



Curriculum Vitae Europass

Personal Information

First name(s) / Surname(s) **Luca Ambrosino**
Address(es) traversa privata Sanseverino n. 8, 80128 Napoli
Telephone(s) Mobile: 3398496090
E-mail Luca.bioinfo@gmail.com
Nationality Italy
Date of birth 08/07/1979
Sex Male

Occupational field **Bioinformatics / Computational Biology**

Employment

Scientific fields Comparative genomics, nucleotide and proteic sequences analyses, networks of ortholog and paralog genes, metabolic pathways analyses, three-dimensional modeling of protein structures, molecular dynamics simulation.

Dates **November 2017 – ongoing**
Qualification Research fellowship
Name and type of organization Research Infrastructures for Marine Biological Resources (RIMAR) - Stazione Zoologica "Anton Dohrn" - Napoli
Areas of research Comparative genomics of marine species
Details Ortholog, paralog and species-specific genes prediction, metabolic network analysis, three-dimensional protein structure prediction

Dates **December 2016 – October 2017**
Qualification Scientific collaboration
Head of research unit Prof. Mazzoleni c/o Università degli Studi di Napoli "Federico II"
Areas of research Functional biology of yeast cells
Details Comparative genomics; orthologs and paralogs prediction.

Dates	June 2016 – November 2016
Qualification	Grant as part of the project of “AIB 2011 Parco Nazionale del Cilento e Vallo di Diano”
Name and type of organization	Università degli Studi di Napoli “Federico II” – Dipartimento di Agraria
Areas of research	Implementation of bioinformatics methodologies for comparative genomics analyses.
Details	Pipelines development for orthologs, paralogs and species-specific genes prediction in <i>Solanum lycopersicum</i> (tomato) and <i>Solanum tuberosum</i> (potato)
Dates	May 2016 – June 2016
Qualification	Italian Co.Co.Co (continuous collaboration contract)
Name and type of organization	NO SELF S.R.L. via Cinthia – Parco San paolo, 10 – 80126 Napoli
Areas of research	Bioinformatics analysis of sequencing data from yeasts.
Details	Orthologs and paralogs network construction in yeast species.
Dates	December 2015 – April 2016
Qualification	Scientific collaboration
Head of research unit	Prof. Maria Luisa Chiusano c/o Università degli Studi di Napoli “Federico II”
Areas of research	Implementation of methods for orthology and paralogy prediction.
Details	Network prediction of orthologs and paralogs in <i>Solanum lycopersicum</i> (tomato) and <i>Vitis vinifera</i> (grapevine)
Dates	February 2015 – November 2015
Qualification	Italian Co.Co.Co (continuous collaboration contract) as part of the project “GENHORT”
Name and type of organization	Università degli Studi di Napoli “Federico II” – Dipartimento di Agraria
Areas of research	Platform development for comparative genomics analyses of Solanaceae
Details	Pipeline development for comparisons based on orthologs and paralogs networks, detection of species-specific genes, functional domains prediction, metabolic networks analysis.
Dates	October 2013 – February 2015
Qualification	Grant as part of the C.A.R.I.N.A. project
Name and type of organization	Consiglio Nazionale delle Ricerche (CNR) – Istituto di Bioscienze e Biorisorse (IBBR)
Areas of research	Implementation and development of bioinformatics platform for comparative genomics of agronomic species.

Details Development of a database of *Arabidopsis thaliana* paralog genes, development of comparative genomics approaches based on mRNA sequences comparison.

Education and training

Dates	May 2013 – May 2016
Title or qualification awarded	PhD in Computational Biology and Bioinformatics
Principal subjects / occupational skills covered	Bioinformatics, computational biology, molecular biology, comparative genomics, gene networking
Thesis	Comparative Approaches for Plant Genomes: Unraveling “Intra” and “Inter” Species Relationships from Preliminary Gene Annotations
Areas of research	<i>Development of a database of Arabidopsis thaliana paralog genes</i> , development of a software for orthologs prediction from mRNA sequences, comparative analysis of <i>Solanum lycopersicum</i> (tomato) e <i>Vitis vinifera</i> (grapevine), prediction of ortholog, paralog and species-specific genes, prediction of functional domains, enzymatic classes and metabolic pathways of <i>Solanum lycopersicum</i> (tomato), <i>Vitis vinifera</i> (grapevine) and <i>Solanum tuberosum</i> (potato)
Name and type of organization	Università degli Studi di Napoli “Federico II” – Dipartimento di Agraria
Dates	December 2012 - May 2013
Title or qualification awarded	Postgraduate training
Principal subjects / occupational skills covered	Computational biology, bioinformatics, Biochemistry, biotechnology
Head of research unit	Dott.ssa Donatella De Pascale
Areas of research	Three-dimensional modeling by homology modeling and molecular dynamics simulations of protein structures from antarctic bacteria.
Name and type of organization	Consiglio Nazionale delle Ricerche (CNR) – Istituto di Biochimica delle Proteine (IBP)
Dates	2009 - 2012
Title or qualification awarded	Molecular and Industrial Biotechnology - 2nd cycle degree - Master
Thesis	A Structural Analysis of Four Novel Disease-Causing PAH Mutants
Areas of research	Three-dimensional modeling of 4 mutants of human enzyme Phenylalanine Hydroxylase (PAH), isolated after a positive neonatal screening to hyperphenylalaninemia pathology.
Vote	107/110
Name and type of organization	Università degli Studi di Napoli “Federico II” - Facoltà di Scienze Biologiche
Dates	2006 - 2009
Title or qualification awarded	Biomolecular and Industrial Biotechnology - 1st level degree – Degree/Bachelor

Thesis Time-solved fluorescence of FAD coenzyme

Areas of research Time-solved fluorescence spectroscopy analysis in order to study conformational dynamics of FAD coenzyme when pH changes.

Vote 110/110

Name and type of organization Università degli Studi di NAPOLI "Federico II" - Facoltà di SCIENZE BIOTECNOLOGICHE

Dates **1995 – 1999**

Title or qualification awarded Secondary school diploma – scientific certificate

Vote 48/60

Name and type of organization Liceo Scientifico Statale L.B. Alberti - Minturno

Personal skills and competences

Mother tongue(s) Italian

Other language(s) English

Self-assessment

European level (*)

English

Understanding				Speaking				Writing	
Listening		Reading		Spoken interaction		Spoken production			
C2	Proficient	C2	Proficient	C1	Proficient	C1	Proficient	C2	Proficient

(*) Common European Framework of Reference for Languages

Bioinformatics and computational skills and competences Excellent knowledge of BLAST software and all its tools for the prediction of similarities between biological sequences.
Excellent knowledge of MODELLER software for the prediction of three-dimensional structures of proteins.
Excellent knowledge of visualization softwares of tridimensional structures of VMD e PYMOL.
Excellent knowledge of GROMACS software for dynamics simulations.
Excellent knowledge of INTERPROSCAN software for functional domains prediction.
Excellent knowledge of CYTOSCAPE software biological network creation and visualization.
Excellent knowledge of main public platforms for -omics science (NCBI, Ensembl, Array Express, RCSB Protein Data Bank, PDB Sum, KEGG, MetaCyc, Reactome)

Informatics skills and competences Excellent knowledge Python programming language.
Good knowledge of JavaScript language.
Good knowledge of MySQL database system management..
Excellent knowledge of main common use softwares(Excel, Access, Power Point, Word, Origin, OpenOffice package).
Excellent knowledge of Windows, and Mac OS system operating systems.
Good knowledge of Unix based operating system.

Technical skills and competences	Technical skills in lab activity (cell growth, purification, spectroscopy and mass spectrometry), acquired during bachelor and master degree, and during the trainings in CEINGE s.c.a.r.l. and IBP – CNR.
Publications	<p>Ambrosino, L., Colantuono, C., Monticolo, F., and Chiusano, M. L. (2017). "Bioinformatics resources for plant genomics: bottlenecks and opportunities in the -omics era." in "Next-generation Sequencing and Bioinformatics for Plant Science" Current Issues in Molecular Biology 71-88 DOI: 10.21775/9781910190654.05 (IMPACT FACTOR: 3,083) (vedi allegato 11 per il preprint) Ambrosino ha supervisionato ed integrato tutti gli sforzi, ha analizzato i dati e ha scritto il manoscritto.</p> <p>Ambrosino, L., Chiusano, M.L. (2017). "Transcriptologs: a transcriptome-based approach to predict orthology relationships." Bioinformatics and Biology Insights 11 DOI: 10.1177/1177932217690136 (IMPACT FACTOR: 2,4) (vedi allegato 12). Ambrosino ha sviluppato il software per la predizione degli ortologi, ha analizzato i dati e scritto il manoscritto.</p> <p>Ambrosino, L., Bostan, H., Ruggieri, V., and Chiusano, M. L. (2016). "Bioinformatics resources for pollen." Plant reproduction 29 (1-2), 133-147 DOI: 10.1007/s00497-016-0284-8 (IMPACT FACTOR: 2,629) (vedi allegato 13). Ambrosino ha supervisionato ed integrato tutti gli sforzi, e ha scritto il manoscritto.</p> <p>De Santi, C., B. Altermark, M. M. Pierechod, L. Ambrosino, D. de Pascale and N. P. Willassen (2016). "Characterization of a cold-active and salt tolerant esterase identified by functional screening of Arctic metagenomic libraries." BMC Biochem 17(1): 1 DOI: 10.1186/s12858-016-0057-x (IMPACT FACTOR: 1,481) (vedi allegato 14). Ambrosino ha effettuato gli allineamenti di sequenze e ha svolto gli studi di modeling tridimensionale per omologia.</p> <p>Ambrosino, L., H. Bostan, P. di Salle, M. Sangiovanni, A. Vigilante and M. L. Chiusano (2016). "pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana." Evol Bioinform Online 12: 1-7 DOI: 10.4137/EBO.S32536 (IMPACT FACTOR: 1,5) (vedi allegato 15). Ambrosino ha costruito i network di paraloghi implementandone la visualizzazione nelle pagine web, e scritto il manoscritto.</p> <p>De Santi, C., L. Ambrosino, P. Tedesco, L. Zhai, C. Zhou, Y. Xue, Y. Ma and D. de Pascale (2015). "Identification and characterization of a novel salt-tolerant esterase from a Tibetan glacier metagenomic library." Biotechnol Prog 31(4): 890-899 DOI: 10.1002/btpr.2096 (IMPACT FACTOR: 1,986) (vedi allegato 16). Ambrosino ha svolto gli esperimenti di Dicroismo Circolare, ha effettuato gli allineamenti di sequenze, ha condotto gli studi di modeling tridimensionale per omologia e le simulazioni di dinamica molecolare, e ha scritto il manoscritto.</p> <p>Maiorano, F., L. Ambrosino and M. R. Guarracino (2015). The MetaboX Library: Building Metabolic Networks from KEGG Database. Bioinformatics and Biomedical Engineering: Third International Conference, IWBBIO 2015, Granada, Spain, April 15-17, 2015, Proceedings, Part I. F. Ortuño and I. Rojas. Cham, Springer International Publishing: 565-576 DOI: 10.1007/978-3-319-16483-0_55 (vedi allegato 17). Ambrosino ha testato il software, effettuato l'analisi metabolica e scritto il manoscritto.</p> <p>De Santi, C., P. Tedesco, L. Ambrosino, B. Altermark, N. P. Willassen and D. de Pascale (2014). "A New Alkaliphilic Cold-Active Esterase from the Psychrophilic Marine Bacterium Rhodococcus sp.: Functional and Structural Studies and Biotechnological Potential." Appl Biochem Biotechnol. DOI: 10.1007/s12010-013-0713-1 (IMPACT FACTOR: 1,751) (vedi</p>

allegato 18). Ambrosino ha effettuato gli studi di modeling tridimensionale per omologia e le simulazioni di dinamica molecolare, e ha scritto il manoscritto.

Oral presentations

L. Ambrosino, H. Bostan, V. Ruggieri, M.L. Chiusano (2016). "An integrated multi-level comparison highlights common aspects and specific features between distantly-related species: Tomato and Grapevine" - BITS 2016, 13th Annual Meeting of the Bioinformatics Italian Society, June 15-17, 2016, University of Salerno, Italy. (presentazione orale sostenuta da **L. Ambrosino**) (abstract vedi allegato 19)

L. Ambrosino, H. Bostan, V. Ruggieri, L. Frusciante, M.L. Chiusano (2015). "*Solanum lycopersicum* versus *Vitis vinifera*: a multilevel gene comparison from fleshy fruit species" – joint Congress SIBV-SIGA 2015, Feeding the planet: plant science and breeding for the future, September 8-11th Milano, Italy. (presentazione orale sostenuta da **L. Ambrosino**) (abstract vedi allegato 20)

H. Bostan, **L. Ambrosino**, V. Ruggieri, M.L. Chiusano – "*Characterization of derivative relationship between tomato and grapevine: a key step to investigate fruit development in the two species*" – Quality Fruit 2014, 3rd Annual Conference of the Cost Action FA1106, September 21-24th Chania, Greece. (presentazione orale sostenuta da **L. Ambrosino**) (abstract vedi allegato 21)

Posters

Colantuono C., **Ambrosino L.**, Chiusano M.L. (2015) "Omics for Plant Sciences: where are the reference resources?" – Third SPOT – ITN conference, March 18-22th Sorrento, Italy (abstract vedi allegato 22)

Chiusano M.L., Colantuono C., **Ambrosino L.** (2015) "Omics for crop improvement: meeting the challenge of integration in a still young, multifaceted world" - joint Congress SIBV-SIGA 2015, Feeding the planet: plant science and breeding for the future, September 8-11th Milano, Italy (abstract vedi allegato 20)

Ambrosino L., Chiusano M.L. (2013). "In Quest of Orthologs" – BBCC 2013 Ottava Edizione, 15 Novembre 2013, Avellino, Italia (abstract vedi allegato 23)

Developed softwares

Transcriptologs: programma per la predizione di relazioni di ortologia basato sull'analisi di sequenze di trascritti provenienti da due specie distinte, scritto nel linguaggio di programmazione Python. *Transcriptologs* è scaricabile gratuitamente presso il link: <https://github.com/LucaAmbrosino/Transcriptologs.git>

Tale software è stato oggetto del lavoro scientifico: **Ambrosino, L.**, Chiusano, M.L. (2017). "Transcriptologs: a transcriptome-based approach to predict orthology relationships." (vedi allegato 12)

pATsi: database di geni paraloghi in *Arabidopsis thaliana*, liberamente consultabile accedendo al sito web: <http://cab.unina.it/athparalog/main2.html>

Tale database è stato oggetto del lavoro scientifico: **Ambrosino, L.**, H. Bostan, P. di Salle, M. Sangiovanni, A. Vigilante and M. L. Chiusano (2016). "pATsi: Paralogs and Singleton Genes from *Arabidopsis thaliana*." (vedi allegato 15)

Bioinformatics courses

Statistics (20 hours - 4 C.F.U.) – Università degli Studi di Napoli “Federico II”, May-June 2015

“A crash-course on Python” – CNR, Napoli, 19-21 Novembre 2014

Bioinformatics (20 hours - 4 C.F.U.) - Università degli Studi di Napoli “Federico II”, February-March 2014

“Intermediate Python programming” – CNR, Napoli, 31 Gennaio 2014

“Python for beginners” – CNR, Napoli, 10 Gennaio 2014

“InterOmics Tutorial Day” – CNR, Napoli, 14 Novembre 2013

**Partecipation to congresses
and seminars**

“Feeding the planet: plant science and breeding for the future”, 8-11 Settembre 2015

“Epigen Chromatin”, 11 maggio 2015

“Agricoltura e Biotecnologie”, 27 Aprile 2015

“Futuro tecnologie NGS”, 26 Aprile 2015

“Stress Biology and Crop Fertility”, 18-22 Marzo 2015

“Evoluzione tecnologie e progressi scienza”, 25 Febbraio 2015

“Global quantitative understanding of a living system”, 20 Febbraio 2015

“Results in GenoPom Projects”, 22-23 Gennaio 2015

“Regressione PLS”, 8 Gennaio 2015

“Gene capture in pepper”, 18 Dicembre 2014

“Metabolomics and heat stress in tomato”, 2 Dicembre 2014

“Ionmica in Pomodoro”, 27 Novembre 2014

“Bringing maths to life”, 27-29 Ottobre 2014

“Abiotic stress on tomato”, 23 Ottobre 2014

“Quality Fruit, cost action FA1106”, 21-24 Settembre 2014

“De novo genome assembly, 17 Giugno 2014

“RNA-seq to non model organism”, 12 maggio 2014

“Pathogen stress in tomato”, 6 Marzo 2014

“Sequenziamento pomacee”, 26 Febbraio 2014

"Sequenziamento solanacee", 25 Febbraio 2014

"Darwin Day", 12 Febbraio 2014

"Tracking genetic variation in potato", 30 Gennaio 2014

"GenoPom Projects", 21-22 gennaio 2014

"Structural properties of protein structures", 20 Dicembre 2013

"Conditional cDNA", 9 Dicembre 2013

"Genomics and computational advances", 5 Dicembre 2013

"Lentils", 27 Novembre 2013

"BBCC 2013", 15 novembre 2013

"Modular organizations of human protein interaction maps", 1 Ottobre 2013

"Solanum dulcamara", 18 Luglio 2013

"Synthetic biology", 16 Luglio 2013

"Working with next generation sequencing data", 9 Luglio 2013

"A biocontrol agent among plant pathogens", 4 Giugno 2013

Partecipazione to National or International Projects

2016 – Grant as part of the italian project "AIB 2011 Parco Nazionale del Cilento e Vallo di Diano (Rif.: Bando AIB DIA, responsabile scientifico: Prof. Stefano Mazzoleni)", carrying out the research activity: "implementation of bioinformatics methodologies for comparative genomics", *with the aim of developing pipelines for prediction of ortholog, paralog and species-specific genes in Solanum lycopersicum (tomato) and Solanum tuberosum (potato).*

2016 – Partecipazione to the international project "Solanaceae Pollen Thermotolerance – Marie Curie Initial Training Network project (Grant agreement no. 289220, coordinatore: Prof. Enrico Schleiff)", contributing as first author to the publication: "*Bioinformatics resources for pollen*", and contributing as co-author to the poster "*Omics for Plant Sciences: where are the reference resources?*" at international congress "*Third SPOT – ITN conference*".

2015/2017 – Italian Co.Co.Co (continuous collaboration contract) as part of the italian project "GENHORT - Valorizzazione di produzioni ortive campane di eccellenza con strumenti di genomica avanzata (PON02_00395_3215002, Rif.: Bando GENHORT/1 piattaforma bioinformatica, responsabile scientifico: Prof. Luigi Frusciante)", carrying out the research activity: *set up of a bioinformatics platform for comparative genomics of Solanaceae*, and contributing as first author to 4 publications: "*Bioinformatics resources for plant genomics: bottlenecks and opportunities in the -omics era*", "*Transcriptologs: a transcriptome-based approach to predict orthology relationships*", "*Bioinformatics resources for pollen*", "*pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana*", contributing as first author to the oral presentation: "*Solanum lycopersicum versus Vitis vinifera: a multilevel gene comparison from fleshy fruit species*", and as co-author to the poster "*Omics for crop improvement: meeting the challenge of integration in a still young, multifaceted world*" to the international congress

"joint Congress SIBV-SIGA 2015, Feeding the planet: plant science and breeding for the future".

2015/2017 – Participation to the national project "GENOPOM PRO Potenziamento della filiera pomodoro attraverso l'uso di piattaforme integrate di post-genomica (PON02_00395_3082360, responsabile scientifico: Prof. Luigi Frusciante)" carrying out the research activity and contributing as first author to: "Bioinformatics resources for plant genomics: bottlenecks and opportunities in the -omics era", "Transcriptologs: a transcriptome-based approach to predict orthology relationships", "Bioinformatics resources for pollen", "pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana", and contributing as co-author to the poster: "Omics for crop improvement: meeting the challenge of integration in a still young, multifaceted world" at the international congress "joint Congress SIBV-SIGA 2015, Feeding the planet: plant science and breeding for the future".

2015 - Participation to the national project "MIUR project PON02_00619" carrying out the research activity of developing an automatized method for metabolic analyses and modeling of metabolic networks, and contributing as co-author to the publication: "*The MetaboX Library: Building Metabolic Networks from KEGG Database*".

2015 - Participation to the national project "Italian Flagship project Interomics" carrying out the research activity of developing an automatized method for metabolic analyses and modeling of metabolic networks, and contributing as co-author to the publication: "*The MetaboX Library: Building Metabolic Networks from KEGG Database*".

2015 – Participation to the international project "CNR-CAS Cooperation Agreement 2011–2013 Discovery of new extremozymes and their potential use in biotechnology", carrying out the research activity and contributing as co-author to the publication: "*Identification and characterization of a novel salt-tolerant esterase from a Tibetan glacier metagenomic library*".

2014/2017 – Participation to the international project "COST Action FA1106 - An integrated systems approach to determine the developmental mechanisms controlling fleshy fruit quality in tomato and grapevine (responsabile scientifico: Prof. Mondher Bouzayen)", and grant winner for the oral presentation: "*Characterization of derivative relationship between tomato and grapevine: a key step to investigate fruit development in the two species*" to the international congress "3rd Annual Conference of the Cost Action FA1106", and contributing as first author to 3 publications: "*Bioinformatics resources for plant genomics: bottlenecks and opportunities in the -omics era*", "*pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana*", "*Transcriptologs: a transcriptome-based approach to predict orthology relationships*".

2014 – Participation to the national project "P.N.R.A. (Italian National Antarctic Research Programme) 2009–2011", carrying out the activity research and contributing as co-author to the publication: "*A New Alkaliphilic Cold-Active Esterase from the Psychrophilic Marine Bacterium Rhodococcus sp.: Functional and Structural Studies and Biotechnological Potential*".

2013 – Grant as part of the regional project "C.A.R.I.N.A. – Sicurezza, sostenibilità e competitività delle produzioni agroalimentari della Campania (P.O.R. Campania FSE 2007-2013, Bando n. IGV-025-2013-NA, Gazzetta Ufficiale n. 67 del 23-08-2013, responsabile scientifico: Dott.ssa Maria Stefania Grillo)", carrying out the research activity: "*Implementation of bioinformatics platforms for comparative genomics of agronomic species*", developing a public database of Arabidopsis thaliana paralog genes, and a comparative strategy based on the comparison of mRNA sequences of Arabidopsis thaliana e Sorghum bicolor.

Collaboration activity for bioinformatics analyses and services.

2014/2015 – Scientific collaboration with Dott.ssa Donatella De Pascale, researcher of the Istituto di Biochimica delle Proteine del Consiglio Nazionale delle Ricerche IBP-CNR sito in via

Pietro Castellino 111, Napoli, carrying out the research activity of tridimensional modeling of protein structures and molecular dynamics activities on proteins from anctartic bacteria. This activity contributed to the publication of: "*A New Alkaliphilic Cold-Active Esterase from the Psychrophilic Marine Bacterium Rhodococcus sp.: Functional and Structural Studies and Biotechnological Potential*", "*Identification and characterization of a novel salt-tolerant esterase from a Tibetan glacier metagenomic library*", "*Characterization of a cold-active and salt tolerant esterase identified by functional screening of Arctic metagenomic libraries*".

2015 – Scientific collaboration with Dott. Mario Guarracino, researcher of Istituto di Calcolo e Reti ad alte prestazioni del Consiglio nazionale delle Ricerche ICAR-CNR sito in via Pietro Castellino 111, Napoli, carrying out the research activity of metabolic network modeling. This activity contributed to the publication of: "*The MetaboX Library: Building Metabolic Networks from KEGG Database*".

2014 – Scientific collaboration with Dott.ssa Stefania Grillo, researcher of the Istituto di Bioscienze e Biorisorse del Consiglio Nazionale delle Ricerche IBBR-CNR sito in via Università 133, Portici (NA), carrying out the research activity of prediction of structural and functional homologs of "sweet-taste proteins" from plant species .

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