

FABRIZIO FERRÈ, PH.D.

INDIRIZZO:

Università di Roma Tor Vergata
Centro di Bioinformatica Molecolare (CBM), Dipartimento di Biologia
Via della Ricerca Scientifica s.n.c, 00133 Roma

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RECAPITI TELEFONICI:

011 39 06 72594320 (ufficio)
011 39 339 3691120 (cellulare)
011 39 06 2023500 (fax)

ESPERIENZA PROFESSIONALE

Giugno 2011 – presente

Assegnista presso il Centro di Bioinformatica Molecolare (CBM)
Università di Roma Tor Vergata, Dipartimento di Biologia

Dicembre 2011 – Marzo 2013

Collaboratore di Ricerca presso il CASPUR/CINECA (Consorzio interuniversitario per Applicazioni di Supercalcolo Per l'Università e la Ricerca).
CASPUR, Roma

Giugno 2008 – Maggio 2011

Ricercatore FIRB nell'unità di Biocomputing.
Università di Roma La Sapienza, Dipartimento di Scienze Biochimiche A. Rossi Fanelli

Novembre 2006 – Giugno 2008

Application Specialist II nel centro di Genomica/Programma per le Cellule Staminali.
Harvard Medical School, Children's Hospital, Dipartimento di Ematologia/Oncologia, Boston MA - USA

Luglio 2003 – Novembre 2006

Ricercatore postdoc.
Boston College, Dipartimento di Biologia, Chestnut Hill MA – USA

Gennaio 2001 – Giugno 2003

Curatore della banca dati di motivi lineari eucariotici di proteine **ELM** (<http://elm.eu.org/>)
Università di Roma Tor Vergata, (in collaborazione con EMBL, Heidelberg – Germania)

Febbraio 2001 – Maggio 2003

Curatore della banca dati di interazioni proteiche **MINT** (<http://cbm.bio.uniroma2.it/mint/>)
Università di Roma Tor Vergata

EDUCAZIONE

Novembre 1999 – Maggio 2003

Dottorato in Biologia Molecolare e Cellulare. Titolo della tesi: “*A computational approach to the analysis and comparison of protein functional surfaces*”.

Università di Roma Tor Vergata

Novembre 1992 – Maggio 1999

Laurea in Biologia (110/110 *cum laude*). Titolo della tesi: “*Methods to modulate peptides exposition on phage capsids in libraries selections*”.

Università di Roma Tor Vergata, Dipartimento di Biologia

PUBBLICAZIONI IN RIVISTE SCIENTIFICHE

1. Via A.*, **Ferrè F.***, Brannetti B., Valencia A. & Helmer-Citterich M. “*3D view of the surface motif associated to the ploop structure: cis and trans cases of convergent evolution*” *Journal of Molecular Biology* 303, 455-465 (2000) (* equal contribution)
2. Via A., **Ferrè F.**, Brannetti B. & Helmer-Citterich M. “*Protein surface similarities: a survey of methods to describe and compare protein surfaces*” *Cellular and Molecular Life Sciences* 57, 1970-1977 (2000)
3. Puntervoll P., Linding R., Gemünd C., Chabanis-Davidson S., Mattingsdal M., Cameron S., Martin D.M.A., Ausiello G., Brannetti B., Costantini A., **Ferrè F.**, Maselli V., Via A., Cesareni G., Diella F., Superti-Furga G., Wyrwicz L., Ramu C., McGuigan C., Gudavalli R., Letunic I., Bork P., Rychlewski L., Küster B., Helmer-Citterich M., Hunter W.N., Aasland R. & Gibson T.J. “*The ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins*” *Nucleic Acids Research* 31(13): 3625-30 (2003)
4. **Ferrè F.***, Via A.*, Ausiello G., Brannetti B., Zanzoni A. & Helmer-Citterich M. “*Development of computational tools for the inference of protein interaction specificity rules and functional annotation using structural information*” *Comparative and Functional Genomics* 4: 416-419. (2003) (* equal contribution)
5. **Ferrè F.**, Ausiello G. & Helmer-Citterich M. “*SURFACE: a database of protein surface regions for functional annotation*” *Nucleic Acids Research* 32 (Database issue) D240-4. (2004)
6. Clote P., **Ferrè F.**, Krizanc D. & Kranakis E. “*Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency*”. *RNA* 11(5): 578-591. (2005)
7. **Ferrè F.** & Clote P. “*Disulfide connectivity prediction using secondary structure information and diresidue frequencies*”. *Bioinformatics* 21(10):2336-46 (2005)
8. **Ferrè F.** & Clote P. “*DiANNA: a web server for disulfide connectivity prediction*”. *Nucleic Acids Research* 33 (Web Server issue):W230-2 (2005)
9. **Ferrè F.**, Ausiello G., Zanzoni A. & Helmer-Citterich M. “*Functional annotation by identification of local surface similarities: a novel tool for structural genomics*” *BMC Bioinformatics* 6:194 (2005)
10. **Ferrè F.** & Clote P. “*DiANNA 1.1: an extension of the DiANNA web server for ternary cysteine classification*” *Nucleic Acids Research* 34 (Web Server Issue): W230-2 (2006)
11. **Ferrè F.** & Clote P. “*BTW: A web server for Boltzmann time warping for gene expression time series*” *Nucleic Acids Research* 34 (Web Server Issue): W482-5 (2006)
12. **Ferrè F.**, Lorenz W.A., Ponty Y. & Clote P. “*DIAL: A web server for RNA structural alignment using dihedral angles*” *Nucleic Acids Research* 35 (Web Server Issue): W659-68 (2007)
13. Ceol C.J., Houvras Y., Jane-Valbuena J., Bilodeau S., Battisti V., Fritsch L., Lin W.M., Hollmann T.J., **Ferrè F.**, Bourque C., Burke C., Turner L., Uong A., Johnson L.A.,

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- Beroukhim R., Mermel C.H., Loda M., Ait-Si-Ali S., Garraway L., Young R.A. & Zon L.I. "The SETDB1 histone methyltransferase is recurrently amplified in and accelerates formation of melanoma" *Nature* 471(7339):513-7 (2011)
14. Leoni G., Le Pera L., **Ferrè F.**, Raimondo D. & Tramontano A. "Coding potential of the products of alternative splicing in human" *Genome Biology* 27(12):1625-9 (2011)
 15. Vecchione L., Diano L., Campagnolo L., Rocchi L., **Ferrè F.**, Siracusa G., Mehta J.L., Novelli G., Amati F. "Functional characterization and expression analysis of novel alternative splicing isoforms of *Olr1* gene during mouse embryogenesis" *Gene* 491(1):5-12 (2012)
 16. Sannella A., Olivieri A., Bertuccini L., **Ferrè F.**, Severini C., Alano P. "Specific tagging of the egress-related osmiophilic bodies in the gametocytes of *Plasmodium falciparum*" *Malar J.* 11:88 (2012)
 17. Parca L., Gherardini P.F., Truglio M., Mangone I., **Ferrè F.**, Helmer-Citterich M., Ausiello G. "Identification of nucleotide-binding sites in protein structures: a novel approach based on nucleotide modularity" *PLOS One* 7(11):e50240 (2012)
 18. Parca L., **Ferrè F.**, Ausiello G., Helmer Citterich M. "Nucleos: a web server for the identification of nucleotide binding sites in protein structures" (in press for *Nucleic Acids Research*)
 19. Bianchi V., Mangone I., **Ferrè F.**, Helmer Citterich M., Ausiello G. "webPDBinder: a server for the identification of ligand binding sites on protein structures" (in press for *Nucleic Acids Research*)
 20. Lanni S., Goracci M., Borrelli L., Chiurazzi P., **Ferrè F.**, Helmer-Citterich M., Tabolacci E., Neri G. "Role of CTCF protein in regulating *FMR1* locus conformation and transcription" (in press for *PLOS Genetics*)

LIBRI

1. **Ferrè F.** "From sequence to structure: an easy approach to protein structure prediction". In "The Internet for cell and molecular biologists" Chapter 10, 233-307. Edited by A. Cabibbo, R.P. Grant and M. Helmer-Citterich, Horizon Scientific Press (2002)
2. **Ferrè F.** "Integrated bioinformatics software at NCBF". In the Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics, Section 4.8: Modern Programming Paradigms in Biology. John Wiley & Sons (2005)
3. Ausiello G., **Ferrè F.**, Zanzoni A., Peluso D. & Helmer-Citterich M. "Annotazione funzionale attraverso l'analisi di similarità locale di superfici proteiche" in "Bioinformatica sfide e prospettive" a cura di Ceccarelli, M., Colantuoni, V., Graziano, G., Rampone, S., Franco Angeli Ed. (2006) – in Italian

MEMBRO DI:

- ISCB (International Society for Computational Biology).
- BITS (Bioinformatics Italian Society).

ORGANIZZAZIONE DI MEETING SCIENTIFICI

- ECCB '08 (European Conference on Computational Biology 2008, Cagliari IT) program committee and local organizing committee
- CASP 8 (Critical Assessment of protein Structure Prediction 2008, Cagliari IT), local organizing committee
- ISMB/ECCB '09 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2009, Stockholm SE) program committee

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- NETTAB '09 (Network Tools and Applications in Biology, Catania IT) program committee
- ISMB '10 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2010, Boston – USA) program committee
- ECCB '10 (European Conference on Computational Biology 2010, Ghent BE) program committee
- Bioinformatics 2011 (International Conference on Bioinformatics Models, Methods and Algorithms), Rome - January 2011, program committee
- BITS (Bioinformatics Italian Society) Annual Meeting 2012, Catania IT, program committee
- Bioinformatics 2013 (International Conference on Bioinformatics Models, Methods and Algorithms), Madrid – February 2013, program committee
- ISMB/ECCB '13 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2013, Berlin) program committee

INSEGNAMENTO

- Attività di supporto per il corso di Bioinformatica, Università di Roma Tor Vergata, Laurea in Biologia (anno accademico 2001/2002)
- Attività di supporto per il modulo di Bioinformatica per la scuola di Applicazioni Biotecnologiche, Università di Roma Tor Vergata (a.a. 2001/2002)
- Seminari per il corso di Bioinformatica, Boston College, Chestnut Hill MA USA (a.a. 2004/2005, 2005/2006)
- Master Inter-Facoltà in Bioinformatica (Medicina, Scienza, Farmacia), Università di Roma La Sapienza (2008/2009)
- Seminari per il corso di Tecnologie Emergenti, Università di Roma La Sapienza, 2010
- Seminari per il corso di Struttura delle Macromolecole, Lauree Magistrali in Ingegneria delle Nanotecnologie, Università di Roma La Sapienza, (a.a. 2010/2011, 2011/2012, 2012/2013)
- *Bioinformatics using Python for Biologists* course, Gulbenkian Training Programme in Bioinformatics (GTPB), Oeiras (Portogallo), Maggio 2011
- Corso di Genomica Computazionale, Laurea Magistrale in Bioinformatica, Università di Roma Tor Vergata (a.a. 2009/2010, 2010/2011, 2011/2012, 2012/2013)
- Corso di Metodi Informatici per la Biologia, Laurea Magistrale in Biologia Cellulare e Molecolare, Biologia ed Evoluzione Umana, Biologia Evoluzionistica ed Ecologica, Università di Roma Tor Vergata (a.a. 2012/2013)

SEMINARI

- Dana Farber Cancer Institute, Boston MA, USA – Gennaio 2003
- Massachusetts Institute of Technology (MIT) Bioinformatics seminar series, Cambridge MA, USA - Ottobre 2003;
- American Mathematical Society 2004 Meeting - Rider University, Lawrenceville NJ, USA- Giugno 2004;
- Massachusetts Institute of Technology (MIT) Bioinformatics seminars series, Cambridge MA, USA - Marzo 2004;
- Istituto Firc di Oncologia Molecolare (IFOM), Milano – Dicembre 2004;
- Scuola Internazionale Superiore di Studi Avanzati (SISSA), Trieste – Gennaio 2005;
- Consorzio Mario Negri Sud, Santa Maria Imbaro (Chieti) – Gennaio 2005;
- Istituto di Ricerca di Biologia Molecolare (IRBM) P. Angeletti, Pomezia (Rome) – Marzo 2005;

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- Istituto Firc di Oncologia Molecolare (IFOM), Milano – Maggio 2005;
- Beth Israel Deaconess/Harvard Cancer Center, Boston MA, USA – Settembre 2006;
- Dipartimento di Scienze Biochimiche, Facoltà di Medicina, Università di Roma La Sapienza – Luglio 2008;
- CE.IN.GE./F.I.Bio., Naples IT, *Next generation sequencing applications and future perspectives* Meeting, Aprile 2012
- PAG (Plant and Animal Genome) XXI meeting, San Diego CA, USA - Gennaio 2013

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011 39 339 3691120 (mobile)
011 39 06 2023500 (fax)

SCIENTIFIC INTERESTS

Application of Next Generation Sequencing technologies for the analysis of the transcriptome, genome sequencing and assembly, epigenetic modification analysis. Analysis of protein function modulation by alternative splicing. Analysis of the impact of mutations on the protein functional sites. Comparative genomics, genome functional annotation and gene expression analysis. MicroRNA and their targets analysis and prediction. Protein structure and protein surface analysis and comparison, and analysis of the relationship between structure, surface and function. Application of machine learning algorithms to biological problems. Analysis of RNA folding, structure, function and evolution.

SUMMARY OF QUALIFICATIONS

- Extensive knowledge of Bioinformatics and Computational Biology; Strong background in Molecular and Cellular Biology;
- More than 14 years of research experience in biomedical sciences;
- More than 12 years of experience in Computational Biology/Bioinformatics (algorithms, applications and databases);
- Two years of experience as experimental biologist, working on phage display technology;
- Proven creativeness in developing novel Computational Biology algorithms;
- Expertise in using many bioinformatics tools, public genomics and proteomics databases; experience as curator of biological databases;
- Expertise in machine learning applications to biomedical problems (neural networks, support vector machines, hidden Markov models, random forests);

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- Expertise in statistical data analysis, data mining, and experimental design;
- Proficiency in programming using many computer languages including Python, C/C++, SQL, R;
- Outstanding ability of carrying out independent research work as well as collaborative projects;
- Reviewer for Nucleic Acids Research, Bioinformatics, FEBS Letters, FEBS Journal, BMC Bioinformatics, Proteins, Journal of Mathematical Biology, Amino Acids.

PROFESSIONAL EXPERIENCE

Jun 2011 – Current

Research fellow at the Centre for Molecular Bioinformatics (CBM), directed by Professor Manuela Helmer-Citterich, working on computational genome analysis.

University of Rome Tor Vergata, Biology Department, Rome – Italy

Dec 2011 – Mar 2013

Research fellow at CASPUR/CINECA (Inter-University Consortium for the Application of Super-Computing for Universities and Research).

CASPUR, Rome – Italy

Jun 2008 – May 2011

FIRB Researcher in the Biocomputing unit (directed by Prof. Anna Tramontano), working on structural bioinformatics and computational genomics.

University of Rome La Sapienza, Biochemical Sciences Department A. Rossi Fanelli, Rome - Italy

Nov 2006 – Jun 2008

Application Specialist II in the Stem Cell Program - Genomics Core (directed by Prof. Leonard Zon), working on comparative genomics and genome annotation.

Harvard Medical School, Children's Hospital, Hematology/Oncology Department, Boston MA - USA

Jul 2003 – Nov 2006

Post-doctoral research fellow in the Computational Biology group of Prof. Peter Clote, working on gene expression time series analysis and clustering, machine learning applied to protein sequences, and different aspects of RNA folding and biology.

Boston College, Biology Department, Chestnut Hill MA – USA

January 2001 – Jun 2003

Curator of the eukaryotic proteins linear motifs database **ELM** (<http://elm.eu.org/>)

University of Rome Tor Vergata, Rome – Italy (partnership with EMBL, Heidelberg – Germany)

February 2001 – May 2003

Curator of the protein-protein interaction database **MINT** (<http://cbm.bio.uniroma2.it/mint/>)

University of Rome Tor Vergata, Rome - Italy

EDUCATION

Nov 1999 – May 2003

Ph.D. in Molecular and Cell Biology, working in the Centre for Molecular Bioinformatics (CBM), directed by Professor Manuela Helmer-Citterich. Thesis title: “*A computational approach to the analysis and comparison of protein functional surfaces*”.

University of Rome Tor Vergata, Biology Department, Rome - Italy

Nov 1992 – May 1999

B.S. – M.Sc. in Biology (110/110 *cum laude*). Experimental thesis in the Molecular Genetics lab, directed by Professor Gianni Cesareni, with the supervision of Professor Franco Felici. Thesis title: “*Methods to modulate peptides exposition on phage capsids in libraries selections*”.

University of Rome Tor Vergata, Biology Department, Rome – Italy

PUBLICATIONS IN PEER REVIEWED JOURNALS

21. Via A.*, Ferrè F.*, Brannetti B., Valencia A. & Helmer-Citterich M. “*3D view of the surface motif associated to the ploop structure: cis and trans cases of convergent evolution*” *Journal of Molecular Biology* 303, 455-465 (2000) (* equal contribution)
22. Via A., Ferrè F., Brannetti B. & Helmer-Citterich M. “*Protein surface similarities: a survey of methods to describe and compare protein surfaces*” *Cellular and Molecular Life Sciences* 57, 1970-1977 (2000)
23. Puntervoll P., Linding R., Gemünd C., Chabanis-Davidson S., Mattingsdal M., Cameron S., Martin D.M.A., Ausiello G., Brannetti B., Costantini A., Ferrè F., Maselli V., Via A., Cesareni G., Diella F., Superti-Furga G., Wyrwicz L., Ramu C., McGuigan C., Gudavalli R., Letunic I., Bork P., Rychlewski L., Küster B., Helmer-Citterich M., Hunter W.N., Aasland R. & Gibson T.J. “*The ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins*” *Nucleic Acids Research* 31(13): 3625-30 (2003)
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25. Ferrè F., Ausiello G. & Helmer-Citterich M. “*SURFACE: a database of protein surface regions for functional annotation*” *Nucleic Acids Research* 32 (Database issue) D240-4. (2004)
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29. Ferrè F., Ausiello G., Zanzoni A. & Helmer-Citterich M. “*Functional annotation by identification of local surface similarities: a novel tool for structural genomics*” *BMC Bioinformatics* 6:194 (2005)
30. Ferrè F. & Clote P. “*DiANNA 1.1: an extension of the DiANNA web server for ternary cysteine classification*” *Nucleic Acids Research* 34 (Web Server Issue): W230-2 (2006)
31. Ferrè F. & Clote P. “*BTW: A web server for Boltzmann time warping for gene expression time series*” *Nucleic Acids Research* 34 (Web Server Issue): W482-5 (2006)

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32. **Ferrè F.**, Lorenz W.A., Ponty Y. & Clote P. “*DIAL: A web server for RNA structural alignment using dihedral angles*” *Nucleic Acids Research* 35 (Web Server Issue): W659-68 (2007)
33. Ceol C.J., Houvras Y., Jane-Valbuena J., Bilodeau S., Battisti V., Fritsch L., Lin W.M., Hollmann T.J., **Ferrè F.**, Bourque C., Burke C., Turner L., Uong A., Johnson L.A., Beroukhim R., Mermel C.H., Loda M., Ait-Si-Ali S., Garraway L., Young R.A. & Zon L.I. “*The SETDB1 histone methyltransferase is recurrently amplified in and accelerates formation of melanoma*” *Nature* 471(7339):513-7 (2011)
34. Leoni G., Le Pera L., **Ferrè F.**, Raimondo D. & Tramontano A. “*Coding potential of the products of alternative splicing in human*” *Genome Biology* 27(12):1625-9 (2011)
35. Vecchione L., Diano L., Campagnolo L., Rocchi L., **Ferrè F.**, Siracusa G., Mehta J.L., Novelli G., Amati F. “*Functional characterization and expression analysis of novel alternative splicing isoforms of Orl1 gene during mouse embryogenesis*” *Gene* 491(1):5-12 (2012)
36. Sannella A., Olivieri A., Bertuccini L., **Ferrè F.**, Severini C., Alano P. “*Specific tagging of the egress-related osmiophilic bodies in the gametocytes of Plasmodium falciparum*” *Malar J.* 11:88 (2012)
37. Parca L., Gherardini P.F., Truglio M., Mangone I., **Ferrè F.**, Helmer-Citterich M., Ausiello G. “*Identification of nucleotide-binding sites in protein structures: a novel approach based on nucleotide modularity*” *PLOS One* 7(11):e50240 (2012)
38. Parca L., **Ferrè F.**, Ausiello G., Helmer Citterich M. “*Nucleos: a web server for the identification of nucleotide binding sites in protein structures*” (in press for *Nucleic Acids Research*)
39. Bianchi V., Mangone I., **Ferrè F.**, Helmer Citterich M., Ausiello G. “*webPDBinder: a server for the identification of ligand binding sites on protein structures*” (in press for *Nucleic Acids Research*)
40. Lanni S., Goracci M., Borrelli L., Chiurazzi P., **Ferrè F.**, Helmer-Citterich M., Tabolacci E., Neri G. “*Role of CTCF protein in regulating FMRI locus conformation and transcription*” (in press for *PLOS Genetics*)

BOOK CHAPTERS

4. **Ferrè F.** “*From sequence to structure: an easy approach to protein structure prediction*”. In “*The Internet for cell and molecular biologists*” Chapter 10, 233-307. Edited by A. Cabibbo, R.P. Grant and M. Helmer-Citterich, Horizon Scientific Press (2002)
5. **Ferrè F.** “*Integrated bioinformatics software at NCBF*”. In the *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, Section 4.8: Modern Programming Paradigms in Biology. John Wiley & Sons (2005)
6. Ausiello G., **Ferrè F.**, Zanzoni A., Peluso D. & Helmer-Citterich M. “*Annotazione funzionale attraverso l'analisi di similarita' locale di superfici proteiche*” in “*Bioinformatica sfide e prospettive*” a cura di Ceccarelli, M., Colantuoni, V., Graziano, G., Rampone, S., Franco Angeli Ed. (2006) – in Italian

SUBMITTED MANUSCRIPTS

- Bianchi V., Colantoni A., Gherardini P.F., Ausiello G., **Ferrè F.**, Helmer-Citterich M. “*DBATE: DataBase of Alternative Transcripts Expression*”
- Palmeri A., Ausiello G., **Ferrè F.**, Helmer-Citterich M., Gherardini P.F. “*A genome-wide domain-centric perspective on protein phosphorylation*”

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- Colantoni A., Bianchi V., Gherardini P.F., Scalia Tomba G., Ausiello G., Helmer Citterich M., Ferrè F. “*Alternative splicing tends to avoid partial removals of protein-protein interaction sites*”

MEMBERSHIPS

- ISCB (International Society for Computational Biology).
- BITS (Bioinformatics Italian Society).

MEETING ORGANIZING COMMITTEE

- ECCB '08 (European Conference on Computational Biology 2008, Cagliari IT) program committee and local organizing committee
- CASP 8 (Critical Assessment of protein Structure Prediction 2008, Cagliari IT), local organizing committee
- ISMB/ECCB '09 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2009, Stockholm SE) program committee
- NETTAB '09 (Network Tools and Applications in Biology, Catania IT) program committee
- ISMB '10 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2010, Boston – USA) program committee
- ECCB '10 (European Conference on Computational Biology 2010, Ghent BE) program committee
- Bioinformatics 2011 (International Conference on Bioinformatics Models, Methods and Algorithms), Rome - January 2011, program committee
- BITS (Bioinformatics Italian Society) Annual Meeting 2012, Catania IT, program committee
- Bioinformatics 2013 (International Conference on Bioinformatics Models, Methods and Algorithms), Madrid – February 2013, program committee
- ISMB/ECCB '13 (Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2013, Berlin) program committee

TEACHING

- Supporting activity for the Bioinformatics course, Tor Vergata University degree in Biology (academic year 2001/2002)
- Supporting activity for the Bioinformatics module in Biotechnology Applications school, Tor Vergata University Specialization Schools (academic year 2001/2002)
- Monographies for the Bioinformatics course, Boston College, Chestnut Hill MA USA (academic year 2004/2005, 2005/2006)
- Bioinformatics Inter-faculty (Medicine, Science, Pharmacy) Master at Sapienza University (2008/2009)
- Seminars for the New Technologies Course (Corso di Tecnologie Emergenti), Sapienza University, November 2010
- Seminars for the Structure of Macromolecules course, Nanotechnology Engineering “Laurea Magistrale”, Sapienza University, academic year 2010/2011, 2011/2012, 2012/2013
- *Bioinformatics using Python for Biologists* course, Gulbenkian Training Programme in Bioinformatics (GTPB), Oeiras (Portugal), May 2011
- *Computational Genomics* course, for the Bioinformatics "Laurea Magistrale", Tor Vergata University, academic year 2009/2010, 2010/2011, 2011/2012, 2012/2013

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- *Informatic methods for Biology* course, for the Molecular Biology “Laurea Magistrale”, Tor Vergata University, academic year 2012/2013

INVITED SPEAKER

- Dana Farber Cancer Institute, Boston MA, USA – January 2003
- Massachusetts Institute of Technology (MIT) Bioinformatics seminar series, Cambridge MA, USA - October 2003;
- American Mathematical Society 2004 Meeting - Rider University, Lawrenceville NJ, USA- June 2004;
- Massachusetts Institute of Technology (MIT) Bioinformatics seminars series, Cambridge MA, USA - March 2004;
- Istituto Firc di Oncologia Molecolare (IFOM), Milan – December 2004;
- Scuola Internazionale Superiore di Studi Avanzati (SISSA), Trieste – January 2005;
- Consorzio Mario Negri Sud, Santa Maria Imbaro (Chieti) – January 2005;
- Istituto di Ricerca di Biologia Molecolare (IRBM) P. Angeletti, Pomezia (Rome) – March 2005;
- Istituto Firc di Oncologia Molecolare (IFOM), Milano – May 2005;
- Beth Israel Deaconess/Harvard Cancer Center, Boston MA, USA – September 2006;
- Biochemical Sciences Department, Faculty of Medicine, Sapienza University – July 2008;
- CE.IN.GE./F.I.Bio., Naples IT, *Next generation sequencing applications and future perspectives* Meeting, April 2012
- PAG (Plant and Animal Genome) XXI meeting, San Diego CA, USA - January 2013

LANGUAGES

- Italian (native)
- English (excellent)
- French (basic)