003.

Compiani M\*, Capriotti E, Casadio R (2003). Minimal models of protein folding dynamics (oral presentation). **V Congresso del Gruppo Italiano di Chimica Computazionale**. Certosa di Pontitignano, Siena (Italy), December 18-19 2003.

Capriotti E, Rossi I, Fariselli P, Casadio R. (2003) Improving the detection of protein remote homologues using Shannon Entropy Information. **BITS Meeting 2004**. Padova (Italy), March 26-27 2004.

Samori B, Grandi F, Guagliarini G, Sandal M, Casadio R, Capriotti E (2004). Mechanochemistry of Human Angiostatin. **American Chemical Society Meeting 2004**. Anaheim, California (USA), March 29-31 2004.

Capriotti E, Fariselli P, Casadio R (2004). I-Mutant: predicting protein stability upon mutation. **Proceedings XII international conference on Intelligent Systems for Molecular Biology, ISMB** Glasgow (Scotland), July 31 – August 04 2004, pag. 117.

Capriotti E, Fariselli P\*, Casadio R (2004). A neural network-based method for predicting protein stability changes upon single point mutations (oral presentation). **Proceedings XII international conference on Intelligent Systems for Molecular Biology, ISMB**. Glasgow (Scotland) July 31 – August 04 2004, pag 50.

Compiani M, Capriotti E, Casadio R (2004). Computation of the folding rates of wild type and mutant proteins. **IV International Workshop on Models and Metaphors from Biology to Bioinformatic Tools, Network Tools and Applications in Biology (NETTAB)**. Camerino, Macerata (Italy), September 5-7 2004.

Capriotti E, Fariselli P, Calabrese R, Casadio R\*. (2005). Predicting protein stability changes from sequences using support vector machines (oral presentation). **V Computational European Conference on Computational Biology (ECCB05)**. Madrid (Spain), September 28 - October 01 2005.

Calabrese R, Capriotti E, Fariselli P, Casadio R (2005). Prediction of the insurgence of human genetic diseases due to single point protein mutation. **I International Student Symposium in V Computational European Conference on Computational Biology (ECCB05)**. Madrid (Spain), September 28 - October 01 2005, SS-54.

Capriotti E, Fariselli P, Rossi I, Casadio R (2006) Improving the quality of the predictions of protein stability changes upon mutation using a multi class predictor. **BITS meeting 2006**. Bologna (Italy) April 28-29 April 2006.

Calabrese R, Capriotti E, Casadio R. (2006) PhD-SNP, a Web Server for the prediction of human genetic diseases associated to single point protein mutation . **VII Jornadas de Bioinformatica**. Zaragoza (Spain), November 20-22 2006.

Capriotti E, Marc A Marti-Renom (2007). RNA structural comparison. **EMBO Workshop: Viral RNA: Structure Function and Targeting**. EMBL Heidelberg (Germany), March 5-7 2007.

Capriotti E, Fariselli P\*, Rossi I, Casadio R. (2007) The effect of mutations on protein stability changes: a three class pair residue-discrimination study. **BITS Meeting 2007** Napoli (Italy), April 26-28 2007.

Capriotti E, Marti-Renom MA. (2007) SARA: tool for Structural Alignment of Ribonucleic Acids. **3DSig Satellite meeting Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria), July 19-20 2007, pag. 21.

Capriotti E, Arbiza L, Casadio R, Dopazo J, Dopazo H, Marti-Renom MA. (2007) Selective pressure at the codon level improves the prediction of disease related protein mutations in human. **Proceedings XV international conference on Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria) July 21-25 2007.

Capriotti E, Arbiza L, Casadio R, Dopazo J, Dopazo H, Marti-Renom MA. (2007) Selective pressure at the codon level improves the prediction of disease related protein mutations in human. **Proceedings 9th International Meeting on Human Genome Variation and Complex Genome Analysis (HGV2007)**. Sitges, Barcelona (Spain) September 6-8 2007, pag 81.

Capriotti E\*, Marti-Renom MA. (2008) SARA: tool for RNA structural alignment. **VIII Jornadas de Bioinformatica**,

Valencia (Spain), February 13-15 2008, pag 246.

*Casadio R\*, Calabrese R, Capriotti E, Fariselli P, Martelli PL.* (2008) Protein folding, misfolding and diseases: the I-Mutant suite. **International Symposium on Health Informatics and Bioinformatics (HiBit 08)**. Istanbul (Turkey) May 18-20, 2008.

*Calabrese R\*, Capriotti E, Casadio R* (2008) A machine learning approach to predict cancer-related mutations. **Bioinformatics Methods for Biomedical Complex System Applications (NETTAB08)**. Varenna, Como (Italy), May 19-21 2008.

*Calabrese R, Capriotti E, Casadio R.* (2008) PhD-SNP1.0: a web server for the Prediction of human genetic Diseases associated to missense Single Nucleotide Polymorphisms. **EMBNet Conference 2008. 20<sup>th</sup> Anniversary Celebration: Programme and Abstract Book**. Martina Franca, Bari (Italy), September 24-26 2008. pag 78.

*Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R.* (2008) Gene Ontology annotation improves the prediction of cancer-related mutations. **Final programme abstract book. Functional Genomics and Disease. 3<sup>rd</sup> ESF Functional Genomics Conference**. Innsbruck (Austria), October 1-4 2008, pag 87.

*Casadio R, Calabrese R, Capriotti E, Fariselli P, Martelli PL,* (2008) Protein destabilization and the Diseaseome. **VIII Congress of the National Institute for Biostructures and Biosystems (INBB)**. Rome (Italy), October 23-24 2008.

*Capriotti E, Altman RB.* (2010) A new disease-specific machine learning approach for the prediction of cancer-related SNPs. **XVII international conference on Intelligent Systems for Molecular Biology (ISMB)**. Boston (USA), July 11-13 2010.

*Baù D, Sanyal A, Lajoie BR, Capriotti E, Dekker J, and Marti-Renom MA.* (2010) The three-dimensional folding of the  $\alpha$ -globin gene domain reveals formation of chromatin globules. **XVII international conference on Intelligent Systems for Molecular Biology (ISMB)**. Boston (USA), July 11-13 2010.

*Capriotti E, Altman RB.* (2010) Predicting cancer-causing single amino acid polymorphisms using functional annotation. **4<sup>th</sup> Comprehensive Cancer Research Training Program (CCRTP) at Stanford University**, Palo Alto California (USA), September 13-17 2010.

*Capriotti E, Marti-Renom MA* (2010). Quantifying the relationship between RNA sequence and three-dimensional structure conservation for homology detection. **Proceedings of IX European Conference on Computational Biology, ECCB Ghent** (Belgium), September 26-29 2010.

*Capriotti E, Marti-Renom\* MA* (2010). Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. **10<sup>th</sup> Spanish Symposium on Bioinformatics (JBI2010)**, Torremolinos-Málaga (Spain), October 27-29 2010

*Capriotti E, Marti-Renom MA* (2010). Defining the relationship between sequence and three-dimensional structure conservation in RNA. **Biomedical Computation at Stanford (BCATS2010)**, Palo Alto (California, USA), November 6 2010.

*Capriotti E, Norambuena T, Marti-Renom AM, Melo F* (2011). All-atom knowledge-based potential for RNA structure prediction and assessment. **XIX international conference on Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria) July 17-19 2011.

*Capriotti E Bromberg Y, Altman RB* (2011). Improving the detection of deleterious mutations integrating the predictions four well-tested methods. **XIX international conference on Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria) July 17-19 2011.

*Thusberg J, Capriotti E, Auer J, Mooney S* (2011). Functional profiling of pharmacogenetics non-synonymous SNPs. **XIX international conference on Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria) July 17-19 2011.

*Seligman C, Thusberg J, Capriotti E, Li B, Miller J, Auer J, Whirl-Carrillo M, Klein T, Mooney S* (2012). Predicting pharmacogenetic protein variants. **XX international conference on Intelligent Systems for Molecular Biology**, Long Beach, California (USA), July 15-17 2012.

*Capriotti E, Fariselli P, Martelli PL, Casadio R* (2012). Predicting the effect of single point mutations on protein stability using evolutionary information. **XX international conference on Intelligent Systems for Molecular Biology**, Long Beach, California (USA), July 15-17 2012.

*Rocha J, Capriotti E* (2012). RNA Structural Alignment by a Flexible Matching (2012). 11th **European Conference on Computational Biology**. Basel (Switzerland), September 9-12 2012.

Capriotti E (2012). DrCancer: a new machine-learning approach for the detection of cancer-causing single amino acid polymorphisms. **UAB Comprehensive Cancer Center, 15th Annual Research Retreat and Research Competition**, Birmingham, Alabama (USA), October 29 2012.

Bromberg Y, Capriotti E (2013). SNP-SIG: Future challenges in the annotation of genetic variations. **Summit on Translational Bioinformatics (TBI)**. San Francisco, California (USA), 18-20 March 2013.

Capriotti E, Bromberg Y (2013). Meta-SNP: meta-predictor of disease causing non-synonymous variants. **Critical Assessment of Genome Interpretation (CAGI)**. Berlin (Germany), 17-18 July 2013

Capriotti E, Bromberg Y (2013). Meta-SNP: meta-predictor of disease causing non-synonymous variants. **SNP-SIG meeting at the XXI international conference on Intelligent Systems for Molecular Biology**. Berlin (Germany), 19 July 2013.

Rocha J, Segura J, Capriotti E (2013). RNADeform: Structural Alignment by Flexible Matching and Basepair Constraints. **XXI international conference on Intelligent Systems for Molecular Biology**, Berlin (Germany), July 21-23 2013.

Khass M, Watkins L, Zhuang V, Capriotti E, Burrows PD Schroeder HW. The surrogate light chain selects Mu heavy chain based on its DH CDR-H3 sequence. **15<sup>th</sup> International Congress of Immunology (ICI)**. Milan (Italy), August 22-27 2013.

Monzon A, Capriotti E, Parisi G. (2014). Conformational diversity of protein functional regions improves the characterization of deleterious mutations. **XIII European Conference on Computational Biology (ECCB)**. Strasbourg (France), September 7-10 2014.

Rocha J, Alberich R, Capriotti E. (2014). DRFLEX: An RNA Structural Classification Database with RNAFlex. **XIII European Conference on Computational Biology (ECCB)**. Strasbourg (France), September 7-10, 2014.

Tian R, Basu MK, Capriotti E\*. (2015). Prioritizing cancer driver genes with ContrastRank. **German Conference on Bioinformatics (GCB) 2015**. Dortmund (Germany), September 27-30, 2015.

Tian R, Basu MK, Capriotti E\*. (2015). ContrastRank: Prioritizing cancer-associated genes using germline mutation rates. **EMBL Conference on Cancer Genomics**. Heidelberg (Germany), 1-4 November 2015.

Emidio Capriotti\*, Piero Fariselli (2016). PhD-SNPg: A new tool for the interpretation of single nucleotide variants. **Vari-SIG 2016 Meeting - international conference on Intelligent Systems for Molecular Biology (ISMB)**. Orlando, FL (USA). 8-12 July 2016.

## Personal oral presentations

Compiani M, Capriotti E\*, Casadio R (2001) A diffusion-collision model uses the thermodynamic information extracted by a neural network to estimate the folding times of all-alpha proteins (oral presentation). **XXXI Congresso Nazionale di Chimica Fisica**. Padova (Italy), June 19-23 2001, pag 20.

Capriotti E\*, Compiani M, Casadio R (2001) Il modello di diffusione-collisione e le reti neurali: un nuovo metodo per stimare il tempo di folding delle proteine all-alpha. **Scuola Nazionale di Biofisica: Biofisica e Biomateriali (IX ciclo)**. Bressanone, Bolzano (Italy), September 3-5 2001 (pag. 35).

Capriotti E\*, Rossi I, Fariselli P, Casadio R (2003) Improving the detection of protein remote homologues using Shannon Entropy Information. **Meeting of the Galileo Cooperation Project**. Marseille (France), June 27-28 2003.

Capriotti E\*, Rossi I, Fariselli P, Casadio R. (2003) Improving the detection of protein remote homologues using Shannon Entropy Information. (oral presentation). **Scuola Nazionale di Biofisica: Biofisica della Cellula (XI ciclo)**. Bressanone, Bolzano (Italy), September 8-10 2003.

Calabrese R, Capriotti E\*, Casadio R (2006). Predicting the insurgence of human genetic diseases due to single point protein mutation using machine learning approach. **VIII Congresso SIMAI**. Baia Samuele, Ragusa (Italy), May 22-26 2006.

Capriotti E\*, Marti-Renom MA. (2007) SARA: tool for RNA structural alignment (oral presentation). **Sixth Meeting on Nucleic Acids and Nucleotides (RANN07)**. Valencia (Spain), November 22-23 2007, pag 43.

Capriotti E\*, Arbiza L, Casadio R, Dopazo J, Dopazo H, Marti-Renom MA. (2008) Selective pressure at the codon level improves the prediction of disease related protein mutations in human. **VIII Jornadas de Bioinformatica**, Valencia,

(Spain), February 13-15 2008, pag 28.

Capriotti E\*, Marti-Renom MA. (2008) SARA: a tool for RNA Structure Alignment, **Non-Coding RNAs: Computational Challenges and Applications**. Antalya (Turkey), April 28-30 2008.

Capriotti E\*, Marti-Renom M. (2008) RNA structure alignment by a unit-vector approach. **Proceedings of VII European Conference on Computational Biology**, ECCB, Cagliari (Italy), September 22-26 2008, pag 47.

Capriotti E\*, Marti-Renom MA. (2009) SARA: a method for RNA structural alignment and function annotation. **Lipari International Summer School on Bioinformatics and Computational Biology**. RNAs: structure, function and therapy. Lipari, Messina (Italy), June 13-20 2009.

Capriotti E\*, Altman RB. (2010) Predicting disease-related single amino acid polymorphisms using protein structure. **9<sup>th</sup> International Conference on Computational Systems Bioinformatics (CSB2010)**. Stanford, Palo Alto, California (USA), August 17-18 2010.

Capriotti E\*, Altman RB. (2010) Improving the prediction of disease-related variants using protein three-dimensional structure. **II Workshop on Annotation, Interpretation and Management of Mutations (AIMM) at the European Conference on Computational Biology (ECCB)**. Ghent, Belgium, September 26-29 2010.

Capriotti E\*, Altman RB. (2010) Improving the detection of deleterious single amino acid polymorphisms using protein functional and structural information. **Exploring the functional consequences of genomic variation (HGVS meeting)**. Washington DC (USA), November 2 2010.

Capriotti E\*. (2010). Predicting deleterious mutation from CAGI. **Critical Assessment of Genome Interpretation (CAGI)**. Berkeley, California (USA), 10 December 2010.

Capriotti E\*, Altman RB. (2011). Predicting deleterious single amino acid polymorphisms using protein functional and structural information. **EMBO Young Scientist Forum**. Warsaw (Poland), June 30<sup>th</sup> – July 1<sup>st</sup> 2011.

Capriotti E\*, Fariselli P, Martell PL, Casadio R (2011). SNPs&GO: predicting the deleterious effect of human mutations using functional annotation. **XIX international conference on Intelligent Systems for Molecular Biology (ISMB)**. Wien (Austria) July 17-19 2011.

Capriotti E\*, Altman RB, Bromberg Y (2013). Collective computational wisdom to predict disease-associated SNVs. **Summit on Translational Bioinformatics (TBI)**. San Francisco, California (USA), 18-20 March 2013.

Capriotti E\* (2013). Predicting deleterious mutations in p16<sup>INK4A</sup> with SNPs&GO. **Critical Assessment of Genome Interpretation (CAGI)**. Berlin (Germany), 17-18 July 2013

Tian R, Basu MK, Capriotti E\* (2014). ContrastRank: a new method for ranking putative cancer driver genes and classification of tumor samples. **XIII European Conference on Computational Biology (ECCB)**. Strasbourg (France), 7-10 September 2014.

Capriotti E\*, Fariselli P (2017). PhD-SNPg: A webserver and lightweight tool for scoring single nucleotide variants. **XXV international conference on Intelligent Systems for Molecular Biology (ISMB)**. Prague (Czech Republic), 21-25 July 2017.

Zhao L, Abedpour N, Blum C, Kolkhof P, Beller M, Kollmann M, Capriotti E (2018). Predicting gene expression changes in *E. coli* from mRNA sequence information. **XXVI international conference on Intelligent Systems for Molecular Biology (ISMB)**. Chicago (USA), 6-10 July 2018.

Capriotti E\* (2018). Evaluating the Frataxin challenge predictions. **V Critical Assessment of Genome Interpretation (CAGI)**. Chicago (USA), 5-7 July 2018

Capriotti E\* (2018). Predicting the effect of variants on GAA function. **V Critical Assessment of Genome Interpretation (CAGI)**. Chicago (USA), 5-7 July 2018

## Italian publications

Casadio R, Capriotti E, Compiani M, Fariselli P, Jacoboni I, Martelli PL, Rossi I, Tasco G. (2002) Large Scale-Modelling Of Membrane And Globular Proteins in Estratti da **5° Workshop sul Calcolo ad Alte Prestazioni in Italia: Supercalcolo In Biotecnologia, Bioinformatica, Bioingegneria** (CILEA ed.) October 21 2001, Milan, Italy.



*Casadio R, Capriotti E, Compiani M, Fariselli P, Jacoboni I, Malaguti L, Martelli PL, Rossi I, Tasco G* (2002). Proc. XV **Convegno internazionale Ordine Nazionale dei Biologi** "Progresso scientifico, etica, tutela delle risorse, Sfide Professionali del Terzo Millennio" October 3-6 2002, Umago, Croazia Vol 1:61-70.

*Casadio R, Capriotti E, Compiani M, Fariselli P, Jacoboni I, Malaguti L, Martelli PL, Rossi I, Tasco G* (2004). La predizione strutturale di proteine nell'era genomica ed i metodi di apprendimento automatico. **Biologi Italiani** 4: 38-42.

*Casadio R, Calabrese R, Tasco G, Capriotti E, Compiani M, Marani P, Montanucci L, Rossi I, Martelli PL, Fariselli P.* (2007). Metodi di Machine Learning per la predizione di strutture proteiche e della loro interazione. **Convegno Bioinformatica: sfide e prospettive**. Università del Sannio, December 17-18 2003, Benevento, Italy. F. Angeli Editore pag 51.