Institutional Biosafety Committee Meeting Minutes

La Jolla Institute FOR IMMUNOLOGY | Life Without Disease.

August 13th, 2025 meeting

A regular meeting of the Institutional Biosafety Committee of the La Jolla Institute for Immunology was held in person on Wednesday, August 13, 2025, at 9:30 AM, with the option to join via Zoom teleconference.

The meeting started at 9:33 AM.

IBC ATTENDANCE: 11 MEMBERS AND 2 ALTERNATES (11 VOTING MEMBERS, 7 MEMBERS REQUIRED FOR QUORUM)

Regular Members	Present
Miguel Reina-Campos, Ph.D. (Chair)	☑
Mike Barajas (Alternate) CMAR, RLATG	☐
Sylvie Blondelle, Ph.D.	☑
Laurence Cagnon, Ph.D.	☑
Beth Ford, D.V.M.	☑
David Hall, CSP	☑
Peter Jones, BS, LATG	☐
Alessandro Sette, Ph.D.	☑
Stephen Schoenberger, Ph.D.	☑
Kristine Suchey, BS, RVT	☑
Renna Wolfe, Ph.D.	☑
Jeremy Young, BS, MBA	☑
Marianne Zupanc, Ph.D.	☑
Others Present: Jason Vo, Hayley Simon	

Note: Stephen Schoenberger joined via zoom.

Miguel Reina-Campos is the new vice-chair, and 2 members resigned from the IBC

REVIEW AND APPROVAL OF THE MINUTES

The June meeting minutes were approved unanimously with the reviewed modifications. They will be the first minutes to be posted on LJI web site.
The new format was reviewed and explained.

PROTOCOL REVIEW

The risk assessment evaluation matrix was discussed by the IBC and the following terms and percentages were proposed for the likelihood of an exposure:

- Very significant (>10% risk)
- Significant (1-10% risk)
- Unlikely (0.1-0.99% risk)
- Very unlikely (<0.01% risk)

NEW PROTOCOLS

PI	**Grifoni**
Protocol #	**BHR01-AG**
Title	Next Generation Immunogen Platform
Experimental Procedures	
Agent	mRNA-LNP saline solution
Project summary (from form)	Lipid Nanoparticles (LNPs) with mRNAs coding for antigens of interest will be injected into rodents as tests for immunogenicity.
Additional details from the protocol	The encapsulated mRNAs will be composed of a string of partial structural or non-structural viral genes sequences.
Manipulations planned	In vivo injection, pipetting, dissection, Flow cytometry and cell sorting
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	Lassa and Junin viruses
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	Partial structural and non-structural viral genes. No expected functionality to remain as only immunogenic sequences are retained.
NA Host(s) and Vector(s)	N/A
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Proposed Biosafety Level	BSL-1 and ABSL-1
CA ATP-L	No
NIH Guidelines	III-D-4-a
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Reina-Campos**
Protocol #	**BHR05-MRC**
Title	Reina-Uropathogenic E. coli strain (UPEC)
Experimental Procedures	
Agent	Uropathogenic Escherichia coli (UPEC) UTI89
Project summary (from form)	There is a gap in the literature regarding tissue-resident memory CD8+ T cells (TRM) in the prostate, despite its widespread research in various non-lymphoid tissues. We will be utilizing uropathogenic E. coli. UTI89 to thoroughly assess prostate TRM immunity in the context of a localized bacterial infection.
Additional details from the protocol	N/A
Manipulations planned	Bacteria culture, pipetting, centrifugation, in vivo infection (via catheter), urine collection, dissection, homogenate preparation, colony-forming unit assay, flow cytometry and histology.
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	N/A
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	N/A
NA Host(s) and Vector(s)	N/A
Risk Assessment/Training	
Proposed Risk Assessment	Low

Training	Verified and on record
IBC Assessment	
Proposed Biosafety Level	BSL-2 and ABSL-2
CA ATP-L	No
NIH Guidelines	N/A
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Shresta**
Protocol #	**BHR24-SS**
Title	Pseudotyped recombinant West Nile Viruses expressing GFP
Experimental Procedures	
Agent	**Pseudotyped replication deficient recombinant WNV**
Project summary (from form)	Neutralization assay developed at Washington University against Flaviviruses will be transferred to LJI to test the capacity of monoclonal antibodies and/or serum samples from vaccinated or infected **subjects** to neutralize recombinant flaviviruses. Recombinant, single-round infectious delta GP West Nile Viruses expressing GFP and structural proteins of other flaviviruses (preMembrane and E of Dengue, Zika, Japanese Encephalitis and WN viruses will be used in the neutralization assays.
Additional details from the protocol	Chimeric and attenuated WNV reporter viruses expressing GFP and structural proteins from various Flaviviruses (DENV, ZIKV, JEV, WNV)
Manipulations planned	Tissue culture, virus production, centrifugation, pipetting
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	West Nile Virus, Zika Virus, Dengue virus, Japanese Encephalitis Virus, Jelly fish
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	Delta env genome, envelope, marker
NA Host(s) and Vector(s)	Mammalian cell lines
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Proposed Biosafety Level	BSL-2
CA ATP-L	No
NIH Guidelines	III-D-1-a and III-D-3-a
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Weiskopf**
Protocol #	**BHR03-DW**
Title	PBMC derived from long term recovered Chikungunya infected subjects
Experimental Procedures	
Agent	PBMCs, plasma and all blood products derived from people previously infected with Chikungunya and obtained seven to ten years post-infection. Samples are expected to be free of virus.

Project summary (from form)	Human PBMC from donors will be examined for the presence of T cell responses specific for Chikungunya Virus. Our goal is to understand the nature of the human immune response to Chikungunya virus as well as detail its mechanisms.
Additional details from the protocol	Samples are not expected to be infectious as they were collected seven to ten years post Chikungunya infection.
Manipulations planned	PBMC purification (ficoll separation), cell culture, fluorospots, ELISA, flow cytometry staining, cell sorting, centrifugation, pipetting
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	N/A
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	N/A
NA Host(s) and Vector(s)	N/A
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Proposed Biosafety Level	BSL-2
CA ATP-L	No. CA ATP-L covers potentially infectious clinical materials. “Samples are expected to be free of virus.”
NIH Guidelines	N/A
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

RENEWALS

PI	**Ay**
Protocol #	**BHR01-FA**
Title	Normal human blood samples
Experimental Procedures	
Agent	Human blood
Project summary (from form)	The search for causal genetic variants associated with specific diseases among many variants identified by genome-wide association studies (GWAS) has been rejuvenated several times by the increase in throughput, resolution and the number/modality of experimental techniques that are broadly available. Advances in capturing cell-type-specific physical proximity among genomic regions also added a new dimension for this search by revealing the importance of 3D genome organization in interpreting the role of genetic variants in gene regulation. A number of combinations of these different techniques have proven useful in identifying a number of causal variants but many major challenges remain in our goal towards creating complete maps of genotype-phenotype associations for complex diseases. Our recent focus has been to address an important gap in the current knowledge of how genetic variants may impact 3D genome organization with or without a measurable impact on gene expression of the cell state/type that is available for molecular characterization. We have identified a number of genetic variants that associate with read coverage, strengths of specific loops and/or overall connectivity of large genomic regions. Leveraging our expertise in computational analysis and the newly established experimental component of our lab, we will address a number of questions emerging from our recent findings within the next five years. We will first define and characterize the role of genetic variants, which we found to be associated with specific chromatin loops and/or overall connectivity of regions harboring regulatory elements in specific human

	immune cell types. Next, we will perform long read-based assays and develop accompanying analysis methods to resolve allele-specificity and connection modality of multi-way interactions involving regulatory elements. Throughout the project period, we will continue developing computational methods for integrative, comparative and high-resolution analysis of conformation capture data. As we have done before, our methods development will be in alignment with biological questions we are trying to answer but with flexibility and generalizability in mind for their broad utility by other researchers.
Additional details from the protocol	N/A
Manipulations planned	PBMC purification, magnetic cell separation, tissue culture, pipetting, centrifugation, high-throughput chromatin conformation capture assay (HiCuT)
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	N/A
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	N/A
NA Host(s) and Vector(s)	N/A
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Assigned Biosafety Level	BSL-2
CA ATP-L	No
NIH Guidelines	N/A
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Benedict**
Protocol #	**BHR01-CB**
Title	MCMV & RCMV
Experimental Procedures	
Agent	WT and recombinant MCMV & RCMV
Project summary (from form)	The overall goals of this project are to use M and R Cytomegalovirus (CMV), in both in vitro and in vivo studies, to further understand the innate and adaptive immune response to infection, elucidating the mechanisms and strategies of infection and immune evasion of the virus. By understanding the latter, a potential more effective and specific CMV treatment or vaccine may be possible to develop.
Additional details from the protocol	Recombinant viruses express reporter genes, nothing hazardous.
Manipulations planned	In vitro and in vivo infection, tissue culture with infected cells, injections, transfection
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	Jellyfish, sea anemones, firefly, mCMV, rCMV
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	reporter genes, genome
NA Host(s) and Vector(s)	Fibroblasts, E. Coli
Risk Assessment/Training	
Proposed Risk Assessment	Low

Training	Verified and on record
IBC Assessment	
Assigned Biosafety Level	BSL-1 and ABSL-2
CA ATP-L	No
NIH Guidelines	III-D-3-e and III-D-4-b
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Benedict**
Protocol #	**BHR03-CB**
Title	Herpes and Anti-Immune Defenses – HCMV & RhCMV
Experimental Procedures	
Agent	HCMV and RhCMV
Project summary (from form)	Cytomegalovirus (CMV, a beta-herpesvirus) infects the majority of the world's population. Even though CMV infection is strictly species specific, RhCMV shows a high amount of genetic similarities to human CMV, which can help us understand this virus behavior in humans as well. CMV successfully establishes a lifelong infection through specific immune evasion strategies and studying the specific viral genes that accomplish this leads to the development of better antiviral therapies. As CMV is also a virus capable of 'remodeling' the human immune system, it could also be possible to elucidate new aspects of our own immune responses. That is why we study both human and rhCMV in cultured cells, and test how specific gene products from these viruses function to dampen immunity.
Additional details from the protocol	N/A
Manipulations planned	Production of virus by infection or transfection, cell culture, pipetting, centrifugation
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	HCMV, RhCMV, jellyfish
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	Genome, modulator of immune response, marker
NA Host(s) and Vector(s)	E. Coli, human cells (primarily fibroblasts), Rh fibroblast cell line culture (negative for Herpes B)
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Assigned Biosafety Level	BSL-2 and BSL-2 with BSL-3 practices aimed at containing the aerosols
CA ATP-L	Yes
NIH Guidelines	III-D-1-a, III-D-2-a, and III-D-3-a
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Kronenberg**
Protocol #	**BHR29-MK**
Title	Francisella tularensis live vaccine strain

Experimental Procedures	
Agent	Francisella tularensis live vaccine strain, subspecies holarctica.
Project summary (from form)	Francisella tularensis is capable of activating a special type of immune cell that is known only to respond against bacteria with a specific metabolism. For this particular infection, this cell type is required to eliminate the bacteria and protect against it. We will use these bacteria to study long term responses of the immune cell to try to understand how it develops immunological memory.
Additional details from the protocol	This strain is excluded from the Select Agent Program. After infection, this agent clears in 10 days.
Manipulations planned	Bacteria culture, in vivo infection (intranasal, intratracheal or IP), organs collection (14 days to 1-year post-infection), sample processing, fixation, flow cytometry and imaging (fixed and unfixed).
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	N/A
Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	N/A
NA Host(s) and Vector(s)	N/A
Risk Assessment/Training	
Proposed Risk Assessment	Low (Medium?)
Training	Verified and on record
IBC Assessment	
Assigned Biosafety Level	BSL-2 with BSL-3 practices aimed at containing the aerosols and ABSL-2
CA ATP-L	Yes – (voluntary use of N95)
NIH Guidelines	N/A
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels with the discussed modifications	

PI	**Shresta**
Protocol #	**RDR07-SS**
Title	RNA silencing in infected or non-infected cells
Experimental Procedures	
Agent	siRNAs
Project summary (from form)	Our goal is to define the host cell factors that regulate arbovirus infection (Dengue virus, Zika virus, Japanese Encephalitis virus, Yellow Fever virus and Chikungunya virus). We will use siRNA technology to downregulate genes or long-non coding RNA of interest in macrophages and dendritic cells (DCs), major cellular hosts of arboviruses. These cells will include both transformed human lines (such as U937, THP-1, U937-DCSIGN and Mutz-3) and primary human macrophages and DCs derived from peripheral blood mononuclear cells (PBMCs). Identification of host cell molecules that regulate arbovirus infection in macrophages and DCs will lead to greater understanding of arbovirus disease pathogenesis and may help develop novel therapeutics against these arboviruses.
Additional details from the protocol	
Manipulations planned	Transfections of mammalian cells
Recombinant or Synthetic Nucleic Acids	
Source of nucleic sequences (e.g., species)	synthetic

Nature of nucleic acid (NA) sequences (e.g., enzyme, oncogene)	Gene silencers
NA Host(s) and Vector(s)	Mammalian cells
Risk Assessment/Training	
Proposed Risk Assessment	Low
Training	Verified and on record
IBC Assessment	
Assigned Biosafety Level	BSL-1 (siRNA) and BSL-2 (mammalian cells)
CA ATP-L	No
NIH Guidelines	III-F (exempt)
Category 1 Research	No
Category 2 Research	No
IBC Approval	
Unanimously approved at the proposed biosafety levels	

AMENDMENTS FOR IBC REVIEW

None

AMENDMENTS APPROVED BY BIOSAFETY

BHR03-ADS

ANNUAL MONITORING

16 protocols due for annual monitoring

These protocols were due for annual monitoring between May 1, 2025, and June 30, 2025. No significant changes were made to the protocols, except for changes related to personnel, funding source, IRB number, IACUC protocol number, or addition of genes, strains or experimental procedures not affecting the approved biosafety levels. These minor changes will be approved administratively by the EH&S office.

CLOSED PROTOCOLS

6 protocols were closed:

- 3 protocol due for annual monitoring were closed (1 from Saphire, 2 from Schmiedel)
- 3 protocol due for renewal were closed (1 from Sette, 2 from Vijayanad)

STORAGE MEMO

None

GENERAL BUSINESS

TPS UPDATES

A new RDR tab was presented.
The questions were updated to reflect the most current updates to the NIH guidelines. The new RDR tab will be inserted into the BHR to merge the existing BHR and RDR protocols. EH&S will send the new RDR tab to the IBC as a PDF for review and approval before the October IBC meeting.

RDR tabs available to review and added to the BHRs

1. BHR01-AG
2. BHR01-CB

3. BHR03-CB
4. BHR24-SS
5. RDR07-SS

BSL-3 INCIDENTS
None

NIH REPORTABLE INCIDENTS
None

DURC
None

Meeting adjourned at 10:44 am