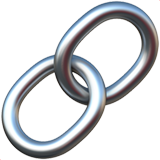
Juliana J. Lee

[juliana\_lee@hms.harvard.edu](mailto:juliana_lee@hms.harvard.edu)

# EDUCATION

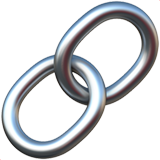
**University of Oxford**, Nuffield Department of Clinical Medicine Oxford, UK

**MSc by Research**, Clinical Medicine 2018-2021



( )

Dissertation: A CRISPR-Cas9 screen for hepatocyte receptors for malaria parasite invasion

[](https://www.ndm.ox.ac.uk/team/alexander-sandy-douglas)Advisor: Dr. Alexander (Sandy) Douglas ( )

**University of Toronto**, Faculty of Arts and Science Toronto, ON, Canada

## Honours Bachelor of Science (with high distinction) 2014-2018

Majors: Immunology and Biochemistry

Dissertation: Effect of Type I and Type II interferons (IFNs) on GITR ligand expression in inflammatory antigen presenting cells (infAPCs).

Undergraduate research advisor: Dr. Tania Watts ([](https://immunology.utoronto.ca/faculty/tania-watts))

# CERTIFICATE

**Harvard Extension School** Boston, MA, US

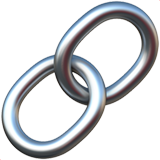
## Bioinformatics Graduate Certificate 2021-2022

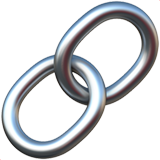
* Relevant courses: Epigenetics (BIOSE30; grade A),

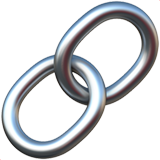
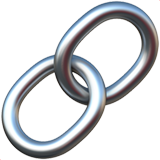
Bioinformatics (BIOTE104; grade A-), Biostatistics (STATS E-102; grade A-), Artificial Intelligence (CSCI E-80; grade B)

# RESEARCH EXPERIENCE

**Harvard Medical School – Harvard University**, Department of Immunology Boston, MA, US

***Research Assistant with Dr. Christophe Benoist ([](https://cbdm.hms.harvard.edu/))*** 2020-present

[](https://www.immgen.org/ImmGenMembers.html)Project 1: Mapping genome-wide association of histone post-translational modifications (H3K4me1, H3K4me3, H3K27me3, H3K36me3, H3K27ac and H3.3) and chromatin-associated proteins (CTCF) in immune cells by using Cleavage Under Targets & Release Using Nuclease (CUT&RUN) as an Immunological Genome (ImmGen) consortium project ( ).

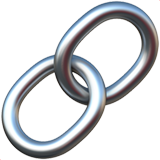
* [](https://www.epicypher.com/technologies/cutana/cut-and-run)Spearheaded a collaborative work with EpiCypher( ), an epigenetics company that launched CUT&RUN, to combat cell population heterogeneity by optimizing their standard CUT&RUN protocol. Success in CUT&RUN optimization and data analysis pipeline were demonstrated in a manuscript submitted to Nature Immunology, currently under revision stage.
  + Extensively tested various cell storage conditions, buffers with different chemical compositions, enzyme:cell ratios and salt:enzyme ratios to decrease the required number of fresh cells from 500,000 to 10,000 (method referred to as ‘low cell input CUT&RUN’). 24 antibodies targeting the six histones and CTCF from various manufacturing companies were tested to choose antibodies most compatible with low cell input CUT&RUN.
  + Developed a data analysis pipeline for processing low cell input CUT&RUN data resulting in in a communal use for other lab members.
  + [](https://www.ncbi.nlm.nih.gov/gds/?term=GSE208138%5bAccession%5d)Led the CUT&RUN project of a submitted manuscript by producing CUT&RUN data of follicular B cells from intraperitoneally injected C57BL/6 mice with IL-4 or PBS. Data can be found through GEO Series accession number [GSE208138](https://www.ncbi.nlm.nih.gov/gds/?term=GSE208138%5bAccession%5d) ( ).
* Led a group of 15 scientists (PhD students and postdoctoral researchers) from eight ImmGen labs to map chromosome structures across 120 immune cell types using the low input CUT&RUN method and the six histones and CTCF.
  + Used C57BL/6 x Cast/EiJ F1 mice to investigate relationships between genetic variants and chromosome structures by comparing allele-specific signals.
  + Performed ultra-low input RNAseq (ULI RNAseq) and ATACseq in parallel to incorporate transcriptome and chromatin accessibility data.
  + Results are soon to be made publicly available on [www.immgen.org](http://www.immgen.org/) for global users.

Project 2: Management of ULI RNAseq samples, and communal lab reagents.

* Collaborated with Broad Institute to facilitate 1) generation of ULI RNAseq data produced by SMART- Seq2 sequencing kits in batch-mode and 2) distribution of data to sample owners.
  + Worked on more than 2,500 ULI RNAseq samples from six labs from Harvard Medical School, one lab from Brigham and Women’s Hospital and one lab from University of California San Diego to help produce high quality data, which are used in two publications, six manuscripts in progress and one grant proposal.
* Carefully planned usage of easily backordered ULI RNAseq materials for 25 lab members to prevent them from being out-of-stock, resulting in expedient and efficient sample collection and data generation without any delays caused by lack of materials.
* Organized and ordered common laboratory materials, resulting in lab members being able to conduct experiments on time with all reagents.

## University of Oxford, Jenner Institute

### Graduate Researcher with Dr. Alexander (Sandy) Douglas

Project: A CRISPR-Cas9 screen for hepatocyte receptors for malaria parasite invasion ( )

Oxford, UK 2018-2020

* Studied liver stage of malaria by performing high-throughput CRISPR-Cas9 screens to uncover new hepatocyte surface receptors involved in sporozoite invasion, resulting in 1) setting a standard CRISPR-Cas9 screen protocol in studying malaria for general lab use, 2) identification of hepatocyte receptors that play a role in sporozoite invasion and 3) a manuscript in progress.
  + Knocked out 470 genes, ranked by most to least abundant human hepatocyte surface protein, in Cas9-expressing HC-04, a human hepatocyte cell line made susceptible to rodent sporozoite invasion, using CRISPR-Cas9.
  + Dissected *Anopheles* mosquitoes to harvest fresh transgenic mCherry-expressing rodent sporozoites and infected mutated HC-04 cells twice a month. Sorted invaded cells, marked by high mCherry fluorescence, 22 hours post infection for next-generation sequencing.
  + Identified *Itgav, Rpn1, Tmem30a, Atp2b1, Itgb5, Slc35a2, Mgat1, Fcgr2b, Emc1* and *Apoh* as significant genes in sporozoite invasion by using MAGeCK-VISPR, a computational tool designed for high-throughput CRISPR screens.
  + Combatted weaknesses in protocol by identifying *Itgav and Itgb5* as false positives using single gene knock-out cell lines and avidity-based extracellular interaction screens (AVEXIS).

After identifying weaker cell-surface adhesion as the source of false positives, application of collagen to cell culture was added to the protocol.

* + Newly identified *Pigs, Pvrl2, Itgb2, Slc35a2, Mgat1, Cd63, Ephb4, Itgb1, Cd163* and *Ins* as significant in sporozoite invasion in second CRISPR-Cas9 screens with the new protocol.
  + Targeted *Slc35a2* and *Mgat1* as candidates for further studies as they were identified in both first and second CRISPR-screens; however, due to laboratory shutdown during COVID-19 pandemic, no further experiments could be performed on the new results.

**University of Toronto, Department of Immunology** Toronto, ON, Canada

***Undergraduate Researcher with Dr. Tania Watts*** Summer 2017-2018

Project 1: Effect of Type I and Type II IFNs on GITR ligand expression in infAPCs.

* Investigated causal transcription factor binding sites for GITR ligand expression in response to type I and II IFNs in RAW264.7, a macrophage-like mouse cell line, using Gaussia-Cypridina dual luciferase reporter assays.
  + Deleted STAT5, IRF7, ISRE, STAT3 and STAT6 transcription factor binding sites on GITR ligand (predicted by using MatInspector) using site-directed mutagenesis on a plasmid vector expressing GITR ligand and Cypridina-luciferase.
  + Transfected RAW264.7 with the mutated GITR ligand-Cypridina expressing plasmid and Gaussia-luciferase plasmid, which was used for background bioluminescence measurement. Then, stimulated RAW264.7 cells with IFN-**α**, IFN-**β** and IFN-**γ** 24 hours post transfection.
  + Recorded GITR ligand activity 24 hours post stimulation by measuring Cypridina:Gaussia bioluminescence ratio and identified ISRE, STAT3 and STAT6 binding sites as players in GITR ligand expression in response to interferon stimulation.

Project 2: Introduction of rs4761847 SNP in Traf1 using CRISPR-Cas9 to investigate its causal relationship with rheumatoid arthritis.

* Used qPCR to confirm A:A rheumatoid arthritis-resistant homozygosity in THP-1 cells, a human monocyte-like cell line. Designed three sgRNA candidates and two repair templates to introduce rs4761847 SNP (which mutates A to G in Traf1 gene) to this THP-1 cell line. Ligated the sgRNAs to a Cas9-expressing vector and transfected THP-1 cells with this mutated vector and repair templates. A to G SNP in all four chromosomes of THP-1 cells was confirmed by qPCR.

**National Institute of Immunology** New Delhi, India

### Queen Elizabeth II Diamond Jubilee Intern with Dr. Prafullakumar Tailor Summer 2016

Project: Interaction between IRF8 and other transcription factors in CD8+ dendritic cell development.

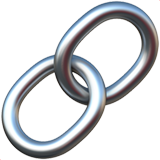
* Generated lentivirus containing plasmid expressing Irf8-targeting sgRNA and Cas9 enzyme from HEK293T. Transduced dendritic cells cultured from Balb/c mice with this lentivirus which resulted in a generation of Irf8-/- cell line for future common lab use.

# PUBLICATIONS

Baysoy A, Seddu K, Salloum T, Dawson C, **Lee J**, [11 authors], Benoist C. (2022) The interweaved signatures of common-gamma-chain cytokines across immunologic lineages. (Submitted to Nature Immunology; under revision)

* Contributed Figure 5A, 5B, 5C, and 5D

Lee, J. (2021). A CRISPR-Cas9 screen for hepatocyte receptors for malaria parasite invasion [Master's thesis]. University of Oxford.



( )

Lee J, Reddy RS, Douglas S. (2022) CRISPR-Cas9 screen for identifying essential hepatocyte receptors in sporozoite invasion [manuscript in preparation]

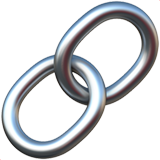
# RELEVANT TECHNICAL SKILLS

* Computational analysis using R, bash, and python
* CUT&RUN, ULI RNAseq, ATACseq, CRISPR-Cas9 screen
* Spleen, thymus, lymph node and peritoneal cavity harvest and preparation
* Intraperitoneal and retroorbital injection of mice
* FACS, flow cytometry and analysis (BD LSR, BD FACSAria, Sony SH800S Sorter)
* Molecular biology techniques such as DNA cloning, transfection, sgRNA library pool generation, PCR, gel electrophoresis, ELISA, luciferase assay, Western Blot, SDS-Page, cell culture, recombinant protein production

# AWARDS

Graduate prize; 2021 (£50)

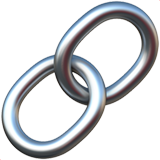
* Awarded yearly to twelve students by Governing Body at Trinity College, University of Oxford

[](https://global.utoronto.ca/u-of-t-covid-19-student-engagement-award-winners/)2020 U of T COVID-19 student engagement award ( ); 2020 ($3000)

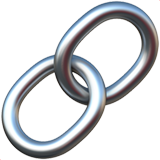
* Awarded grant for COVID19 Recovery project for the summer of 2020

The Provost W.T. Delworth Graduation Scholarship + secondary merit award; 2018 ($3,500)

* Awarded to the graduating class of Trinity College, University of Toronto based on their student debt and grade point average.

[](https://immunology.utoronto.ca/issrp)Immunology Summer Student Research Program ( ); 2017 ($4,800)

* Awarded to undergraduate summer research interns to conduct laboratory research project at a lab from the Department of Immunology, University of Toronto from May to August.
* Successful internship resulted in project continuation from September 2017 to April 2018 as a part of IMM450, a full-year research course.

[](https://www.trinity.utoronto.ca/study-arts-science/research-courses-experiential-learning/international-experience/queen-elizabeth-ii-scholarships/#%3A~%3Atext%3DQUEEN%20ELIZABETH%20II%20DIAMOND%20JUBILEE%20SCHOLARSHIP%20PROGRAM%26text%3DTrinity%20College%20submitted%20successful%20proposals%2Cmajor%20component%20of%20both%20programs)Queen Elizabeth II Diamond Jubilee Scholarship ( ); 2016 ($7,000)

* Awarded to 15 students every year to conduct a research project as an intern at a lab in a commonwealth country for three months

Dean’s List Scholar (2016 – 2018)

* + Yearly awarded for receiving cGPA of higher than 3.50 (top 20%)

Chemistry Connections Challenge, winning entry; 2017 Trinity College Admission Scholarships; 2014 ($1,000)

* Awarded to 90 incoming first-year students

University of Toronto President’s Entrance Scholarship; 2014 ($2,000)

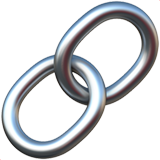
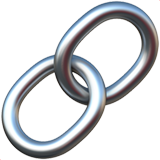
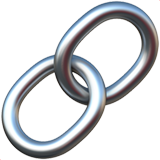
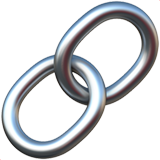
* Awarded to incoming first-year students with a final admission grade of 95% and above

# PUBLIC ENGAGEMENT

## COVID19 Recovery Project – wake up to positive news ( )

### Founder and Team Leader

2020-2021

* To bring positive, heartwarming news and lessen negative impact the COVID19 pandemic had on everyone around the world, [www.covid19recovery.net](http://www.covid19recovery.net/) website was created (total of 55,000+ visitors and 200 visits/day).
* Led a group of 15 students from five countries to update website with positive news articles, pictures, and interviews with people of various occupations from professor to social worker.
* Managed social media accounts such as Instagram and Facebook to bring news about website updates and guidelines on how to stay safe during the pandemic. Service was provided in three languages: English, French and Mandarin.
* [](https://global.utoronto.ca/u-of-t-covid-19-student-engagement-award-winners/)Received COVID-19 Student Engagement Award ($3000) from the University of Toronto ( ).
* [](https://www.11alive.com/article/news/health/coronavirus/friends-band-together-to-highlight-good-news-in-the-midst-of-coronavirus/85-9562f3ff-d758-492c-8b99-4a9810ad7563)[](https://toronto.citynews.ca/2020/03/30/silver-linings-some-good-news-in-these-trying-times/)Project success was featured on 11Alive ( ), University of Toronto News ( ), and Toronto CityNews ( ) news articles.

**KSEAUK Bio-Medical Symposium** Nov 2019

### Invited presenter

* Presented research work on how CRISPR-Cas9 helps to understand human-parasite relationship

## Jenner Institute Student Symposium Oct 2019

### Invited presenter

* Highlighted and shared research discoveries to other students, research assistants and group leaders of the Jenner Institute, University of Oxford

**Trinity College MCR Gaudy** May 2019

### Invited presenter

* Invited to showcase research to the benefactors as one of the representatives of the Trinity College Middle Common Room (MCR) community

**Trinity College MCR Committee** 2019-2020

### Secretary

* Managed more than 200 MCR and SCR members, and successfully organized college-wide events such networking with alumni and other Oxford college students.
* Organized committee meetings and produced weekly newsletters with updates on college activity.

**Toronto Life Sciences** Toronto, ON, Canada

***Staff member*** Sept 2016 – Sept 2017

* Organized seminars for 200 undergraduate students in preparation for their course examinations

**Mount Sinai Hospital** Toronto, ON, Canada

***Volunteer***

* Unit 1) Ben and Hilda Katz Acute Care for Elders (ACE) unit Sept 2015 – Nov 2016
  + Prepared meals, helped mobility and provided entertainment to elderly patients for 100+ hours
  + Occasionally contributed as a Korean interpreter for Korean patients
* Unit 2) Pathology and Laboratory Medicine May 2015 – Aug 2015
  + Organized patients’ blood, stool, and urine samples to different testing stations for 40+ hours

**Smart Abacus Academy** Markham, ON, Canada

***Class instructor*** June – July 2015

* Organized course curriculum and taught French, Math, Science, Korean and English to 30 grade 4, 5 and 6 students