Maria Secrier

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Current Position

Lecturer, Computational Cancer Biology   *11/2017 - present*
UCL Genetics Institute, Department of Genetics, Evolution and Environment, London, UK
- Research programme in computational cancer genomics and immunology.

Education

PhD, Computational Biology - *magna cum laude* (4 publications, 3 first author) *10/2009 - 06/2013*
European Molecular Biology Laboratory (EMBL) and the *University of Heidelberg*, Germany
-Mentors: Dr. Reinhard Schneider, Dr. Wolfgang Huber
- Thesis topic: Visualization and analysis strategies for dynamic gene-phenotype relationships

BSc, Bioinformatics and Computational Biology (2 publications, 1 first author) *08/2006 - 06/2009*
Jacobs University, Bremen, Germany
- Thesis topic: Mutational robustness in gene regulatory networks

Research Experience

Senior Scientist: bioinformatics and immuno-oncology   *07/2016 - 10/2017*
AstraZeneca, Cambridge, UK
- Led projects in the area of immuno-oncology, disease bioinformatics and CRISPR-Cas9 screens.

Visiting Scientist: cancer genomics   *07/2016 - 07/2017*
Cancer Research UK Cambridge Institute, Cambridge, UK
- Led the genomic analyses of the first ever derived oesophageal adenocarcinoma organoids.

Research Associate: cancer genomics   *01/2014 - 07/2016*
Cancer Research UK Cambridge Institute, University of Cambridge, Cambridge, UK
- Mentors: Prof. Simon Tavaré, Prof. Rebecca Fitzgerald
- Headed the computational analysis efforts of the group on whole-genome sequencing data from >100 samples of oesophageal adenocarcinoma, as part of the International Cancer Genome Consortium (ICGC).

Short-term Postdoc: cancer bioinformatics   *07/2013 - 11/2013*
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
- Mentors: Dr. Reinhard Schneider, Dr. Wolfgang Huber, Dr. Toby Gibson
- Evaluated the impact of perturbing motif-mediated protein interactions in different types of cancer.

Research Assistant (multiple): bioinformatics and systems/network biology   *2007-2009*
Imperial College (London), Max Planck Institute (Bremen), University of Maynooth (Ireland)

Honours, Awards and Funding

Wellcome Institutional Strategic Support Fund (£19,802 for 2 years)	*2018–2020*
Wellcome Trust, BBSRC and BSGCT student bursaries (£5,440)	*2018*
Bye Fellowship, *Murray Edwards College*, University of Cambridge	*2014–2016*
Special Distinction for Excellency at postgraduate level in Europe (from Romanian Government)	*2013*
Graduate Research Fellowship, *EMBL*, Heidelberg - funding for the duration of the PhD	*2009–2013*
Merit-based Scholarship/Distinction for Academic Achievement, *Jacobs University*	*2006–2009*

Co-chair of the UCL Cancer Domain Early Careers Network	*2018 - present*
Senior Editor - Annals of Human Genetics	*2017 - present*
Member of the Cambridge Cancer Centre Aerodigestive Commitee	*2015 - 2016*

Established bioinformatic infrastructure/expertise as one of top 3 priorities for the Cambridge Cancer Centre.

Member of the Garuda Core Alliance Consortium - Systems Biology knowledge platform *2011 - 2013*

SELECTED PUBLICATIONS (TOTAL - 18, FIRST AUTHOR - 6, † JOINT FIRST AUTHORSHIP)

Li, X.†, Francies, H.†, **Secrier, M.**, .., Garnett, M. Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. *Nat Commun* 2018; 9(1):2983

Talukdar, F.R., di Pietro, M., **Secrier, M.**, .., Herceg, Z., OCCAMS Consortium*. Molecular landscape of esophageal cancer: implications for early detection and personalized therapy. *Ann N Y Acad Sci* 2018

Noble, F., .., Underwood, T.J., **OCCAMS Consortium***. Multicentre cohort study to define and validate pathological assessment of response to neoadjuvant therapy in oesophagogastric adenocarcinoma. *Br J Surg* 2017; 104(13):1816-1828 (* includes **Secrier M**)

Garcia, E., .., Underwood, T.J., **OCCAMS Consortium***. Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. *Sci Rep* 2016; 6:32417. (* includes **Secrier M**)

Noorani, A.†, Bornschein, J.†, Lynch, A.G.†, **Secrier, M.**,.., Fitzgerald, R.C. A comparative analysis of whole genome sequencing of esophageal adenocarcinoma pre- and post-chemotherapy. *Genome Res* 2017;27(6):902-912

Secrier, M.†, Li, X.†, .. Fitzgerald, R.C. Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. *Nat Genetics* 2016; 48(10):1131-41

Contino, G., Eldridge, M., **Secrier, M.**, .., Fitzgerald, R.C. Whole-genome sequencing of nine esophageal adenocarcinoma cell lines. *F1000Res* 2016; 5:1336.

Secrier, M., Fitzgerald, R.C. Signatures of mutational processes and associated risk factors in esophageal squamous cell carcinoma: a geographically independent stratification strategy? *Gastroenterology* 2016; 150(5):1080-3.

De Silva, N., Schulz, L., Paterson, A., Qain, W., **Secrier, M.**, .., Fitzgerald, R.C., Ford, H. Molecular effects of Lapatinib in the treatment of HER2 overexpressing oesophago-gastric adenocarcinoma. *Br J Cancer* 2015 Nov 3;113(9):1305-12.

Ross-Innes, C.S., .., Fitzgerald, R.C., **OCCAMS Consortium***. Whole-genome sequencing provides new insights into the clonal architecture of Barrett's esophagus and esophageal adenocarcinoma. *Nat Genetics* 2015 Sep;47(9):1038-46. (* includes **Secrier M**)

Secrier, M., Schneider, R. Visualizing time-related data in biology, a review. *Brief Bioinform* 2014 Sep;15(5):771-82. *corresponding author*

Weaver, J.M., .., Fitzgerald, R.C., **OCCAMS Consortium***. Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. *Nat Genetics* 2014 Aug;46(8):837-43. (* includes **Secrier M**)

Secrier, M., Schneider, R. PhenoTimer: Software for mapping time-resolved phenotypic landscapes. *PLOS ONE* 2013 Aug 12;8(8):e72361. *corresponding author*

Secrier, M., Pavlopoulos, G.A., Aerts, J., Schneider, R. Arena3D: visualizing time-driven phenotypic differences in biological systems. *BMC Bioinform* 2012 Mar 22;13:45. *highly accessed, corresponding author*

Setty, Y., Chen, C.C., **Secrier, M.**, .., Kalamatianos, D., Emmott, S. How neurons migrate: a dynamic in-silico model of neuronal migration in the developing cortex. *BMC Syst Biol* 2011 Sep 30;5:154.

Pavlopoulos, G.A., **Secrier, M.**, .., Schneider, R., Bagos, P.G. Using graph theory to analyze biological networks. *BioData Min* 2011 Apr 28;4:10. *highly accessed*

Secrier, M.†, Toni, T.†, Stumpf, M.P. The ABC of reverse engineering biological signalling systems. *Mol Biosyst* 2009 Dec;5(12):1925-35.