CURRICULUM VITAE ET STUDIORUM

CONTACT DETAILS

Name: Domenico Giosa
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PROFESSIONAL POSITIONS

31/12/2021 – present: Researcher (fixed-time, RTD-A; art.24 c.3 Italian law 240/2010) in Genetics (SSD: BIO/18), Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Italy.

PON "Research and Innovation" 2014-2020 – CUP J45F21001750007

Project Title: "Decipher genomes and transcriptomes of *Sporothrix spp.* using Next Generation Sequencing and bioinformatics tools".

2021: Temporary Research Fellow, Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Italy.

PRIN 2017 project entitled "Natural and pharmacological inhibition of the early phase of viral replication (VirSudNet)", project code 2017M8R7N9, CUP Code J44I19000670006.

01/03/2016 – 31/03/2017: Temporary Research Fellow, IRCCS Hospital Centro Neurolesi "Bonino Pulejo", Messina, Italy.

Research Project GR-2011-02347606 for "The surveillance and control of hospital-acquired infections" entitled "Application of molecular methodologies including multi locus sequence typing (MLST) and microsatellite-based genotyping to determine the frequency and distribution of clinically important *Candida* species in hospital care units and use of the whole genome mapping (WGM) technology as tool for comparative genome analysis of *Candida parapsilosis* epidemic clones".

TEACHING ACTIVITIES

2021-2024: Teaching assistant and exam committee member as "Subject Expert" for "Molecular Techniques for the Study of Microorganisms" (SSD: BIO/19 - Microbiology) and "Bioinformatics and Molecular Networks" (SSD: BIO/18 - Genetics), at the University of Messina

2023-2024: Professor of "Bioinformatics and Genetics with application in forensic sciences", The Department of Mathematics and Computer Sciences, Physical Sciences and Earth Sciences (MIFT), University of Messina, Italy.

2022-2023: Professor of "Applied Genomics and Bioinformatics", Master's Degree Course in Biology of Health, Applied technologies and Nutrition, University of Messina, Italy

2021-2022: Professor of "Bioinformatics & Molecular Networks", Master's Degree Course in Medical Biotechnology, Department of Biomedical, Dental, Morphological and Functional Imaging Sciences, University of Messina, Italy.

2020-2021: Lecturer for the course "Microbial Biotechnologies" of the Master's Degree Course in Biology (LM-6), Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina.

2019-2020: Professor of "Emerging role of bioinformatics in computer studies of epigenetics and implications for pathologies", First level Master in "OCCUPATIONAL AND ENVIRONMENTAL RISK MANAGEMENT", Department of Biomedical, Dental, Morphological and Functional Imaging Sciences, University of Messina, Italy.

2018-2019: Lecturer for the courses "Animal Genomics and Zootechnical Selection" and "General Zootechnics and Principles of Selection" for the Master's Degree Course in Science, Technologies and Safety of Animal Production, Department of Veterinary Sciences, University of Messina, Messina.

Lecturer for the "Integrated Course of Microbiology: Pathogenesis of liver diseases", Master's Degree in Biotechnology for Health, Department of Human Pathology of Adults and Developmental Age, University of Messina, Italy.

2017-2018: Lecturer for the "Integrated Course of Microbiology: Pathogenesis of liver diseases", Master's Degree in Biotechnology for Health, Department of Human Pathology of Adults and Developmental Age, University of Messina, Italy.

2015-2016: Lecturer for the course "Molecular Genetics", Master's Degree in Biology, Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Italy.

INTERNATIONAL TEACHING ACTIVITIES

2022-2023: Professor of the summer school international course "Topics in Microbiology and Parasitology", Doctoral Program at University of Concepción, Concepción, Chile.

2017-2018: Professor of the course "Bioinformatics", Master in Plant Protection and Biotechnology, Moulay Ismail University, Faculty of Science, Meknés, Morocco.

PROFESSIONAL EXPERIENCES

2020: Research Activity at Genomix4Life s.r.l. (6 months)
Baronissi, Salerno, Italy.
2018/2019: Research Activity at Sequentia Biotech SL (6 months)
Barcelona, Spain.
2017: Trainee at Sequentia Biotech SL (2 months)
Barcelona, Spain.
2015: Erasmus Trainee at CBS-KNAW Fungal Biodiversity Centre (3 months)
Utrecht, The Netherlands.
2011: Trainee at Bianchi – Melacrinò – Morelli Hospital (3 months)
Reggio Calabria, Italy.

EDITORIAL ACTIVITY

2022: Guest Associate Editor in Fungal Pathogenesis (Frontiers in Cellular and Infection Microbiology)
2018-presente: Reviewer for: Frontiers, MDPI, PLOS ONE, INFEZMED

SCIENTIFIC SOCIETIES MEMBERSHIP

2023-present: Italian Genetic Association (AGI)
2022-present: International Society of Human & Animal Mycology (ISHAM)

FUNDING AWARDS

2022-2023: FABBR-UniME 2022 competition within the University of Messina: funding for research activities on the basis of competitive calls that provide for peer review

ACADEMIC DEGREES

2017-2020: Ph.D. in Medical and Surgical Biotechnology
XXXIII Cycle (PON DOT1314013) - CUP: J78G17000110007
University of Messina, Italy.
Thesis entitled “Development of a custom NGS method and of a pipeline ad hoc bioinformatics for the characterization of the integrations of Hepatitis B virus in hepatocellular carcinoma”.
Tutor: Prof. Teresa Pollicino
Degree Mark: summa cum laude

2015: Master’s Degree in Biology (LM-6)
University of Messina, Italy.
Thesis in Genetics (BIO/18) entitled "Parallel Massive Sequencing of the entire genome of *Sporothrix pallida*".
Tutor: Prof. Orazio Romeo
Degree Mark: 110/110 cum laude

PROFESSIONAL SKILLS

Bioinformatics analysis of DNA- and RNA-sequencing data (Sanger, Next Generation Sequencing, Third Generation Sequencing, Optical mapping); de-novo and reference-guided genome/transcriptome assembly; Variant calling (SNPs and SVs); Comparative genomics; Structural and Functional genome/transcripome annotation; Differential Gene Expression Analysis; Gene Ontology Enrichment Analysis, Pathway Enrichment Analysis; Metagenomics and Metatranscriptomics (target and whole-genome/transcriptome); Sequence Alignments (pairwise- and multiple sequence alignments); Molecular phylogeny (target and whole genome); miRNA-target interactions; ad hoc development of bioinformatics pipeline.

Studies were mainly, but not exclusively, focused on fungal organisms (*Sporothrix spp., Candida spp., Cryptococcus spp., Fusarium spp., Hortaea spp.*), viruses (HSV, HBV, HCV) and mammals (*Homo sapiens sapiens, Sus scrofa*).

RESEARCH PRODUCTS

PUBLICLY AVAILABLE PROJECTS

GENOMES: JNEX02000000; LVYW01000000; LVYX01000000; GCA_006511355.1; CP025717-CP025731; JACSRB000000000; JACSRC000000000; JADMNF000000000; JADMNG000000000; JADMNH000000000; JADMNI000000000; CP071552-CP71572;
TRANSCRIPTOMES: GEVW00000000.2, GEVV00000000.2

BIOPROJECTS: PRJNA650273; PRJNA539953; PRJNA641248; PRJNA428229; PRJNA327736; PRJNA327731; PRJNA633855; PRJNA418771.

GENE EXPRESSION OMNIBUS (GEO): GSE145856.
DATABASE: http://sporothrixgenomedatabase.unime.it/

ARTICLES PUBLISHED IN INTERNATIONAL JOURNALS

1. Du W[†], **Giosa D**[†], Wei J[†], Giuffrè L, Shi G, El Aamri L, D’Alessandro E, Hafidi M, de Hoog S,Romeo O, Huang H. Long-read PacBio genome sequencing of four environmental saprophytic *Sporothrix* species spanning the pathogenic clade. *BMC Genomics* **23,** 506 (2022). doi:10.1186/s12864-022-08736-w.
2. Dougue AN, El-Kholy MA, Giuffrè L, Galeano G, D′Aleo F, Kountchou CL, Nangwat C, Dzoyem JP, **Giosa D**, Pernice I, Shawky SM, Ngouana TK, Boyom FF, Romeo O. Multilocus sequence typing (MLST) analysis reveals many novel genotypes and a high level of genetic diversity in *Candida tropicalis* isolates from Italy and Africa. *Mycoses*. 2022; 00: 1-12. doi: 10.1111/myc.13483.
3. Lui M, **Giosa D**, Romeo O,Bitto A. Computational Pathways Analysis and Personalized Medicine in HER2-Positive Breast Cancer, Current Pharmacogenomics and Personalized Medicine 2022; 19() . https://dx.doi.org/10.2174/1875692119666220407114044.
4. Giuffrè L, **Giosa D**, Galeano G, Aiese Cigliano R, Paytuví-Gallart A, Sutera A M, Tardiolo G, Zumbo A, Romeo O, D’Alessandro E (2021). Whole-metagenome shotgun sequencing of pig faecal microbiome. Italian Journal of Animal Science, 20(1), 1147-1155. doi:10.1080/1828051X.2021.1952910.
5. Chen C, Wang X, Zong W, D’Alessandro E, **Giosa D**, Guo Y, Mao J, Song C. Genetic Diversity and Population Structures in Chinese Miniature Pigs Revealed by SINE Retrotransposon Insertion Polymorphisms, a New Type of Genetic Markers. *Animals*. 2021; 11(4):1136. https://doi.org/10.3390/ani11041136.
6. Chen C, D'Alessandro E, Murani E, Zheng Y, **Giosa D**, Yang N, Wang X, Gao B, Li K, Wimmers K, Song C. SINE jumping contributes to large-scale polymorphisms in the pig genomes. *Animals* 2021, 11, 1136. DOI: 10.3390/ani11041136.
7. **Giosa D**, Felice MR, Giuffrè L, Aiese Cigliano R, Paytuví-Gallart A, Lo Passo C, Barresi C, D'Alessandro E, Huang H, Criseo G, Mora-Montes HM, de Hoog S, Romeo O. Transcriptome-wide expression profiling of Sporothrix schenckii yeast and mycelial forms and the establishment of the Sporothrix Genome DataBase. Microb Genom. 9.10 (2020), doi: 10.1099/mgen.0.000445.
8. Romeo O, Marchetta A, **Giosa D**, Giuffrè L, Urzì C, De Leo F. Whole Genome Sequencing and Comparative Genome Analysis of the Halotolerant Deep Sea Black Yeast Hortaea werneckii. Life (Basel). 2.10 (2020), 10(10):E229. doi: 10.3390/life10100229.8.
9. Tricomi G, **Giosa D**, Merlino G, Romeo O, Longo F. Toward a Function-as-a-Service Framework for Genomic Analysis. *2020 IEEE International Conference on Smart Computing (SMARTCOMP)*, 2020, pp. 314-319, doi: 10.1109/SMARTCOMP50058.2020.00070.
10. Lombardo, D., Saitta, C., **Giosa, D**., Casuscelli di Tocco, F., Musolino, C., Caminiti, G., Chines, V., Franzè, M. S., Alibrandi, A., Navarra, G., Raimondo, G., Pollicino, T."Frequency of somatic mutations in TERT promoter, TP53 and CTNNB1 genes in patients with hepatocellular carcinoma from Southern Italy". *Oncology Letters* 19.3 (2020): 2368-2374.
11. Nnadi, N.E., **Giosa, D.**, Ayanbimpe, G.M. *et al.* Whole-Genome Sequencing of an Uncommon *Cryptococcus neoformans* MLST43 Genotype Isolated in Nigeria. *Mycopathologia* **184,** 555–557 (2019). https://doi.org/10.1007/s11046-019-00376-1.
12. D'Alessandro, E., Sapienza, I., **Giosa, D.**, Giuffrè, L., & Zumbo, A. (2019). In silico analysis of meat quality candidate genes among Nero Siciliano, and Italian heavy pigs genomes. *Large Animal Review*, *25*(4), 137-140.
13. D'Alessandro E, **Giosa D**, Sapienza I, Giuffrè L, Cigliano RA, Romeo O, Zumbo A. Whole genome SNPs discovery in Nero Siciliano pig. *Genet Mol Biol*. 2019;pii: S1415-47572019005021102.
14. D'Aliberti D, Cacciola I, Musolino C, Raffa G, Filomia R, Alibrandi A, Benfatto S, Beninati C, Saitta C, **Giosa D**, Romeo O, Raimondo G, Pollicino T. NS3 Variability in Hepatitis C Virus Genotype 1A Isolates from Liver Tissue and Serum Samples of Treatment-Naïve Patients with Chronic Hepatitis C. July 2018 *Intervirology* 61(1):1-8. DOI: 10.1159/000489307
15. Scordino F., Giuffrè L., Barberi G., Marino Merlo F., Orla.ndo M. G., **Giosa D.**, Romeo O. Multilocus Sequence Typing Reveals a New Cluster of Closely Related Candida tropicalis Genotypes in Italian Patients With Neurological Disorders. *Front. Microbiol.*, 06 April 2018 | https://doi.org/10.3389/fmicb.2018.00679.
16. **Giosa, D.,** Felice, M. R., Lawrence, T. J., Gulati, M., Scordino, F., Giuffrè, L., Lo Passo, C., D’Alessandro, E., Criseo, G., Ardell, D. H., Hernday, A. D., Nobile, C. J., Romeo, O. (2017). Whole RNA-sequencing and transcriptome assembly of *Candida albicans* and *Candida africana* under chlamydospore-inducing conditions. *Genome Biology and Evolution*, 9(7), 1971-1977.
17. Chowdhary, A., Hagen, F., Sharma, C., Al-Hatmi, A. M. S., Giuffrè, L., **Giosa, D.,** Fan, S., Badali, H., Felice, M. R., de Hoog, S., Meis, J. F., Romeo, O. (2017). Whole Genome-Based Amplified Fragment Length Polymorphism Analysis Reveals Genetic Diversity in *Candida africana*. *Frontiers in microbiology*, 3;8:556. doi: 10.3389/fmicb.2017.00556.
18. Huang, L., Gao, W., **Giosa, D.,** Criseo, G., Zhang, J., He, T., Huang, X., Sun, J., Sun, Y., Huang, J., Zhang, Y., Brankovics, B., Scordino, F., D'Alessandro, E., van Diepeningen, A., de Hoog, S., Huang, H., Romeo, O. (2016). Whole-genome sequencing and in silico analysis of two strains of *Sporothrix globosa*. *Genome biology and evolution*, 8(11), 3292. doi:10.1093/gbe/evw230.
19. D’Alessandro, E., **Giosa, D.,** Huang, L., Zhang, J., Gao, W., Brankovics, B., Oliveira, M. M. E., Scordino, F., Lo Passo, C., Criseo, G., van Diepeningen, A. D., Huang, H., de Hoog, G. S., Romeo, O. (2016). Draft genome sequence of the dimorphic fungus *Sporothrix pallida*, a nonpathogenic species belonging to Sporothrix, a genus containing agents of

human and feline sporotrichosis. *Genome announcements*, 4(2), e00184-16. doi:10.1128/genomeA.00184-16.

20 Felice, M. R., Gulati, M., Giuffrè, L., **Giosa, D.,** Di Bella, L. M., Criseo, G., Nobile, C. J., Romeo, O., Scordino, F. (2016) Molecular Characterization of the N-Acetylglucosamine Catabolic Genes in *Candida africana*, a Natural NAcetylglucosamine Kinase (HXK1) Mutant. *PLoS ONE* 11(1): e0147902. doi:10.1371/journal.pone.0147902.

21 Rharmitt, S., Hafidi, M., Hajjaj, H., Scordino, F., **Giosa, D.,** Giuffrè, L., Barreca, D., Criseo, G., Romeo, O. (2016). Molecular characterization of patulin producing and non-producing Penicillium species in apples from Morocco. *International journal of food microbiology*, 217, 137-140. doi:10.1016/j.ijfoodmicro.2015.10.019.

CONFERENCE PAPERS

1 A Bonomo, G Rigano, M Lui, L Giuffrè, R Aiese Cigliano, O Romeo, **D Giosa**. Sporothrix genome database update and whole phylogenomic analysis. Bioinformatics and Computational Biology Conference (BBCC), 2022. https://doi.org/10.7490/f1000research.1119311.1.

2 Maria Lui, Gabriele Rigano, Andrea Bonomo, Letterio Giuffrè, Orazio Romeo, **D Giosa**. Bioinformatics analysis of six Candida parapsilosis genome assemblies obtained using whole-genome optical maps and Illumina short-read data. Bioinformatics and Computational biology Conference (BBCC), 2022. https://doi.org/10.7490/f1000research.1119306.1.

3 **D Giosa**, L Giuffrè, MR Felice, G Rigano, M Lui, R Aiese Cigliano, LM Lopes Bezerra, O Romeo. Whole-transcriptome analysis of *Sporothrix brasiliensis* grown in mold- and yeast-inducing conditions (P421), *Medical Mycology*, Volume 60, Issue Supplement_1, Sept 2022, myac072P421, https://doi.org/10.1093/mmy/myac072.P421.

4 Ragno A, **Giosa D**, Marzico C, Mastino A, Marino-Merlo F. Exploration of possible role of cellular micro-RNA in HSV-1/cell interaction by a bioinformatic and experimental dual approach. Topic: Viral pathogenesis and virus-host interactions. 6TH National Congress of the Italian Society for Virology SIV-ISV (p.143) Naples, Italy, 3-5 Jul 2022.

5 Albano M, Savoca S, Romeo O, **Giosa D**, Spanò N, Capillo G. Occurrence of Zu cristatus (Bonelli, 1819) in the Ionian Sea at unusual depth. 94th National Congress of the Italian Society for Experimental Biology, Palermo, Italy, 6-9 Apr 2022.

6 **Giosa D**, Lombardo D, Musolino C, Navarra G, Raimondo G, Pollicino T. A new high-throughput HBV integration sequencing approach shows that mitochondrial DNA is frequently targeted by virus integration in liver cells with active HBV replication. *Digestive and Liver Disease 54*, eS8-S9. https://doi.org/10.1016/j.dld.2022.01.020.

7 Marco Tolone, **Domenico Giosa**, Rosalia Di Gerlando, Anna Maria Sutera, Angelo Moscarelli, Ilaria Rizzuto, Baldassarre Portolano, Salvatore Mastrangelo. Whole-genome resequencing reveals specific genomic variants in Italian insular sheep breeds. ASPA 24 th Congress. Ital J Anim Sci vol.20:s1,2021. https://doi.org/10.1080/1828051X.2021.1968170.

8 Tricomi G., **Giosa D.,** Merlino G., Romeo O., Longo F. Toward a Function-as-a-Service Framework for Genomic Analysis. *SmartSys* 2020 workshop in Smartcomp 2020.

9 **D Giosa,** F Casuscelli di Tocco, G Raffa, C Musolino, D Lombardo, C Saitta, R Aiese Cigliano, W Sanseverino, O Romeo, G Navarra, G Raimondo, T Pollicino**.** Comprehensive characterization of HBV in tumor and non-tumor liver tissues from patients with HBV related-HCC. *Digestive and Liver Disease* 52, e3-e4. https://doi.org/10.1016/j.dld.2019.12.014.

10 D Lombardo, C Saitta, **D Giosa**, F Casuscelli di Tocco, C Musolino, G Caminiti, Valeria Chines, MS Franzè, G Navarra, G Raimondo, T Pollicino. Frequency of TP53, CTNNB1, and TERT promoter mutations in patients with hepatocellular carcinoma. *Digestive and Liver Disease* 52, e52-e53. https://doi.org/10.1016/j.dld.2019.12.055.

11 **Domenico Giosa**, Deborah D'Aliberti, Francesca Casuscelli di Tocco, Giuseppina Raffa, Cristina Musolino, Gianluca Tripodi, Daniele Lombardo, Carlo Saitta, Riccardo Aiese Cigliano, Orazio Romeo, Giuseppe Navarra, Giovanni Raimondo, Teresa Pollicino. Characterization of Hepatitis B Virus integration landscape patients with Hepatocellular Carcinoma and in PLC/PRF/5 cell lines. "*34th SIPMeT National Congress*, 4th Joint Meeting of Pathology and Laboratory Medicine, Second Joint Meeting in collaboration with ASIP-AMP-UEMS-WASPALM, Patologia e Medicina di Laboratorio 4.0". 23-25 Oct 2018, Aci Castello, Catania, Italy.

12 C. Barresi, L. Moreno, M. G. Orlando, M. R. Felice, D. Barreca, **D. Giosa**, G. Criseo, B. G. van den Ende, A. van Diepeningen, S. de Hoog, O. Romeo. Susceptibility to hydrogen peroxide and molecular characterization of catalase-encoding genes in different Sporothrix species. *ISHAM* 2018, Jul 2018, Amsterdam, The Netherlands.

13 D. D'aliberti, **D. Giosa**, G. Raffa, C. Musolino, G. Tripodi,D. Lombardo, F.C.D. Tocco, C. Saitta, O. Romeo, G. Navarra,G. Raimondo, T. Pollicino. Analysis of HBV DNA integration in tumor and non-tumor livertissues by a high-throughput viral integration detection method. EASL LiverTree™, Ginevra (Swiss), 14 Apr 2018. *Journal of Hepatology* 68:S688. DOI: 10.1016/S0168-8278(18)31636-2.

14 D. D'Aliberti, **D. Giosa**, G. Raffa, C. Musolino, G. Tripodi, D. Lombardo, F. Casuscelli di Tocco, C. Saitta, O. Romeo, G. Navarra, G. Raimondo, T. Pollicino. Characterization of HBV integration landscape in tumor and non-tumor liver tissues by a high-throughput viral integration detection method. Febbraio 2018. DOI: https://doi.org/10.1016/j.dld.2018.01.095. *51th Annual Meeting A.I.S.F.* Roma, Italy, 22-23 Feb 2018.

15 L. Giuffrè, **D. Giosa,** F. Scordino, I. Sapienza, G. Criseo, O. Romeo, E. D'Alessandro. Nero Siciliano pig's intestinal mycobiota: phenotypic and molecular characterization. *90° Convegno SIBS* "Biologia sperimentale nella ricerca di base ed applicata all'ambiente ed alla salute umana", Trapani, Italy, 27-28 Oct 2017.

16 I. Sapienza, M. Pugliese, L. Sinagra, **D. Giosa,** L. Giuffrè, O. Romeo, E. D'alessandro. Analysis of the titin-cap gene as candidate for dilated cardiomyopathy in Great Dane. *90° Convegno SIBS* "Biologia sperimentale nella ricerca di base ed applicata all'ambiente ed alla salute umana", Trapani, Italy, 27-28 Oct 2017.

17 I. Sapienza, C. Rifici, A. Sanfilippo, L. Giuffrè, **D. Giosa,** O. Romeo, E. D'alessandro. c-KIT mutation analysis and its relationship with degree of aggression in mast cell tumors in two dog breeds. *90° Convegno SIBS* "Biologia

sperimentale nella ricerca di base ed applicata all'ambiente ed alla salute umana", Trapani, Italy, 27-28 Oct 2017.

18 **D. Giosa,** M.R. Felice, L. Giuffré, F. Scordino, C. Lo Passo, G. Criseo, E. D'Alessandro, O. Romeo. Whole mRNA sequencing and transcriptome assembly of Candida albicans and *Candida africana* under chlamydospore-inducing conditions. *Journal of Biological Research* 2016; 89:s1

19 **D. Giosa,** I. Sapienza, L. Giuffré, O. Romeo, E. D'Alessandro. Toward KIT and RXFP2 genes SNPs discovery in goat (*Capra hircus*) using NGS technology approach. *Journal of Biological Research* 2016; 89:s1.

20 L. Giuffré, **D. Giosa,** F. Scordino, G. Criseo, E. D'Alessandro, O. Romeo, M.R. Felice. Sequencing and preliminary analysis of genes involved in iron metabolism in *Candida africana* CBS11016 strain. *Journal of Biological Research* 2016; 89:s1

21 F. Scordino, **D. Giosa,** G. Barberi, O. Romeo. Molecular epidemiology of pathogenic Candida species in hospital environments. *Journal of Biological Research* 2016; 89:s1

22 L. El Aamri, M. Hafidi, G. Criseo, L. Giuffre, H. Ghalfi, C. Barresi, M.G. Orlando, A. Lebrihi, **D. Giosa,** O. Romeo. Molecular identification of lipase producing yeasts isolated from moroccan strawberry and olive pomace. *Journal of Biological Research* 2016; 89:s1

23 D. A. van Diepeningen, A. al-Hatmi, B. Dalyan Cilo, **D. Giosa,** W. J. Bartstra and G. S. de Hoog. Azole susceptibility and resistance in *Fusarium spp*. *Mycoses* 2015 Blackwell Verlag GmbH, 58 (Suppl. 4), 51–226.

24 S. Rharmitt, M. Hafidi, H. Hajjaj, **D. Giosa,** L. Giuffrè, D. Barreca, G. Criseo, F. Scordino, O. Romeo. Molecular and biochemical characterization of patulin producing and non-producing Penicillium species in apples fruits from Morocco. Conference: *37th Mycotoxin Workshop*, At Bratislava, Slovakia. doi:10.13140/RG.2.1.2439.9208

ORAL COMMUNICATIONS

1 Domenico Giosa. "The complete genome of thermodimorphic fungi in the long-read sequencing era.", PacBio DISCOVERIES ROADSHOW 2023 – 30 May 2023, Milan, Italy

2 Domenico Giosa. "Il Supporto della Bioinformatica". Course ECM "Le emopatie, dalla clinica al laboratorio", 09 Sep 2022, Messina, Italy;

3 Domenico Giosa. "Applicazioni NGS nello studio delle infezioni virali". Bioinformatics new generation professional: biologists in-silico ENPAB conference, 14 Jun 2019, Messina, Italy.

4 D. Giosa, F. Casuscelli di Tocco, G. Raffa, C. Musolino, D. Lombardo, C. Saitta, R. Aiese Cigliano, W. Sanseverino, O. Romeo, G. Navarra, G. Raimondo, T. Pollicino. Comprehensive characterization of HBV in tumor and non-tumor liver tissues from patients with HBV related-HCC. Digestive and Liver Disease 52, e3-e4. https://doi.org/10.1016/j.dld.2019.12.014

5 Domenico Giosa, Deborah D'Aliberti, Francesca Casuscelli di Tocco, Giuseppina Raffa, Cristina Musolino, Gianluca Tripodi, Daniele Lombardo, Carlo Saitta, Riccardo Aiese Cigliano, Orazio Romeo, Giuseppe Navarra, Giovanni Raimondo, Teresa Pollicino. Characterization of Hepatitis B Virus integration landscape patients with Hepatocellular Carcinoma and in PLC/PRF/5 cell lines. "34th SIPMeT National Congress, 4th Joint Meeting of Pathology and Laboratory Medicine, Second Joint Meeting in collaboration with ASIP-AMP-UEMS-WASPALM, Patologia e Medicina di Laboratorio 4.0". 23-25 Oct 2018, Aci Castello, Catania, Italy.

6 Domenico Giosa, Deborah D'Aliberti, Francesca Casuscelli di Tocco, Giuseppina Raffa, Cristina Musolino, Gianluca Tripodi, Daniele Lombardo, Carlo Saitta, Riccardo Aiese Cigliano, Orazio Romeo, Giuseppe Navarra, Giovanni Raimondo, Teresa Pollicino. Study of HBV DNA integration in patients with HCC and PLC/PRF/5 cells by a high-throughput viral integration detection method. 2018 International HBV Meeting, 03-06 Oct 2018, Taormina, Messina, Italy.

7 Domenico Giosa, Letterio Giuffrè, Riccardo Aiese Cigliano, Maria Rosa Felice, Giuseppe Criseo, Enrico D'alessandro, Orazio Romeo. Bioinformatics analysis of Next-Generation Sequencing data in microbiology. 90° Convegno SIBS "Biologia sperimentale nella ricerca di base ed applicata all'ambiente ed alla salute umana", Trapani, Italy, 27-28 Oct 2017.

8 Domenico Giosa, Alessandro Zumbo, Irene Sapienza, Letterio Giuffrè, Riccardo Aiese Cigliano, Orazio Romeo, Enrico D'alessandro. Whole genome SNPs discovery and analysis of genetic diversity in Nero Siciliano Pig. 90° Convegno SIBS "Biologia sperimentale nella ricerca di base ed applicata all'ambiente ed alla salute umana", Trapani, Italy, 27-28 Oct 2017.

9 Domenico Giosa, Maria Rosa Felice, Letterio Giuffre', Fabio Scordino, Carla Lo Passo, Giuseppe Criseo, Enrico D'alessandro, Orazio Romeo. Whole mRNA sequencing and transcriptome assembly of Candida albicans and Candida africana under chlamydospore-inducing conditions. 89° Convegno SIBS "Clima e Vita", Bologna, Italy, 1-2 Dec 2016.

10 Domenico Giosa. Next Generation Sequencing (NGS): una rivoluzione nella biologia di base e applicata. Corso "Genomica, proteomica e bioinformatica per lo studio e l'identificazione dei microrganismi", Messina, Italy, 29 May 2015.

11 Domenico Giosa, Enrico D'Alessandro, Fabio Scordino, Francesca Bertolini, Salvatore Brosio, Leandro F. Moreno, Balazs Brankovics, Manoel Marques Evangelista Oliveira, Giuseppe Criseo, Carla Lo Passo, Anne D. van Diepeningen, Sybren de Hoog, Orazio Romeo. Draft genome of Sporothrix pallida, a non-pathogenic member of the genus Sporothrix. Workshop "Genomics of Neglected Pathogens" (Utrecht, The Netherlands, 20-21 Apr 2015.