FRANCESCA MENGHI The Jackson Laboratory for Genomic Medicine Ten Discovery Drive Farmington, CT 06032 (+1) 860 837 2451; (+1) 860 278 6216 francesca.menghi@jax.org

I am currently working as an associate research scientist at The Jackson Laboratory (JAX) for Genomic medicine. JAX Genomic Medicine is a non-profit research institute which focuses on the understanding of the fine molecular changes at the basis of human diseases and aims at the discovery of novel means towards the early diagnosis and the individualised treatment of diseased patients with the ultimate goal of developing efficient protocols for personalised medicine.

Here, I am involved in several projects that explore the genome-wide patterns of genetic and transcriptional alterations characterising human cancers. In particular, I am interested in the identification of key regulatory genes and/or pathways which may explain tumour initiation and progression as well as provide valuable targets for the development of novel therapeutic approaches and prognostic biomarkers. At present, I am investigating critical genomic aberrations implicated in ovarian and breast cancer tumorigenesis. By exploiting next-generation sequencing technologies I aim at a better understanding of the individuality of cancer genomes and at the development of novel approaches towards the personalised management of cancer patients.

EDUCATION

PhD (Cancer Biology)

University College London, Institute of Child Health, UK, 2006 – 2010

- Sponsored by the Olivia Hodson Cancer Fund and the Annabel McEnery Children's Cancer Fund
- Supervised by Dr J Ham and Dr TS Jacques
- Title of PhD thesis: *Genome-wide analysis of gene expression and alternative splicing in human medulloblastomas.*

MRes Bioinformatics

University of Milan, Bicocca, Italy, 2005 - 2006

- Sponsored by the European Social Fund
- Supervised by Dr M Foti and Pr P Ricciardi-Castagnoli
- Title of Mres project: *Time-course gene expression profiling for the study of the molecular mechanisms of host-pathogen interactions.*

Laurea degree in Medical Biotechnology

University of Milan, Italy, 1999-2004

- Supervised by Pr G Finocchiaro and Pr D Fornasari
- Title of graduation thesis: *Molecular characterization of benign, atypical and malignant meningiomas by DNA microarray and loss of heterozygosity analysis.*

RESEARCH AND TEACHING EXPERIENCE

Associate Research Scientist (July 2013 - present) – Exploring the molecular mechanisms of cellular transformation at a genomic level.

The Jackson Laboratory for Genomic Medicine, Farmington, CT. Mentored by *Prof. Edison Liu*. Role involves:

- Investigating the role of chromosome X in breast cancer tumorigenesis
- Exploring the molecular basis of gender-specific susceptibility to cancer
- Identifying genomic "cancer-cassettes" which play fundamental roles in tumour initiation and maintenance

Postdoctoral Fellow (January 2011-September 2011) / Reasearch Associate (October 2011-May 2013) – Studying cancer genomes through the integrative analysis of genome-wide biological data (next-generation sequencing and hybridisation array).

Genome Institute of Singapore. Mentored by *Prof. Edison Liu* Role involved:

- Identification of somatic single nucleotide changes affecting cancer genomes (based on analysis of RNA-Seq and exome-capture sequencing data)
- Analysis of somatic structural rearrangements affecting putative oncogenes and tumour suppressor genes in cancer samples using distant paired-end tag DNA sequencing.
- Identifying cancer-specific somatic alterations with potential as tumour biomarkers.
- Developing analysis approaches for the integration of genome-wide biological data to investigate tumorigenesis in ovarian, melanoma and breast cancer.
- Exploring mechanism of acquired drug resistance in human melanoma cancer cells.

PhD Student. – Investigating genome-wide patterns of gene expression and differential splicing in human medulloblastoma.

University College London, Institute of Child Health, 2006-2010 Role involved:

- Analysis of differential gene expression and splicing in paediatric medulloblastomas using the Affymetrix Human Exon 1.0 ST array.
- Setting up of *in vitro* mouse cerebellar granule cell progenitor primary cultures as a model of cerebellar development.
- Investigating the role of candidate genes in *in vitro* mouse and human medulloblastoma cell lines.

Research Fellow. - Investigating molecular prognostic markers in human brain tumours.

Isituto Nazionale Neurologico Carlo Besta, Milan, Italy, 2004-2006 Role involved:

- Investigating prognostic markers in gliomas (LOH analysis, TP53, EGFR, MGMT);
- Analysing gene expression profile data generated within the group and validating the expression level of candidate genes;
- Keeping a bio-bank of DNA isolated from patients' tumour specimens and normal lymphocytes;
- Taking care of a database of the molecular aberrations identified in patients' tumour specimens.

Undergraduate Tutor. - Research dept. of Genetics, Evolution and Environment.

University College London, London, UK, 2008 (fall)

PRIZES AND CONFERENCES

Prizes awarded

- ICH open day poster special commendation, 2008
- Regional prize winners in Biotechnology YES business course, Newcastle/London, UK, 2008
- Best contribution award at the IX National Congress of the Italian Association of Neuro-Oncology, 2004

Grants and scholarships

- Awarded Olivia Hodson Cancer Fund PhD studentship 10/2006 to 03/2010
- Awarded Annabel McEnery Children's Cancer Fund 04/2010 to 09/2010

Conferences attended

- AACR 102nd annual meeting, Chicago, Illinois, USA, 2012, presented poster
- Frontiers in Cancer Science, Singapore, 2011
- Personalized Cancer Medicine Conference, Singapore, 2011
- 14th Human Genome meeting 2010, Montpellier, France, presented poster
- AACR 100th annual meeting, Denver, Colorado, USA, 2009, presented poster
- 110th British Neuropathological Society meeting, London, UK, 2009, presented poster
- AACR 98th annual meeting, Los Angeles, California, USA, 2007
- AACR 96th annual meeting, Anaheim, California, 2005, presented poster
- International symposium & annual meeting of the Neuro-Oncology working group of the German Cancer Society, Düsseldorf, Germany, 2004
- IX National Congress of the Italian Association of Neuro-Oncology, 2004, oral presentation
- AACR 95th annual meeting, Orlando, Florida, USA, 2004

PUBLICATIONS

Inaki K*, **Menghi F***, Woo XY*, Wagner JP, Jacques PÉ, Lee YF, Shreckengast PT, Soon WW, Malhotra A, Teo AS, Hillmer AM, Khng AJ, Ruan X, Ong SH, Bertrand D, Nagarajan N, Karuturi RK, Hidalgo Miranda A, Liu ET. Systems consequences of amplicon formation in human breast cancer.

Genome Res. 2014 Oct 24(10):1559-71. (* Inaki K, Menghi F and Woo XY contributed equally to this work)

Sandhu KS, Li G, Poh HM, Quek YL, Sia YY, Peh SQ, Mulawadi FH, Lim J, Sikic M, **Menghi F**, Thalamuthu A, Sung WK, Ruan X, Fullwood MJ, Liu E, Csermely P, Ruan Y. Large-scale functional organization of long-range chromatin interaction networks. **Cell Rep**. 2012 Nov 29;2(5):1207-19.

Kristiansen M, **Menghi F**, Hughes R, Hubank M, Ham J. Global analysis of gene expression in NGF-deprived sympathetic neurons identifies molecular pathways associated with cell death. **BMC Genomics**. 2011 Nov 8;12:551.

Menghi F, Orzan FN, Eoli M, Farinotti M, Maderna E, Pisati F, Bianchessi D, Valletta L, Lodrini S, Galli G, Anghileri E, Pellegatta S, Pollo B, Finocchiaro G. DNA microarray analysis identifies CKS2 and LEPR as potential markers of meningioma recurrence. **Oncologist**. 2011;16(10):1440-50.

Salsano E, Paterra R, Figus M, **Menghi F**, Maderna E, Pollo B, Solero CL, Massimi L, Finocchiaro G. Expression profile of frizzled receptors in human medulloblastomas. **J Neurooncol**. 2011 Aug 18.

Menghi F, Jacques TS, Barenco M, Schwalbe EC, Clifford SC, Hubank M, Ham J. Genome-wide analysis of alternative splicing in medulloblastoma identifies splicing patterns characteristic of normal cerebellar development. **Cancer Res**. 2011 Mar 15;71(6):2045-55.

Orzan F, Pellegatta S, Poliani PL, Pisati F, Caldera V, **Menghi F**, Kapetis D, Marras C, Schiffer D, Finocchiaro G. Enhancer of Zeste 2 (EZH2) is up-regulated in malignant gliomas and in glioma stem-like cells. **Neuropathol Appl Neurobiol**. 2011 Jun;37(4):381-94.

Gladin CR, Salsano E, **Menghi F**, Grisoli M, Ghielmetti F, Milanesi I, Pollo B, Brock S, Cusin A, Minati L, Finocchiaro G, Bruzzone MG.

Loss of heterozygosity studies in extracranial metastatic meningiomas. J Neurooncol. 2007 Oct;85(1):81-5.

Eoli M*, **Menghi F***, Bruzzone MG, De Simone T, Valletta L, Pollo B, Bissola L, Silvani A, Bianchessi D, D'Incerti L, Filippini G, Broggi G, Boiardi A, Finocchiaro G.

Methylation of O6-methylguanine DNA methyltransferase and loss of heterozygosity on 19q and/or 17p are overlapping features of secondary glioblastomas with prolonged survival.

Clin Cancer Res. 2007 May 1;13(9):2606-13 (* Eoli M and Menghi F contributed equally to this work)

Pellegatta S, Poliani PL, Corno D, **Menghi F**, Ghielmetti F, Suarez-Merino B, Caldera V, Nava S, Ravanini M, Facchetti F, Bruzzone MG, Finocchiaro G.

Neurospheres enriched in cancer stem-like cells are highly effective in eliciting a dendritic cell-mediated immune response against malignant gliomas.

Cancer Res. 2006 Nov 1;66(21):10247-52.