

INFORMAZIONI PERSONALI

Paolo Uva

Le attività di ricerca correnti sono centrate sull'analisi data-intensive e l'integrazione di dati biologici generati con tecnologie high-throughput. Gli aspetti più rilevanti della mia ricerca riguardano lo sviluppo di pipeline computazionali per l'analisi bioinformatica di dati di sequenziamento NGS per applicazioni alla ricerca biomedica e in ambito clinico. I domini specifici di applicazione sono il sequenziamento genomico (exome, whole-genome) per l'identificazione delle basi genetiche di patologie rare e lo studio del trascrittoma (RNA-Seq).

AMBITO DI RICERCA

FEB. 2016 – oggi

Ricercatore Senior

CRS4, Biosciences, Pula CA

Next Generation Sequencing Core, Program Head

APR. 2011 – 17 SET. 2015

Ricercatore Expert

CRS4, Laboratorio di Bioinformatica, Pula CA

APR. 2009 – MAR. 2011

Ricercatore

CRS4, Laboratorio di Bioinformatica, Pula CA

ESPERIENZE PROFESSIONALI

FEB. 2006 – FEB. 2009

Ricercatore in Bioinformatica

IRBM-Merck MSD, Roma

- Attività di ricerca e sviluppo in bioinformatica per il design e l'analisi di microarray custom per lo studio di anticorpi:
- Integrazione, analisi data-intensive e interpretazione di dati trascrizionali per l'identificazione di biomarcatori in ambito oncologico:

SET. 2004 – DIC. 2005

Post-doc in Bioinformatica

Istituto Nazionale di Ricerca per gli Alimenti e la Nutrizione (INRAN), Roma

- Sviluppo di metodi per l'annotazione di microarray tramite analisi di sequenza per la ricerca di omologie e l'interrogazione di banche dati genomiche.

GEN. 2004 – GIU. 2004

Post-doc in Bioinformatica

Università di Losanna, Svizzera

- Analisi data-intensive di dati biologici (high-throughput Expressed Sequence Tags, ESTs) e partecipazione allo sviluppo di "Fourmidable", una piattaforma web-based per la gestione e l'analisi automatizzata di dati genomici.

ISTRUZIONE E FORMAZIONE

OTT. 2003 – GIU. 2004

Master in Bioinformatica

Swiss Institute of Bioinformatics, Univ. Ginevra e Losanna, Switzerland

1999 – 2002

Dottorato in Scienze della Vita (Honors)

CNRS, Marseilles / Tours, France

1992 – 1999 **Laurea in Scienze Biologiche (110/110 lode)**
University of Rome La Sapienza, Italy

COMPETENZE PERSONALI

Lingue	Italian (native), French (fluent), English (proficient)
OS	Linux, OSX, Windows
Programming	R, Perl, PHP, Python
Versioning	Git
Databases	SQL language, MySQL DBMS administration
Markup languages	HTML, CSS
Database	Conoscenza delle principali banche dati biologiche (InterPro, Gene Ontology, Kegg, UCSC, Ensembl, NCBI)
Framework computazionali	Galaxy
Programmi bioinformatici per analisi NGS	Conoscenza ed esperienza nell'uso dei principali software per l'analisi di dati di esoma, whole-genome, RNA-Seq, microbiologia

ATTIVITA' DI INSEGNAMENTO

19-20 SET. 2016	Exome analysis with Galaxy – Elixir Training Course, Milano
18-20 NOV. 2014	Hands-on Workshop on NGS data analysis using Galaxy – 4 th edition". CRS4, Pula CA, IT
23-25 SET. 2014	Hands-on Workshop on NGS data analysis using Galaxy – 4 th edition". CRS4, Cagliari, IT
18-20 GIU. 2014	Hands-on Workshop on NGS data analysis using Galaxy – 3 rd edition". CRS4, Cagliari, IT
8-11 OTT. 2013	Hands-on Workshop on NGS data analysis using Galaxy – 2 nd edition". CRS4, Pula CA, IT
18-21 GIU. 2013	Hands-on Workshop on NGS data analysis using Galaxy – 1 st edition". CRS4, Pula CA, IT
12-16 NOV. 2012	Course in Next Generation Sequencing data analysis using Galaxy". Istituto Zooprofilattico di Teramo, Teramo, IT.
26 SET. 2012	Master in Bioinformatics, Cagliari, IT. Topics: RNA-Seq and expression microarrays data analysis.
10-16 LUG. 2011	Bilbao Advanced School in Biophysics, Bilbao, ES. Analisi di microarray con R
29 GIU. 2011	Short Course in Bioinformatics, organizzato dalla « Scuola di Dottorato di Ricerca in Scienze Matematiche e Informatiche » dell'Università di Cagliari

1. Eleonora Palagano, Lucia Susani, Ciro Menale, Ugo Ramenghi, Massimo Berger, **Paolo Uva**, Manuela Oppo, Paolo Vezzoni, Anna Villa, Cristina Sobacchi. Synonymous Mutations Add a Layer of Complexity in the Diagnosis of Human Osteopetrosis. *Journal of Bone and Mineral Research* - 2016 doi: 10.1002/jbmr.2929
2. Andrea Angius, **Paolo Uva**, I Buers, Manuela Oppo, Alessandro Puddu, Stefano Onano, Ivana Persico, Angela Loi, Loredana Marcia, Wolfgang Höhne, Gianmauro Cuccuru, Giorgio Fotia, ..., G Zampino, Giangiorgio Crisponi, Laura Crisponi, Frank Rutsch. Bi-allelic Mutations in KLHL7 Cause a Crisponi/CISS1-like Phenotype Associated with Early-Onset Retinitis Pigmentosa. *American Journal of Human Genetics* pages 236-245 vol. 99 num. 1 - july 2016 doi: 10.1016/j.ajhg.2016.05.026
3. Federico Punelli, Mohamad Al Hassan, Veronica Fileccia, **Paolo Uva**, Graziella Pasquini, Federico Martinelli. A microarray analysis highlights the role of tetrapyrrole pathways in grapevine responses to "stolbur" phytoplasma, phloem virus infections and recovered status. *Physiol. and Mol. Plant Pathol.* 01/2016; DOI:10.1016/j.pmpp.2016.01.001
4. Json, J, Ison J, Rapacki K, Ménager H, Kalas M, Rydza E, Chmura P, Anthon C, Beard N, Berka K, Bolser D, Booth T, Bretaudeau A, Brezovsky J, Casadio R, Cesareni G, Coppens F, Cornell M, Cuccuru G, Davidsen K, Vedova GD, Dogan T, Doppelt-Azeroual O, Emery L, Gasteiger E, Gatter T, Goldberg T, Grosjean M, Gruning B, Helmer-Citterich M, Ienasescu H, Ioannidis V, Jespersen MC, Jimenez R, Juty N, Juvan P, Koch M, Laibe C, Li JW, Licata L, Mareuil F, Micetic I, Friberg RM, Moretti S, Morris C, Moller S, Nenadic A, Peterson H, Profiti G, Rice P, Romano P, Roncaglia P, Saidi R, Schafferhans A, Schwummle V, Smith C, Sperotto MM, Stockinger H, Varekova RS, Tosatto SC, de la Torre V, **Uva P**, Via A, Yachdav G, Zambelli F, Vriend G, Rost B, Parkinson H, Longreen P, Brunak S. Tools and data services registry: a community effort to document bioinformatics resources. *Nucleic Acids Res.* 2016 Jan 4;44(D1):D38-47. doi: 10.1093/nar/gkv1116. Epub 2015 Nov 3. PubMed PMID: 26538599
5. Paulis M, Castelli A, Susani L, Lizier M, Lagutina I, Focarelli ML, Recordati C, **Uva P**, Faggioli F, Neri T, Scanziani E, Galli C, Lucchini F, Villa A, Vezzoni P. Chromosome transplantation as a novel approach for correcting complex genomic disorders. *Oncotarget.* 2015 Nov 3;6(34):35218-30. doi: 10.18632/oncotarget.6143. PubMed PMID: 26485770
6. Andrea Masotti, **Paolo Uva**, Laura Davis-Keppen, Lina Basel-Vanagaite, Lior Cohen, Elisa Pisaneschi, Antonella Celluzzi, Paolo Bencivenga, Mingyan Fang, Mingyu Tian, Xun Xu, Marco Cappa, Bruno Dallapiccola. Keppen-Lubinsky syndrome is caused by mutations in the inwardly-rectifying K⁺ channel encoded by KCNJ6. *American Journal of Human Genetics* - 2015 doi: 10.1016/j.ajhg.2014.12.011. PubMed PMID: 25620207
7. Eleonora Palagano, Harry C. Blair, Alessandra Pangrazio, Irina Tourkova, Dario Strina, Andrea Angius, Gianmauro Cuccuru, Manuela Oppo, **Paolo Uva**, Wim Van Hul, Eveline Boudin, Andrea Superti-Furga, Flavio Faletta, Agostino Nocerino, Matteo C. Ferrari, Marta Monari, Alessandro Montanelli, Paolo Vezzoni, Anna Villa, Cristina Sobacchi. Buried in the Middle, But Guilty: Intronic Mutations in the TCIRG1 Gene Cause Human Autosomal Recessive Osteopetrosis. *Journal of Bone and Mineral Research Wiley* - 2015 doi: 10.1002/jbmr.2517 PubMed PMID: 25829125
8. Maria Carmina Castiello, Samantha Scaramuzzi, Francesca Pala, Francesca Ferrua, **Paolo Uva**, Immacolata Brigida, Lucia Sereni, Mirjam van der Burg, Giorgio Ottaviano, Michael H. Albert, Maria Grazia Roncarolo, Luigi Naldini, Alessandro Aiuti, Anna Villa, Marita Bosticardo. B-cell reconstitution after lentiviral vector-mediated gene therapy in patients with Wiskott-Aldrich syndrome. *Journal of Allergy and Clinical Immunology* num. 3 - march 2015 doi: 10.1016/j.jaci.2015.01.035 PubMed PMID: 25792466
9. Luiz Miguel Camargo, Xiaohua Douglas Zhang, Patrick Loerch, Ramon Miguel Caceres, Shane Marine, **Paolo Uva**, Marc Ferrer, Emanuele de Rinaldis, David Stone, John Majercak, William Ray, Chen Yi-An, Mark Shearman, Kenji Mizuguchi. Pathway-Based Analysis of Genome-Wide siRNA Screens Reveals the Regulatory Landscape of App Processing. *PLoS ONE* pages e0115369 - 2015 doi: 10.1371/journal.pone.0115369 PubMed PMID: 26030410
10. Massimo Pilotti, Angela Brunetti, **Paolo Uva**, Valentina Lumia, Lorenza Tizzani, Fabio Gervasi, Michele Iacono, Massimo Pindo. Kinase domain-targeted isolation of defense-related receptor-like kinases (RLK/Pelle) in *Platanus x acerifolia*: phylogenetic and structural analysis. *BMC Plant Biology* pages 884 vol. 7 num. 1 - december 2014 PubMed PMID: 25486898
11. Cuccuru, G., Orsini, M., Pinna, A., Sbardellati, A., Soranzo, N., Travaglione, A., **Uva, P.**, Zanetti, G., Fotia, G. (2014). Orione, a web-based framework for NGS analysis in

- microbiology. *Bioinformatics*. 2014 Jul 1;30(13):1928-9. doi: 10.1093/bioinformatics/btu135. Epub 2014 Mar 10. PubMed PMID: 24618473
12. Cuccuru, G., Leo, S., Lianas, L., Muggiri, M., Pinna, A., Pireddu, L., **Uva, P.**, Angius, A., Fotia, G., Zanetti, G. (2014). An Automated Infrastructure to Support High-throughput Bioinformatics. *Proc. IEEE International Conference on High Performance Computing & Simulation (HPCS 2014)*: 600-607
13. Odorisio, T., Di Salvio, M., Orecchia, A., Di Zenzo, G., Piccinni, E., Cianfarani, F., Travaglione, A., **Uva, P.**, Bellei, B., Conti, A., Zambruno, G., Castiglia, D. (2014). Monozygotic twins discordant for recessive dystrophic epidermolysis bullosa phenotype highlight the role of TGF- β signalling in modifying disease severity. *Human Molecular Genetic*, published online March 5, 2014 PubMed PMID: 24599399
14. Orecchia, A., Mettouchi, A., **Uva, P.**, Simon, G., Arcelli, D., Avitabile, S., Ragone, G., Meneguzzi, G., Pfenninger, K., Zambruno, G., Failla, CM (2013). Endothelial cell adhesion to soluble vascular endothelial growth factor receptor-1 triggers a cell dynamic and angiogenic phenotype. *FASEB J.*, 28(2):692-704 PubMed PMID: 24174428
15. Reverberi M, Punelli M, Scala V, Scarpari M, **Uva P**, et al. (2013). Genotypic and Phenotypic Versatility of *Aspergillus flavus* during Maize Exploitation. *PLoS ONE* 8(7): e68735 doi: 10.1371/journal.pone.0068735 PubMed PMID:23894339
16. Orsini, M., S. Carcangiu, G. Cuccuru, **P. Uva**, and A. Tramontano (2013). The PARIGA Server for Real Time Filtering and Analysis of Reciprocal BLAST Results. *PLoS One*. 2013 May 7;8(5):e62224. doi: 10.1371/journal.pone.0062224. Print 2013. PubMed PMID:23667459
17. **Uva, P.**, L. Da Sacco, M. Del Cornò, A. Baldassarre, P. Sestili, M. Orsini, A. Palma, S. Gessani, and A. Masotti (2013). Rat mir-155 generated from the lncRNA Bic is 'hidden' in the alternate genomic assembly and reveals the existence of novel mammalian miRNAs and clusters. *RNA*, vol. 19, pp. 365–379. doi: 10.1261/rna.035394.112. Epub 2013 Jan 17. PubMed PMID: 23329697
18. **Uva, P.**, Lahm, A., Sbardellati, A., Grigoriadis, A., Tutt, A. and de Rinaldis, E. (2010). Comparative membranome expression analysis in primary tumors and derived cell lines. *PloS ONE* 5(7): e11742 doi: 10.1371/journal.pone.0011742. PubMed PMID: 20668533
19. Marra E., **Uva P.**, Viti V., Simonelli V., Dogliotti E., De Rinaldis E., Lahm A., La Monica N., Nicosia A., Ciliberto G. and Palombo F. (2010). Growth delay of human bladder cancer cells by Prostate Stem Cell Antigen downregulation is associated with activation of immune signaling pathways. *BMC Cancer*. 2010 Apr 7;10:129. doi: 10.1186/1471-2407-10-129. PubMed PMID: 20374648
20. **Uva, P.**, Aurisicchio, L., Watters, J., Loboda, A., Kulkarni, A., Castle, J., Palombo, F., Viti, V., Mesiti, G., Zappulli, V., Marconato, L., Abramo, F., Ciliberto, G., Lahm, A., La Monica, N. and de Rinaldis E. (2009). Comparative expression pathway analysis of human and canine mammary tumors. *BMC Genomics*. 2009 Mar 27;10:135. doi: 10.1186/1471-2164-10-135. PubMed PMID: 19327144
21. Wurm, Y., **Uva, P.**, Ricci, F., Wang, J., Jemielity, J., Iseli, C., Falquet and L. Keller L. (2009). Fourmidable: a database for ant genomics. *BMC Genomics*. 2009 Jan 6;10:5. doi:10.1186/1471-2164-10-5. PubMed PMID: 19126223
22. Leniaud, L., Pichon, A., **Uva, P.** and Bagnères A.-G. (2009). Unicolonality in *Reticulitermes urbis*: a novel feature in a potentially invasive termite species. *Bull Entomol Res*. 2009 Feb;99(1):1-10. doi: 10.1017/S0007485308006032. Epub 2008 Jul 1. PubMed PMID: 18590600
23. **Uva, P.** and de Rinaldis E. (2008). CrossHybDetector: detection of cross-hybridization events in DNA microarray experiments. *BMC Bioinformatics*. 2008 Nov 17;9:485. doi:10.1186/1471-2105-9-485. PubMed PMID: 19014642
24. Monaci, P., Luzzago, A., Santini, C., De Pra, A., Arcuri, M., Magistri, F., Bellini, A., Ansuini, H., Ambrosio, M., Ammendola, V., Bigotti, M. G., Cirillo, A., Nuzzo, M., Nasti, A. A., Neuner, P., Orsatti, L., Pezzanera, M., Sbardellati, A., Silvestre, G., **Uva, P.**, Viti, V., Barbato, G., Colloca, S., Demartis, A., de Rinaldis, E., Giampaoli, S., Lahm, A., Palombo, F., Talamo, F., Vitelli, A., Nicosia, A. and Cortese, R. (2008). Differential screening of phage-Ab libraries by oligonucleotide microarray technology. *PLoS One*. 2008 Jan 30;3(1):e1508. doi: 10.1371/journal.pone.0001508. PubMed PMID: 18231595
25. Wang, J., Jemielity, S., **Uva, P.**, Wurm, Y., Gräff, J. and Keller L. (2007). An annotated cDNA library and microarray for large-scale gene-expression studies in the ant *Solenopsis invicta*. *Genome Biol*. 2007;8(1):R9. PubMed PMID: 17224046

26. Kutnik, M., **Uva, P.**, Brinkworth, L., and Bagnères A.-G. (2004). Phylogeography of two European *Reticulitermes* (Isoptera) species: the Iberian refugium. *Mol Ecol.* 2004 Oct;13(10):3099-113. PubMed PMID: 15367123
27. **Uva, P.**, Clément, J.-L., and Bagnères, A.-G. (2004). Colonial and geographic variations in agonistic behaviour, cuticular hydrocarbons and mtDNA of Italian populations of *Reticulitermes lucifugus* (Isoptera, Rhinotermitidae). *Insectes Soc.* 51: 163-170
28. **Uva, P.**, Clément, J.-L., Austin, J.W., Aubert, J., Zaffagnini, V., Quintana, A., and Bagnères, A.-G. (2004). Origin of a new *Reticulitermes* termite (Isoptera, Rhinotermitidae) inferred from mitochondrial and nuclear DNA data. *Mol Phylogenet Evol.* 2004 Feb;30(2):344-53. PubMed PMID: 14715226
29. Bagnères, A.-G., **Uva, P.**, and Clément, J.-L. (2003). Description d'une nouvelle espèce de Termite : *Reticulitermes urbis* n. sp. (Isopt., Rhinotermitidae). *Bull. Soc. Entomol. France* 108 (4): 435-436
30. Quintana, A., Reinhard, J., Faure, R., **Uva, P.**, Bagnères, A.-G., Massiot, G., and Clément, J.-L. (2003). Interspecific variation in terpenoid composition of defensive secretions of European *Reticulitermes termites*. *J Chem Ecol.* 2003 Mar;29(3):639-52. PubMed PMID: 12757325
31. Austin, J.W., Szalanski, A.L., **Uva, P.**, Bagnères, A.-G., and Kence, A. (2002). A comparative genetic analysis of the subterranean termite genus *Reticulitermes* (Isoptera: Rhinotermitidae). *Ann. Entomol. Soc. Am.* 95 (6): 753-760
32. Clément, J.-L., Bagnères, A.-G., **Uva, P.**, Wilfert, L., Quintana, A., Reinhard, J., and Dronnet, S. (2001). Biosystematics of *Reticulitermes* termites in Europe: morphological, chemical and molecular data. *Insectes Soc.* 48: 202-215

CAPITOLI DI LIBRI

1. M. Orsini, G. Cuccuru, **P. Uva** and G. Fotia. Bacterial genomics data analysis in the next-generation sequencing era. *Data Mining Techniques for the Life Sciences* (Second Edition), Springer, *in press*, June 2015
2. Tkacz, A., Rychlewski, L., **Uva, P.** and Plewczynski, D. (2006). Supervised classification of genes and biological samples. In: *DNA Microarrays: Current Applications*. Ed. de Rinaldis E. and Lahm A. Horizon Bioscience

CONFERENZE (Talk e Posters)

1. P.Uva ,E.Diaconu ,S.Onano ,R.Atzeni ,C.Cossu ,C.Gianmauro ,R.Cusano ,M.Oppo ,I.Zara, A.Angius, L. Crisponi, G. Fotia. The importance of an Italian exome database for the study of rare diseases, SIGU 2016, 23-26 Novembre, Torino
2. Rusmini M, Grossi A, Caroli F, Caorsi R, Musso V, Papa R, Volpi S, Cusano R, Uva P, Ravazzolo R, Martini A, Gattorno M, Ceccherini I. Ricerca di geni coinvolti in immunodeficienze primarie (PID) e in malattie autoinfiammatorie (AIDs) tramite whole-exome sequencing (WES), SIGU 2016, 23-26 Novembre, Torino
3. L. Crisponi, A. Angius, P. Uva, I. Buers, M. Oppo, A. Puddu, S. Onano, I. Persico, A. Loi, L. Marcia, W. Höhne, G. Cuccuru, G. Fotia, M. Deiana, M. Marongiu, H. Atalay, S. Inan, O. El Assy, L. Smit, I. Okur, E. Kılıç, G. Zampino, G. Crisponi, F. Rutsch. Mutations in KLHL7, a Dominant Retinitis Pigmentosa - Locus, Cause a Recessive Crisponi/CISS1-like phenotype, SIGU 2016, 23-26 Novembre, Torino
4. L. Crisponi, A. Angius, P. Uva, I. Buers, M. Oppo, A. Puddu, S. Onano, I. Persico, A. Loi, L. Marcia, W. Höhne, G. Cuccuru, G. Fotia, M. Deiana, M. Marongiu, H. Atalay, S. Inan, O. El Assy, L. Smit, I. Okur, E. Kılıç, G. Zampino, G. Crisponi, F. Rutsch. Mutations in KLHL7, a Dominant Retinitis Pigmentosa - Locus, Cause a Recessive Crisponi/CISS1-like phenotype, ESHG 2016, Barcelona, Spain
5. Eleonora Palagano, Giulia Zuccarini, Stefano Mantero, Daniele Conte, Andrea Angius, Paolo Uva, Paolo Prontera, Paolo Vezzoni, Anna Villa, Giorgio Merlo, Cristina Sobacchi. NBAS is the gene mutated in two patients affected by Acrofrontofacionasal Dysostosis type 1. 43rd Annual European Calcified Tissue Society Congress, Rome, Italy, May 2016
6. Paolo Uva. Next Generation Sequencing: dal gene al genoma. Invited speaker at Convegno NGS: esperienze del gruppo di lavoro a Genova, Genova, 15 gennaio 2016.
7. Paolo Uva. Workflow nell'analisi SGS: allineamento e chiamata delle varianti. Invited speaker at XVIII Congresso Nazionale SIGU 2015, Rimini, 24 ottobre 2015.

8. Gianmauro Cuccuru, Paolo Uva, Stefano Onano, Rossano Atzeni, Simone Leo, Luca Lianas, Manuela Oppo, Luca Pireddu, Andrea Angius, Laura Crisponi, Gianluigi Zanetti, Giorgio Fotia. Exploiting a large scale biodata management system to support NGS variant detection studies. Poster presentation at ISMB/ECCB 2015, Dublin - 2015
9. Marianna Paulis, Alessandra Castelli, Lucia Susani, Michela Lizier, Irina Lagutina, Camilla Recordati, Paolo Uva, Francesca Faggioli, Tui Neri, Eugenio Scanziani, Cesare Galli, Franco Lucchini, Anna Villa, Paolo Vezzoni. Chromosome transplantation: a novel strategy for correcting genomic disorders resistant to classical gene therapy approaches. Poster presentation at ISSCR Annual Meeting 2015, 24-27 June, Stockholm - 2015
10. Paolo Uva, Alessandro Puddu, Manuela Oppo, Stefano Onano, Loredana Marcia, Manila Deiana, Angela Loi, Mara Marongiu, Gianmauro Cuccuru, Giorgio Fotia, Frank Rutsch, Francesco Cucca, Giangiorgio Crisponi, Andrea Angius, Laura Crisponi. Identification of novel gene(s) associated with Crisponi/cold induced sweating syndrome-like phenotype by whole-exome sequencing. Poster presentation at Telethon Convention, Riva del Garda, March 9-11, 2015 - march 2015
11. Eleonora Palagano, Dario Strina, Ciro Menale, Stefano Mantero, Paolo Prontera, Maria Leine Guion-Almeida, Paolo Uva, Andrea Angius, Gianmauro Cuccuru, Manuela Oppo, Anna Villa, Cristina Sobacchi. Understanding the genetic basis of Acrofrontofacionasal Dysostosis 1. Poster presentation at Telethon Convention, Riva del Garda, March 9-11, 2015 - march 2015
12. Gianmauro Cuccuru, Rossano Atzeni, Giorgio Fotia, Paolo Uva, Gianluigi Zanetti. A Galaxy based infrastructure. Oral presentation at ELIXIR All hands meeting - Hinxton - march 2015
13. Palagano, E., Pangrazio, A., Strina, D., Puddu, A., Oppo, M., Valentini, M., Uva, P., Cuccuru, G., Angius, A., Vezzoni, P., Villa, A., Sobacchi, C. New insights on bone biology from exome sequencing of osteopetrotic patients with atypical presentations. Invited talk at 5th International Conference on Osteoimmunology: Interactions of the Immune and Skeletal Systems, Kos, Greece, June 15-20 - 2014
14. Cuccuru, G., M. Orsini, N. Soranzo, A. Pinna, A. Sbardellati, A. Travaglione, P. Uva, G. Zanetti, G. Fotia. Engaging Galaxy in Microbiology. Poster presentation at the Galaxy Community Conference 2013, Oslo, Norway, 30 June - 2 July 2013
15. Soranzo, N., S. Onano, G. Cuccuru, M. Orsini, A. Pinna, A. Sbardellati, P. Uva, G. Fotia. Microbiome profiling on a Galaxy-based framework for Microbiology. Poster presentation at the Galaxy Community Conference 2013, Oslo, Norway, 30 June - 2 July 2013
16. Di Salvio, M., E. Piccinni, A. Orecchia, G. Di Zenzo, F. Cianfarani, A. Travaglione, P. Uva, B. Bellei, A. Conti, G. Zambruno, T. Odorisio, D. Castiglia. Diverse TGF- β signalling activation in fibroblasts from monozygotic twins affected by recessive dystrophic epidermolysis bullosa: role of decorin as modifier gene. Poster contribution at the Gordon Research Conference Epithelial Differentiation & Keratinization, Lucca (Barga), Italy, May 12-17, 2013
17. Onano, S., P. Uva, and M. Orsini. Host profiling from intestinal microbiota sequencing. Talk at the Microbiota and Immunity in Human Diseases (MIHD-OBG 2013) international symposium, Rome, Italy, May 3-4 2013
18. Onano, S., M. Orsini, G. Cuccuru, and P. Uva. Comparison of computational pipelines for microbiome profiling. Talk at the Microbiota and Immunity in Human Diseases (MIHD-OBG 2013) international symposium, Rome, Italy, May 3-4 2013
19. Cuccuru, G., Giorgio Fotia, Simone Leo, Luca Lianas, Massimiliano Orsini, Andrea Pinna, Luca Pireddu, Andrea Sbardellati, Nicola Soranzo, Paolo Uva, Gianluigi Zanetti. Scalability, Reproducibility and Traceability in Large Scale NGS Facilities. Contributed presentation to Clinical Genomics & Informatics Europe, Lisbon, Portugal - 4, 6 December - 2013
20. Cuccuru, G., Massimiliano Orsini, Nicola Soranzo, Andrea Pinna, Andrea Sbardellati, Antonella Travaglione, Paolo Uva, Gianluigi Zanetti, Giorgio Fotia, Engaging Galaxy in Microbiology. Poster presentation at the Galaxy Community Conference 2013, Oslo, Norway - 30 June, 2 July - 2013
21. Nicola Soranzo, Stefano Onano, Gianmauro Cuccuru, Massimiliano Orsini, Andrea Pinna, Andrea Sbardellati, Paolo Uva, Giorgio Fotia. Microbiome profiling on a Galaxy-based framework for Microbiology. Poster presentation at the Galaxy Community Conference 2013, Oslo, Norway - 30 June, 2 July - 2013
22. Orecchia, A., A. Mettouchi, P. Uva, G. Simon, D. Arcelli, S. Avitabile, G. Ragone, G. Meneguzzi, K. Pfenninger, G. Zambruno, and C. M. Failla. Soluble VEGFR-1 interaction with $\alpha 5 \beta 1$ integrin triggers an endothelial cell dynamic and angiogenic phenotype. Poster

- presentation at the Frontiers in Cardiac and Vascular Regeneration conference, May 30 - June 2 2012, Trieste, Italy
23. Fraumene, C., M. Cosso, A. Sassu, G. Maninchedda, F. Serra, F. Marras, P. Ledda, P. Uva, M. Orsini, M. Pirastu, A. Bulfone, A. Angius, and I. Piras. Caratterizzazione del genoma mitocondriale in Ogliastra (Sardegna). Poster presentation at the XIX Congresso dell'Associazione Antropologica Italiana, Torino, 21-24 September 2011.
 24. Mentzen, W. I., M. Floris, and P. Uva. Epigenetic regulation of microRNAs during embryonic stem cell differentiation. Poster presentation at the ISMB/ECCB 2011, Vienna, 17-19 July 2011.
 25. Uva, P., W. I. Mentzen, U. Orfanelli, and S. Cenci. A package for the genome wide dissection of miRNA-mRNA interactions applied to the plasma cell differentiation process. Talk at the BITS 8th Annual Meeting 2011, Pisa, 20-22 June 2011.
 26. Punelli F, Pasquini G, Faggioli F, Uva P, Ferrarini A, Pasquini G. (2010). Gene expression in grapevine cultivars affected by phytoplasma and viruses. CRA-VIT Centro di Ricerca per la Viticoltura (Conegliano - TV): "Il contributo del CRA per la ricerca e l'innovazione del settore vitivinicolo", Conegliano, 15-16 Aprile 2010
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Pula, 14 Febbraio 2017

Paolo Uva

