Dear Faculty Members,

My name is Brian and I am currently completing my M.S. in Bioinformatics at Johns Hopkins University. My programming studies so far have included computer algorithms and machine learning, while my biology studies have included molecular biology of the gene, epigenetics, and protein bioinformatics. While I have wet lab experience in DNA transformation and isolating genes in E. coli and cell biology wet lab I favor performing analysis in the computer lab. I have 3 years programming experience in Python, R and Java in biological and non-biological topics. My studies this fall will continue with implementing databases, Next-gen sequencing including ChIP- and RNA-seq, RNA microarray analysis and Perl programming while next spring I will finish my degree with Cancer biology, more database modelling, and advanced genomics and genetic analyses of splice variants, mutation analysis and copy number variation. Additionally, I completed and continue to use in my studies the material learned in organic chemistry and biochemistry when studying biotherapeutics and protein bioinformatics.

I am interested in the field of high-throughput computing in proteomics, signal pathways, metabolic regulation, and gene networks to define therapeutic targets in hematological cancers. Not only do I enjoy researching the pathology in these cancers but my goal during the MS in Computational and Medicinal Chemistry and my career are to use computational tools and algorithms to model small molecules, and protein drugs as therapies. I hope to narrow down a specific type of hematological cancer throughout your program. I completed a project on Leukemia stems cells in my Epigenetics course on the role of differentiation in ALL and AML which was really exciting however I am also interested in immunotherapies targeting receptors in aggressive B-cell lymphomas and B-cell acute lymphoblastic leukemia. I would like to also indicate how I got to this point of my life and interest in studying chemotherapy drugs for cancer. I graduated with a BS in Finance in 2008 and worked in insurance for a few years but I just was not excited to wake up to go to work. Luckily in 2012 I was hired at SAP to work as a CRM expert and other integrated technologies and little by little my interested grew from data analytics, to computational statistics, to bioinformatics which is where I am now and I know I will need more experience in chemical biology to pursue my career goals. I get really excited to work on computational problems. I started preparing for my fall semester before the summer semester was even over. I woke up early the morning writing this statement of purpose because I was excited to learn a new program for differential expression in RNA-seq applications. The one thing I know in cancer research is that I will never be bored. It is impossible!

During the completion of your program I wish to obtain the skills to collaborate with bench scientists and cheminformaticians to design workflows that increase efficiency of drug targeting in leukemia and lymphoma and personalized drug targeting of mutations in protein expressing genes and fusion proteins. I am fascinated when reading about topics that use the coined phase “drugging the undruggable” in proteomics and protein-protein interactions which attracts me to the lab of Dr. Windsor. I also want to collaborate with laboratories in pharmaceutical chemistry and biophysics to learn more about requirements for designing drug modelling software. I am interested in taking classes in these two disciplines to better sort through databases, implement physical chemistry algorithms and learn computational chemistry programs like Maestro and OpenEye. What attracted me to the program at Stevens Institute was the ability to complete program part time as well as the curriculum. When I was looking for career positions in “Computational Drug Discovery” the backgrounds included physical chemistry, cheminformatics, or computational chemistry and most if not all these programs did not have courses that focused on the medicinal implementation as does the curriculum at Stevens. I cannot wait for the Computational and Medicinal Chemistry courses. The final topic on my protein bioinformatics course touched on protein docking and ligand receptor binding and this was the most interesting topic to me. I always knew about computational modelling in drug design as this was the topic of my statement of purpose to the Bioinformatics program at Johns Hopkins so I would love to continue study at Stevens. I am also aware that there are many job opportunities in New York City in Bio- and Cheminformatics for which I will be applying to the summer before the start of your program.