Dear reader,

I was fortunate to be funded by the NENS during my training stay at the Social, Genetic and Developmental Psychiatry Centre (SGDP), Institute of Psychiatry, King’s College in London, from June 2008 till September 2008.

During my stay I had the privilege to work with Dr. Cathy Fernandes and Dr. Jonathan Mill on the project with the title: Using mouse models to identify the molecular mechanisms mediating gene by environment interactions in depressive illness.

After I had finished my behavioural experiment with mice in Utrecht, the Netherlands, I collected the brain tissue and took it with me to London. At the SGDP I analysed the tissue of different brain regions for methylation patterns in the DNA.

In the beginning of my stay I was shown around in the lab by the deputy of the lab manager to get acquainted to the safety instructions and all other basic rules in the lab. Cathy introduced me to many people at the Institute, which made it easy for me to integrate in this new environment. Jon, Cathy and I sat together to discuss my project and they gave me lots of reading material to be prepared for the upcoming work in the lab.

I started off extracting DNA, RNA and microRNA using the Qiagen Kit from the mice brain tissue which I had collected in Utrecht. I determined the amount of DNA and RNA using a NanoDrop spectrophotometer. The next step was to exchange all the unmethylated cytosines to uracils and all the methylated cytosines stayed cytosines using the Bisulphite treatment. In this way I was able to map the methylation pattern of the Bisulphite treated DNA using the Sequenom (www.sequenom.com). The Sequenom sequences the Bisulphite treated DNA, so methylation patterns can be visualised. We chose to focus on the Bdnf gene, as this gene is a candidate gene for depressive illness and is located on chromosome 2. Jon had designed 8 primers to amplify the Bdnf gene using Polymerase Chain Reaction. I have managed to optimise 7 out of 8 primers, and I managed to run 4 out of 8 primers on the Sequenom in the time I was working at the SGDP. I have collected some interesting data on the methylation pattern of CpG islands in the Bdnf gene using the Sequenom.

Next to my work in the lab I have learned how to design primers using the computer program Epityper and Cathy has learned me more about bioinformatics and statistics. There were also lab meetings and interesting talks from people from the institute which have inspired me very much. The SGDP is a great department to work at, because the people are very friendly and welcoming. I had a chance to meet Professor Michael Rutter, Ian Craig, Avshalom Caspi, David Collier, and many other people from whom I had read their articles before I went to London, but never thought of getting the chance to meet them. The SGDP is quite a new building and the lab was equipped with high-tech machinery, for example pipetting robots and the Sequenom. The lab was spacious and tidy so in sum a great place to do research!

I have had a great time in London and I have learned a lot about the research field in general. For me it has also been a great experience to work at a different institute for three months. This training stay has had an enormous positive influence on my upcoming career as a researcher and on my life.

Yours sincerely,
Miss Fieke Everts