**CAMPUS-WIDE RESOURCES**

School of Medicine BSL-3 Facility

The BSL-3 suite is located on the third floor of the school of medicine research building. The suite consists of four BSL-3 tissue culture laboratories of ~400ft2 each, an ante­room with adjacent shower room, a containment corridor, and access to an autoclave and maintenance closet. Two of the four laboratories have provisions for ducted biosafety cabinets that exhaust to a HEPA bag-in bag-out filtration system and the other two laboratories will be provided with self-contained bio-safety cabinets with integral HEPA filtration. Each laboratory has independent HVAC supply and exhaust ducts connected to the system via a system of automatic and manual bubble dampers. Each laboratory is equipped with a stainless steel wash sink with drain boards; effluent from the sinks will be transported via double wall piping and decontaminated by a two-tank heat treatment system. Entrance to these BSL-3 laboratories is contingent upon successful training and approval by the environmental health and safety department. The suite is in the process of securing certification. These laboratories will contain Class II Type A2 biological biosafety cabinets, CO2 incubators, centrifuges, ultralow freezers and microscopes and a pass-through autoclave is already in place. Security will be provided via access controls (i.e., proximity readers) at the entry to the anteroom and at each laboratory as required. Security cameras will monitor the entry to the ante­room, corridor, and individual laboratories.

Orbach Science Library (UCR Campus)

The School of Medicine Education Building is adjacent to the Raymond L. Orbach Science library, which houses physical resources (e.g., books, maps, journal volumes, etc.) in the physical, natural, biomedical, and engineering/computer sciences. The library also has available 25 group study rooms, 8 of which can be reserved for a period of time, several hundred individual study carrels, as well as tables available. Either the library’s individual computers or student personal computers can be used to access the library catalog, the California Digital Library, many licensed online resources, as well as the Internet. Scanners and Printers are available, and the library also hosts a United States Patent and Trademark Resource Center.

UCR Palm Desert Center.

The UCR Palm Desert Center is a teaching and research center that extends the reach of the campus and offers an extensive array of educational and cultural programming to this region of 450,000 people. The School of Medicine has dedicated space within one of the center’s two buildings, which can be used for small group meetings. A variety of meeting spaces (auditorium seating nearly 300, lecture hall and classrooms) can also be reserved by the CHC as needed.

Central Facility for Advanced Microscopy and Microanalysis (CFAMM)

The Central Facility for Advanced Microscopy and Microanalysis (CFAMM) is a research, service, and consulting laboratory for microscopic characterization of organic and inorganic materials, biological tissue and minerals applying electron beam techniques. The facility utilizes state-of-the-art equipment and its personnel conducts research and provides collaborative assistance, training and service to faculty, staff, and students at UC Riverside as well as to clients in industry, government, and academia. Several electron microscopes are available in the Center: The FEI CM300 TEM features a high, 300 kV accelerating voltage, with a Gatan MSC794 digital camera and EDAX® Genesis Energy Dispersive Spectroscopy system with a liquid N2 cooled 30 mm2 Si(Li) detector with energy resolution of 129 eV for Mn Kα. Detection and analysis of all elements with atomic number 5 (Boron) or higher. The FEI Tecnai12 is a versatile, user-friendly, computer-controlled, conventional TEM. The FEI NNS450 combines high- and low-voltage ultra-high resolution capabilities with variable pressure specimen chamber vacuum. The analytical system allows to perform qualitative and quantitative chemical analysis, image capture, X-ray spectral mapping and line scanning by Energy Dispersive X-ray Spectroscopy (EDX) complemented by structural and crystallographic information including crystal orientation and mis-orientation, accurate phase identification, and phase mapping by Electron Backscattered Diffraction (EBSD). The FEI XL30-FEG is a user-friendly, versatile, high performance SEM. It employs Schotiky-based electron source optimized for brightness/ high beam current operation that significantly extends the use of high spatial resolution combined with quality elemental analysis.

Analytical Chemistry Instrumentation Facility

The ACIF is a campus wide facility housed in the Department of Chemistry and consists of four components, Mass Spectrometry, Nuclear Magnetic Resonance (NMR) Spectroscopy, Optical Spectroscopy and X-ray Crystallography. A faculty director oversees the ACIF as a whole and a support staff of four spectroscopists manage and maintain the various facilities. The ACIF includes the following resources:

* The Regional Mass Spectrometry Facility (RMSF), established in late 1983, is available to any researcher with the need for mass spectrometry analyses. The RMSF analyzes a wide variety of chemical species, including up to 49 elements from the periodic table (i.e., Na-U). Combined, RMSF staff has nearly 60 years experience analyzing samples from a variety of sources. The facility’s philosophy is to work closely with users in determining the best approach to efficiently perform the analyses. Three of the four RMSF instruments have the ability to obtain accurate mass data to provide molecular formula information. The remaining instrument provides MS/MS data in lieu of exact mass measurements.
* The Nuclear Magnetic Resonance (NMR) facility houses seven NMR spectroscopy devices to determine the physical or chemical properties of atoms or the molecules in which they are contained. One such device, the 700 MHz Nuclear Magnetic Resonance (NMR) spectrometer, has been used in structure-based drug design.
* The Optical Facility
* The X-ray Facility, equipped with two Bruker single crystal X-ray diffraction systems, has low temperature capability and a vacuum atmospheres glove box with video microscope for handling air/moisture/oxygen-sensitive samples. Structures can be determined within 2-3 hours, though publication-quality structures take longer. Thin plate crystals (>10µm) can be handled and their structure determined. Crystal face indexing is possible if the sample has well defined faces.

Nanofabrication Cleanroom Facility

The Bourns College of Engineering also houses a Nanofabrication Cleanroom Facility, which features an air filtration and delivery system, along with temperature and humidity control systems, and it houses $7M of equipment for building small-scale circuits and machines, as well as Atomic Force Microscopes used in the present proposal.

Genomics Core Facility

In close proximity to the SOM Research Building is a 10,000ft2 instrumentation facility (Keen Hall) offering advanced tools in bioinformatics, microscopy/imaging, proteomics and genomics. The Genomics Core Facility at the IIGB provides technical, instrument, and professional development. The Core has two suites of instrumentation. In the Genomics Suite, capabilities include automated extraction and purification of plasmids from bacterial cultures in deep-well plates (Beckman Multimek robot), automated handling of liquids for DNA sequencing reactions and PCR. For routine sequencing, the facility utilizes a 96-capillary sequencer (ABI 3730xl), whereas for genotyping, amplified microsatellites can be detected using a 16-capillary instrument (ABI 3100) and appropriate computer software (ABI GeneMapper). In the Gene Expression Suite, commercial microarray services are available. For custom arrays, the core offer two arrayers, a macroarrayer with 96 pins (Genetix Qpix) and a microarrayer with 1~48 pins (BioRad VersArray ChipWrite Pro spot arrayer). Three scanners are available. For microarrays and nucleic acid and protein blots, a Typhoon scanner (GE) with a resolution of 10~500uM can generate and quantify images from a variety of fluorophores and phosphoimage screens. For microarrays, the core offers two different scanners, the GenePix 4000B (Molecular Devices) and the ScannArray Express (Perkin Elmer) along with appropriate software for analysis. For commercial Affymetrix arrays, hybridization (Hybridization Oven 640), staining and washing (Fluidics Station 450), and quality control of RNAs (Bioanalyzer, Agilent) are offered. For array data analysis, two software packages (Molecular Devices Acuity and Stratagene ArrayAssist) are available.

The Genomics Core houses a state-of-the-art Illumina HiSeq 2500HT, MiSeq and Genome Analyzer (GA) IIx. The facility can routinely run 76 or 100 cycle paired-end reads as well as shorter single reads. The Genomics Core employs a full-time Specialist with in-depth knowledge to operate these instruments, as well as additional personnel, including the Administrator of the Cores, who have in-depth knowledge of next generation sequencing to ensure the highest quality services. Full bioinformatics support of instrument system operations is crucial and is provided by a full-time administrator/programmer. For custom data analysis services, programming resources are available within the IIGB Bioinformatics Core. To assist in library preparation, the Genomics Core houses instrumentation for DNA fragmentation (Biodisruptor, Hydroshear), size selection (eGel system), and quality control libraries (Bioanalyzer). The Core provides guidance to customers, workshops and campus-wide seminars in next generation sequencing to promote methods sharing and broader campus-wide research. The Core has broad experience with small RNA, genomic, ChIPseq, RNAseq, bisulfite sequencing, and custom library applications.

UCR Institute for Integrative Genome Biology (IIGB)

The dedicated interdisciplinary Genomics Building ($53.8 million, 64,000ft2, four-story) accommodates over 200 faculty members, graduate students, and postdoctoral and staff researchers. The building brings bioinformaticians and life scientists together under one roof to utilize modern genetic tools, genomics and bioinformatics in addressing basic and applied questions in biology and human health. The laboratories and student/researcher office spaces are an open plan design to stimulate interactivity between members of different research groups, and the 100-seat auditorium regularly hosts symposiums and training sessions dedicated to chemical genomics research.

IIGB's Bioinformatics Facility is located in 1207/1208 Genomics Building. The facility consists of a dedicated office for two systems administrators, one office for up to seven programmers and one for the director of the facility. A multifunctional bioinformatics laboratory that can accommodate twelve programmers and students is part of this infrastructure. In addition, the facility has a dedicated 600ft2 server room with a state-of-the-art raised floor AC system and uninterrupted power supplied by a large UPS and a backup power generator. A bioinformatics laboratory is available for workshops with 10 triple-bootable Windows/OSX/Linux workstations and one molecular modeling workstation from Silicon Graphics. The most relevant HPC resources include the following components: 1) twelve 16-48 CPU core production server systems with 200TB storage space which manages large databases, data storage and multi-user activities; 2) four 8-48 CPU web/database servers with an attached 48TB storage area network (SAN) to manage network intensive web services, such as public databases (all hardware components of this high-availability SAN system are redundant in order to avoid downtime during hardware failures); 3) three super-computing Linux clusters that are fully integrated into this hardware infrastructure; 4) an older 64-CPU Linux cluster and a new one with 348 CPU cores, 3TB of total RAM and the latest Infiniband interconnect; and 5) a dedicated cluster for memory intensive tasks consisting of nodes with a total of 160 CPU cores and 256-512GB of RAM per node. The data from all workstations and servers are automatically replicated every night onto a 250TB backup server system that is located in a geographically separated server room. A strong focus on remote access systems maximizes the availability of all hardware and software resources for many simultaneous users. Online information on this hardware infrastructure, including its usage, is available here: http://manuals.bioinformatics.ucr.edu/home/hpc. The facility is strongly committed to maintaining a comprehensive open-source and open-access software infrastructure for Linux- and Unix-based operating systems. This approach supports access to the widest spectrum of software tools with the most advanced algorithms, and it maximizes the freedom to operate in a highly diverse and multidisciplinary academic research environment. The Debian Linux distribution is used on all workstations and servers to synchronize and automate software and OS updates on all machines of the facility. In addition, a centralized le system maximizes the efficiency and security of data management tasks. Currently, the facility maintains over 300 open-source bioinformatics/cheminformatics software packages for high-throughput data analysis, data mining, molecular modeling, cheminformatics, evolutionary biology, ecology, statistical analysis, etc. In areas that depend on industrial software applications, the facility also owns various commercial software tools. The most important commercial tools are the Insight II environment for protein modeling and ligand docking; the Catalyst software for pharmacophore modeling and pharmacophore-based database searching; and the Cerius2 package for large-scale small molecule mining and QSAR analyses. As much as possible, the facility provides access to various web-based data analysis tools. Many of these tools were developed by the IIGB's Bioinformatics Facility.

Bioinformatics Facility and Equipment Description

IIGB's Bioinformatics Facility is located in 1207/1208 Genomics Building. The facility consists of a dedicated office for two systems administrators, one office for up to seven programmers and one for the director of the facility. A multifunctional bioinformatics lab that can accommodate twelve programmers and students is part of this infrastructure. In addition, the facility has a dedicated 600 ft2 server room with a state-of-the-art raised floor AC system and uninterrupted power supplied by a large UPS and a backup power generator. A bioinfor­matics laboratory is available for workshops with 10 triple-bootable Windows/OSX/Linux workstations and one molecular modeling workstation from Silicon Graphics. The most relevant HPC resources include the following components: 1) twelve 16-48 CPU core production server systems with 200TB storage space which manages large databases, data storage and multi-user activities; 2) four 8-48 CPU web/database servers with an attached 48TB storage area network (SAN) to manage network intensive web services, such as public data­bases (all hardware components of this high-availability SAN system are redundant in order to avoid downtime during hardware failures); 3) three super-computing Linux clusters that are fully integrated into this hardware infrastructure; 4) an older 64-CPU Linux cluster and a new one with 348 CPU cores, 3TB of total RAM and the latest Infiniband interconnect; and 5) a dedicated cluster for memory intensive tasks consisting of nodes with a total of 160 CPU cores and 256-512GB of RAM per node. The data from all workstations and servers are automatically replicated every night onto a 250TB backup server system that is located in a geographically separated server room. A strong focus on remote access systems maximizes the availability of all hardware and software resources for many simultaneous users. Online information on this hardware infrastructure, including its usage, is available here: http://manuals.bioinformatics.ucr.edu/home/hpc. The facility is strongly committed to maintaining a comprehensive open-source and open-access software infrastructure for Linux- and Unix-based operating systems. This approach supports access to the widest spectrum of software tools with the most advanced algorithms, and it maximizes the freedom to operate in a highly diverse and multidisci­plinary academic research environment. The Debian Linux distribution is used on all workstations and servers to synchronize and automate software and OS updates on all machines of the facility. In addition, a centralized le system maximizes the efficiency and security of data management tasks. Currently, the facility maintains over 300 open-source bioinformatics/cheminformatics software packages for high-throughput data analysis, data mining, molecular modeling, cheminformatics, evolutionary biology, ecology, statistical analysis, etc. In areas that depend on industrial software applications, the facility also owns various commercial software tools. The most important commercial tools are the Insight II environment for protein modeling and ligand docking; the Catalyst software for pharmacophore modeling and pharmacophore-based database searching; and the Cerius2 package for large-scale small molecule mining and QSAR analyses. As much as possible, the facility provides access to various web-based data analysis tools. Many of these tools were developed by the IIGB's Bioinformatics Facility.

Next Generation Sequencing

The Genomics Core houses a state-of-the-art Illumina HiSeq 2500HT, MiSeq and Genome Analyzer (GA) IIx. The facility can routinely run 76 or 100 cycle paired-end reads as well as shorter single reads. The Genomics Core employs a full-time Specialist with in-depth knowledge to operate these instruments, as well as additional personnel, includ­ing the Administrator of the Cores, who have in-depth knowledge of next generation sequencing to ensure the highest quality services. Full bioinformatics support of instrument system operations is crucial and is provided by a full-time administrator/programmer. For custom data analysis services, programming resources are available within the IIGB Bioinformatics Core. To assist in library preparation, the Genomics Core houses instrumentation for DNA fragmentation (Biodisruptor, Hydroshear), size selection (eGel system), and quality control libraries (Bioanalyzer). The Core provides guidance to customers, workshops and campus-wide semi­nars in next generation sequencing to promote methods sharing and broader campus-wide research. The Core has broad experience with small RNA, genomic, ChIPseq, RNAseq, bisulfite sequencing, and custom library applications.

Libraries

The University of California, Riverside Library system contains more than 3.7 million volumes, which include more than 400,000 e-books; 87,000 print and electronic serial subscriptions; 2.3 million microforms; and 281,000 government information sources. The UCR Library has access through the California Digital Library to all 10 UC libraries, together constituting one of the largest academic research libraries in the United States.

Reference librarians are available in-person, online, and by telephone to provide general information to in-depth research assistance, including help with database searches, interlibrary loan, document delivery, understanding the research process, and course-specific library instruction.

The Library’s hundreds of workstations allow access to internal, UC-wide, and licensed resources including the Library Catalog, SCOTTY, the UC-wide California Digital Library featuring the Melvyl® Catalog, and hundreds of licensed online resources. The UCR Library system consists of the following:

*Tomás Rivera Library*, which supports Business, Education, Humanities, Fine Arts, and Social Sciences. Rivera Library houses collections that include Government Publications, the Tuskegee Airmen Archive, Education Services, and the famed Eaton Collection, the world's largest publicly-accessible collection of science fiction and fantasy.

*Raymond L. Orbach Science Library* holds more than 533,000 cataloged books, maps, journal volumes, and media supporting Physical Sciences, Natural and Agricultural Sciences, Biomedical Sciences, Engineering and Computer Science. The collection is especially rich in citrus and sub-tropical horticulture, entomology, arid lands agriculture, and soil sciences. Orbach Science Library houses the Map Collection, GIS electronic cartographic resources, and the Patent and Trademark Depository, part of the U.S. Patent and Trademark Office.

*UCR Multimedia Library* contains entertainment and educational materials on video tapes (VHS), DVDs, Blu-Ray, laserdiscs, CD-ROMs, CDs, audio cassettes, and 16mm film.

*UCR Music Library*, encompassing a range of music genres and styles, includes an authoritative collection of music reference books and scores, along with CDs, LPs, DVDs and VHS tapes of performances and equipment to play items in the collection.