Curriculum vitae

General informations

Name: Emanuele Bosi
Place and date of birth: Firenze, 19/10/1987
Nazionality: Italian
Residence: Via Montello 11, Pisa
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Education

• Date (from – to)	2012 - 2015
• Title	**Doctoral degree in Plant science, microbiology and genetics (SSD: BIO/18 - Genetics)**
• Institute	Università degli studi di Firenze
• Level	Doctoral degree
• Thesis title	FROM SEQUENCE TO FUNCTION, FROM GENOMES TO MODELS
• Date (from – to)	2010 - 2012
• Title	**LM-6 - Laurea magistrale in Bioinformatics**
• Institute	Alma Mater Studiorum - Università di Bologna
• Level	Master degree
• Thesis title	DEVELOPMENT OF A GENOME CONTEXT ORIENTED SCAFFOLDING PIPELINE TO IMPROVE BACTERIAL DRAFT GENOME ASSEMBLIES
• Date (from – to)	2006 - 2010
• Title	**1-Classe delle lauree in biotecnologie** **Denominazione corso: BIOTECNOLOGIE**
• Institute	Università degli studi di Firenze
• Level	Bachelor degree
• Thesis title	IDENTIFICATION AND ANALYSIS OF ATYPICAL PLASMID GENES

Abroad periods

• Date (from - to)	01/04/2017 – 31/05/2017
• Institute	Wellcome Trust Sanger Institute
• Department	Host Microbiota interaction lab
• Qualification	Visiting Scientist
• Activities	Research on *Fusobacterium nucleatum*:

- Metabolic modeling and phenotypical predictions
- Anaerobic growth and transcriptomics

• Date (from - to)	30/09/2013-01/04/2014
• Institute	University of California San Diego UCSD
• Department	Department of Bioengineering
• Qualification	Visiting graduate student
• Activities	Integration of *S. aureus* comparative genomics with metabolic modeling

Research experience

• Date (from - to)	01/12/2021 - Presente
• Employer	University of Genova
• Department	DISTAV
• Qualification	Senior researcher (RTD-B) in Genetics (SSD BIO18)
• Description	Genomics analysis of marine bacteria and reconstruction of metabolic models to validate with chemostat experiments

• Date (from - to)	03/08/2019 - 30/11/2021
• Employer	University of Pisa
• Department	Deparment of clinical and experimental medicine
• Qualification	Post-doc (project title **"Systems biology of pancreatic islet cells and their role in diabetes"**)
• Description	Computational analysis of different omics data from pancreatic islets to highlight molecular mechanisms associated with type 1 and type 2 diabetes

• Date (from - to)	01/06/2017 - 31/05/2019
• Employer	Università degli studi di Firenze
• Department	Department of biomedical, clinical and experimental sciences "Mario Serio"
• Qualification	Post-doc (project title **"Development of computational methods to analyse NGS data for the study of pediatric nephropaties"**)
• Description	Development and implementation of methods to identify and prioritise genomic variants associated with rare pediatric disorders.

• Date (from - to)	01/12/2016 - 31/05/2017
• Employer	Università degli studi di Firenze
• Department	Biology department
• Qualification	Post-doc (project title *"Development of metabolic model of microbiota associated with colorectal cancer"*
• Description	Reconstruction of *Fusobacterium nucleatum* metabolic model from genomic data to predict phenotypes associated with colorectal cancer

• Date (from - to)	01/01/2012 - 31/08/2012
• Employer	Università degli studi di Firenze
• Department	Biology department
• Qualification	Trainee
• Description	Development of graph-based methods for genome assembly

• Date (from - to)	01/04/2009-01/10/2009
• Employer	Università degli studi di Firenze
• Department	Biology department
• Qualification	Trainee
• Description	Computational analysis of plasmid sequences to identify putative horizontal gene transfer events

Pubblications

*=Co-first author

1. **Bosi E**, Fani R, Fondi M. The mosaicism of plasmids revealed by atypical genes detection and analysis. **BMC genomics (IF 3.73)**, 12,1,403, 2011.
2. Maida I, **Bosi E**, Perrin E, Papaleo MC, Orlandini V, Fondi M, Fani R, Wiegel J, Bianconi G, Canganella F. Draft genome sequence of the fast-growing bacterium Vibrio natriegens strain DSMZ 759. **Genome announcements (IF 0.89)**, 1,4,e00648-13, 2013.
3. Orlandini V, Maida I, Fondi M, Perrin E, Papaleo MC, **Bosi E**, de Pascale D, Tutino ML, Michaud L, Lo Giudice A. Genomic analysis of three sponge-associated Arthrobacter Antarctic strains, inhibiting the growth of Burkholderia cepacia complex bacteria by synthesizing volatile organic compounds. **Microbiological research (IF 3.97)**, 169,7,593- 601, 2014.
4. Fondi M, Orlandini V, Perrin E, Maida I, **Bosi E**, Papaleo MC, Michaud L, Lo Giudice A, de Pascale D, Tutino ML, Liò P, Fani R. Draft genomes of three Antarctic Psychrobacter strains producing antimicrobial compounds against Burkholderia cepacia complex, opportunistic human pathogens. **Marine genomics (IF 2.385)**, 13,37-38, 2014
5. Maida I, **Bosi E**, Fondi M, Perrin E, Orlandini V, Papaleo MC, Mengoni A, de Pascale D, Tutino ML, Michaud L, Lo Giudice A, Fani R. ,Antimicrobial activity of Pseudoalteromonas strains isolated from the Ross Sea (Antarctica) versus Cystic Fibrosis opportunistic pathogens. **Hydrobiologia (IF 2.385)**, 761,1,443-457, 2015
6. **Bosi E**, Donati B, Galardini M, Brunetti S, Sagot MF, Lió P, Crescenzi P, Fani R, Fondi M. MeDuSa: a multi-draft based scaffolder. **Bioinformatics (IF 5.61)**, 31,15,2443-2451, 2015

7. Maida I, Chiellini C, Mengoni A, **Bosi E**, Firenzuoli F, Fondi M, Fani R. Antagonistic interactions between endophytic cultivable bacterial communities isolated from the medicinal plant Echinacea purpurea. **Environmental microbiology (IF 4.933)**, 2015,

8. **Bosi E**, Fondi M, Maida I, Perrin E, de Pascale D, Tutino ML, Parrilli E, Lo Giudice A, Filloux A, Fani R. Genome-scale phylogenetic and DNA composition analyses of Antarctic Pseudoalteromonas bacteria reveal inconsistencies in current taxonomic affiliation. **Hydrobiologia (IF 2.385)**, 761,1,85-95, 2015

9. Fondi M, Karkman A, Tamminen MV, **Bosi E**, Virta M, Fani R, Alm E, McInerney J. "Every Gene Is Everywhere but the Environment Selects": Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. **Genome Biology and Evolution (IF 3.462)**, 8, 5, 1388-1400, 2016

10. Presta L, Inzucchi I, **Bosi E**, Fondi M, Perrin E, Maida I, Miceli E, Tutino ML, Lo Giudice A, de Pascale D, Fani R. Draft Genome Sequences of the Antimicrobial Producers Pseudomonas sp. TAA207 and Pseudomonas sp. TAD18 Isolated from Antarctic Sediments. **Genome Announcements (IF 0.89)**, 4 (4), e00728-16. 2016

11. Presta L, Inzucchi I, **Bosi E**, Fondi M, Perrin E, Miceli E, Tutino ML, Lo Giudice A, de Pascale D, Fani R. Draft genome sequence of Flavobacterium sp. strain TAB 87, able to inhibit the growth of cystic fibrosis bacterial pathogens belonging to the Burkholderia cepacia complex. **Genome Announcements (IF 0.89)**, 4 (3), e00410-16. 2016

12. Presta L, **Bosi E**, Fondi M, Maida I, Perrin E, Miceli E, Maggini V, Bogani P, Firenzuoli F, Di Pilato V, Rossolini GM, Mengoni A, Fani R. Draft Genome Sequence of Pseudomonas sp. EpS/L25, Isolated from the Medicinal Plant Echinacea purpurea and Able To Synthesize Antimicrobial Compounds. **Genome Announcements (IF 0.89)**, 4 (3), e00346-16. 2016

13. Fondi M, Maida I, Perrin E, Orlandini V, La Torre L, **Bosi E**, Negroni A, Zanaroli G, Fava F, Decorosi F, Giovannetti L, Viti C, Vaneechoutte M, Dijkshoorn L, Fani R. Genomic and phenotypic characterization of the species Acinetobacter venetianus. **Scientific reports (IF 3.998)**, 6, 2016

14. **Bosi E**, Monk JM, Aziz RK, Fondi M, Nizet V, Palsson BO. Comparative genome-scale modelling of S. aureus strains identifies strain-specific metabolic capabilities linked to pathogenicity. **Proceedings of the National Academy of Sciences (IF 9.412)**, 2016

15. Fondi M, **Bosi E***, Presta L, Natoli D, Fani R. Modelling microbial metabolic rewiring during growth in a complex medium. **BMC genomics (IF 3.73)** 17 (1), 970. 2016

16. **Bosi E**, Fondi M, Orlandini V, Perrin E, Maida I, de Pascale D, Tutino ML, Parrilli E, Lo Giudice A, Filloux A, Fani R. The pangenome of (Antarctic) Pseudoalteromonas bacteria: evolutionary and functional insights. **BMC genomics (IF 3.73)** 18 (1), 93. 2017

17. Chiellini C, Maida I, Maggini V, **Bosi E**, Mocali S, Emiliani G, Perrin E, Firenzuoli F, Mengoni A, Fani R. Preliminary data on antibacterial activity of Echinacea purpurea-associated bacterial communities against Burkholderia cepacia complex strains, opportunistic pathogens of Cystic Fibrosis patients. **Microbiological Research (IF 3.970)** 196, 34-43. 2017

18. Mocali S, Chiellini C, Fabiani A, Decuzzi S, de Pascale D, Parrilli E, Tutino ML, Perrin E, **Bosi E**, Fondi M, Lo Giudice A, Fani R. Ecology of cold environments: new insights of bacterial metabolic adaptation through an integrated genomic-phenomic approach. **Scientific Reports (IF 3.998)** 7 (1), 839. 2017

19. Presta L, **Bosi E**, Fondi M, Maida I, Perrin E, Miceli E, Maggini V, Bogani P, Firenzuoli F, Di Pilato V, Rossolini GM, Mengoni A, Fani R. Phenotypic and genomic characterization of the antimicrobial producer Rheinheimera sp. EpRS3 isolated from the medicinal plant Echinacea purpurea: insights into its biotechnological relevance. **Research in microbiology (IF 3.970)** 168 (3), 293-305. 2017

20. Miceli E, Presta L, Maggini V, Fondi M, **Bosi E**, Chiellini C, Fagorzi C, Bogani P, Di Pilato V, Maria G, Mengoni A, Firenzuoli F, Perrin E, Fani R. New Genome Sequence of an Echinacea purpurea Endophyte, Arthrobacter sp. Strain EpSL27, Able To Inhibit Human-Opportunistic Pathogens. **Genome Announcements (IF 0.89)**. 5.25: e00565-1. 2017

21. Maggini V, Presta L, Miceli E, Fondi M, **Bosi E**, Chiellini C, Fagorzi C, Bogani P, Di Pilato V, Maria G, Mengoni A, Firenzuoli F, Perrin E, Fani R Draft genome sequence of pseudomonas sp. strain ep r1 isolated from echinacea purpurea roots and effective in the growth inhibition of human opportunistic pathogens belonging to the burkholderia cepacia complex. **Genome Announcements (IF 0.89)**. 5.20: e00351-17. 2017

22. Perrin E, Fondi M, **Bosi E**, Mengoni A, Buroni S, Scoffone VC, Valvano M, Fani R. Subfunctionalization influences the expansion of bacterial multidrug antibiotic resistance. **BMC genomics (IF 3.73)** 18.1, 834. 2017

23. Presta L, **Bosi E**, Mansouri L, Dijkshoorn L, Fani R, Fondi M. Constraint-based modeling identifies new putative targets to fight colistin-resistant A. baumannii infections. **Scientific Reports (IF 3.998)**, 7(1), 3706. 2017
24. **Bosi E**, Bacci G, Mengoni A, Fondi M. Perspectives and challenges in microbial communities metabolic modeling. **Frontiers in Genetics (IF 3.789)**, 8: 88. 2017
25. **Bosi E**, Mascagni F. Less Is More: Genome Reduction and the Emergence of Cooperation—Implications into the Coevolution of Microbial Communities. **International journal of genomics (IF 2.414)**. 2019
26. Landini S, Mazzinghi B, Becherucci F, Allinovi M, Provenzano A, Palazzo V, Ravaglia F, Artuso R, **Bosi E**, Stagi S, Sansavini G, Guzzi F, Cirillo L, Vaglio A, Murer L, Peruzzi L, Pasini A, Materassi M, Roperto RM, Anders HJ, Rotondi M, Giglio SR and Romagnani P. Reverse phenotyping after whole-exome sequencing in steroid-resistant nephrotic syndrome. **Clinical Journal of the American Society of Nephrology (IF 6.628)** 15 (1), 89-100. 2020
27. Usai G, Mascagni F, Giordani T, Vangelisti A, **Bosi E**, Zuccolo A, Ceccarelli M, King R, Hassani-Pak K, Zambrano LS, Cavallini A, Natali L. Epigenetic patterns within the haplotype phased fig (Ficus carica L.) genome. **The Plant Journal (IF 6.141)** 102 (3), 600-614. 2020
28. Marchetti P, Suleiman M, De Luca C, Baronti W, **Bosi E**, Marselli L. A direct look at the dysfunction and pathology of the β cells in human type 2 diabetes. **Seminars in Cell & Developmental Biology (IF 6.138).** 2020
29. **Bosi E**, Marselli L, De Luca C, Suleiman M, Tesi M, Ibberson M, Eizirik DL, Cnop M, Marchetti P. Integration of single-cell datasets reveals novel transcriptomic signatures of β-cells in human type 2 diabetes. **NAR Genomics and Bioinformatics (IF TBD)** 2 (4), lqaa097. 2020
30. Marselli L, Piron A, Suleiman M, Colli ML, Yi X, Khamis A, Carrat GR, Rutter GA, Bugliani M, Giusti L, Ronci M, Ibberson M, Turatsinze JV, Boggi U, De Simone P, De Tata V, Lopes M, Nasteska D, De Luca C, Tesi M, **Bosi E**, Singh P, Campani D, Schulte AM, Solimena M, Hecht P, Rady B, Bakaj I, Pocai A, Norquay L, Thorens B, Canouil M, Froguel P, Eizirik DL, Cnop M, Marchetti P. Persistent or Transient Human β Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. **Cell Reports (IF 8.109)** 33 (9), 108466. 2020
31. Tesi M, Bugliani M, Ferri G, Suleiman M, De Luca C, **Bosi E**, Masini M, De Tata V, Gysemans C, Cardarelli F, Cnop M. Pro-Inflammatory Cytokines Induce Insulin and Glucagon Double Positive Human Islet Cells That Are Resistant to Apoptosis. **Biomolecules (IF 4.65)** 11(2):320. 2021
32. **Bosi E**, Marchetti P, Rutter GA, Eizirik DL. Human alpha cell transcriptomic signatures of types 1 and 2 diabetes highlight disease-specific dysfunction pathways. iScience (**IF 6.107**). 2022 Sep 3:105056.
33. **Bosi E**, Marselli L, Suleiman M, Tesi M, De Luca C, Del Guerra S, Cnop M, Eizirik DL and Marchetti P, 2022. A single-cell human islet interactome atlas identifies disrupted autocrine and paracrine communications in type 2 diabetes. **NAR Genomics and Bioinformatics (IF TBD)**, 4(4), p.lqac084. 2022

Book chapters

1. **Bosi E**, Fani R, Fondi M. Defining orthologs and pangenome size metrics. **Bacterial Pangenomics: Methods and Protocols** 191-202, 2015
2. Fondi M, **Bosi E**, Fani R. A Systems Biology View on Bacterial Response to Temperature Shift. **Biotechnology of extremophiles** 597-618, 2016
3. Monk J, **Bosi E**. Integration of comparative genomics with genome-scale metabolic modeling to investigate strain-specific phenotypical differences. **Metabolic Network Reconstruction and Modeling**. Humana Press, New York, NY, 2018. 151-175.