CDU Exosome Core

The Exosome Core at Charles R. Drew University's Institute for Advanced Biomedical Research (IABR) can help investigators to elucidate the role of exosomes in biological and disease processes. The Exosome Core provides a range of comprehensive end-to-end services for exosome research, including exosome purification, characterization, and engineering.

The Exosome Core provides high-quality exosome purification services by using ultracentrifugation from various types of biological material. High-purity and intact exosomes

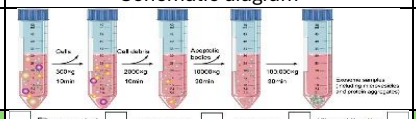
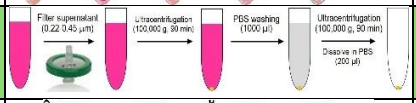
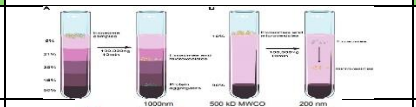
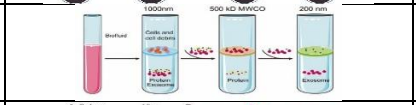
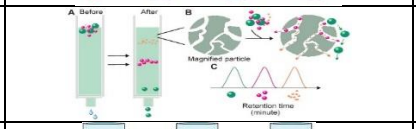
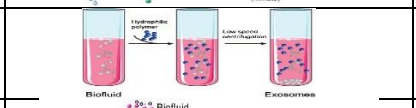
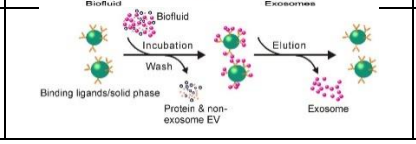
For information regarding experiments, or questions about the services, please contact Dr. Qiongyu Hao (QiongyuHao@cdrewu.edu). There is no charge for consultation and assistance with experimental design.

Exosome Research Services

1. Exosome Isolation

Our Exosome Isolation Services can reliably and reproducibly isolate exosomes from cells and cell culture media, serum/plasma, urine, saliva, cerebrospinal fluid. We can also isolate exosomes from plants as well as bacteria and fungi. Exosomes can be isolated by ultracentrifugation method, but we can provide other options such as differential/gradient ultracentrifugation, immunoaffinity, size exclusion chromatography, and precipitation/low-speed centrifugation.

Table 1. Methods Overview for Exosome Isolation

Methods	Principle	Schematic diagram	Advantages	Disadvantages
Differential Ultracentrifugation	Exosomes are separated based on their density using high-speed centrifugation.		Established and widely used methods can purify exosomes from different biological fluids—large exosome production.	Labor-intensive, time-consuming, may co-precipitate non-exosome materials, potential damage to exosomes due to high forces.
Filter Ultracentrifugation	Exosomes are separated based on their density using high-speed centrifugation.		Improved methods can purify exosomes from different biological fluids. Skip the low-speed centrifugation steps. Large exosome production.	may co-precipitate non-exosome materials, potential damage to exosomes due to high forces.
Density Gradient Centrifugation	Exosomes are separated based on their buoyant density by gradient centrifugation.		Good purity.	Complex, requires careful gradient preparation, longer procedure.
Ultrafiltration	Exosomes are filtered through a membrane with a specific pore size to separate them from larger particles.		Simple and relatively quick, suitable for large-volume samples.	This may result in co-isolation of proteins and contaminants.
Size-Exclusion Chromatography (SEC)	Exosomes are separated based on size by passing through a porous column.		The gentle method preserves exosome integrity.	Possible co-eluttion with proteins, which requires specialized equipment.
Polymer precipitation	Polymers are added to induce exosome aggregation and precipitation.		Easy and rapid process, good yield from various biological fluids.	Contamination with polymers, potential disruption of exosome integrity.
Immunoaffinity-based capture	Antibodies are used to capture exosomes based on specific surface markers.		High specificity enables targeted isolation of exosome subpopulations.	Limited by the availability of well-characterized antibodies, potential loss of non-targeted exosomes.

2. RNA and Protein Quantification
RNA and protein from exosomes can be quantitated.

3. Exosome Characterization
Exosomes are characterized using Nanoparticle Tracking Analysis (NTA). NTA measurements rely on light scattering to extract particle size and the number of particles in a sample. Results are provided as a concentration in particles per ml, a size distribution graph of extracellular vesicle diameters, and a video of the collected data, all gathered in triplicate.

4. Exosome Surface Marker Analysis
Capillary western analysis is used to measure protein markers on exosomes. The capillary western blot assay provides a sensitive, quantitative readout via image and densiometric conversion for all markers tested.

5. Exosome miRNA Isolation & Sequencing
For exosomal miRNA isolation and sequencing, we use Small RNA-Seq (Illumina Platform). Basic analysis of the raw data is performed as part of the service.

6. Functional Studies

We also provide a wide range of exosome functional assays:
- ❖ Exosome-induced inhibition of inflammatory cytokines.
- ❖ Exosome-induced cell proliferation.
- ❖ Exosome-induced cell migration and invasion.
- ❖ Exosome-induced *In vitro* wound healing (scratch assay). The standard scratch assay will be performed using monolayered cells in each well, with photomicrographs taken at 12 hr intervals over a 72 hr period.

7. Pricing

Table 3. Standard User Rates

Service/Unit		CTSI Members	Non-CTSI	Notes
Exosome Isolation	Tissue culture media	$75/sample (1-6) $70/sample (7-12) $60/sample (13-24)	$80/sample (1-6) $75/sample (7-12) $75/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 2 ml. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Serum	$75/sample (1-6) $70/sample (7-12) $60/sample (13-24)	$80/sample (1-6) $75/sample (7-12) $75/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 100 µl. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Cerebrospinal fluid	$75/sample (1-6) $70/sample (7-12) $60/sample (13-24)	$80/sample (1-6) $75/sample (7-12) $75/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 2 ml. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Interstitial fluid.	$75/sample (1-6) $70/sample (7-12) $60/sample (13-24)	$80/sample (1-6) $75/sample (7-12) $75/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 2 ml. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Urine	$85/sample (1-6) $80/sample (7-12) $70/sample (13-24)	$90/sample (1-6) $85/sample (7-12) $85/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 5 ml. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Saliva	$85/sample (1-6) $80/sample (7-12) $70/sample (13-24)	$90/sample (1-6) $85/sample (7-12) $85/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 1 ml. Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
	Plant Homogenates	$75/sample (1-6) $70/sample (7-12)	$80/sample (1-6) $75/sample (7-12)	Minimum samples: 2. Samples Minimum volume: 2 ml. Method: Filter Ultracentrifugation. Other

		$60/sample (13-24)	$75/sample (13-24)	methods can also be used depending on customer preference and sample source.
	Bacterial Exosomes	$75/sample (1-6) $70/sample (7-12) $60/sample (13-24)	$80/sample (1-6) $75/sample (7-12) $75/sample (13-24)	Minimum samples: 2. Samples Minimum volume: 200 ml of supernatant . Method: Filter Ultracentrifugation. Other methods can also be used depending on customer preference and sample source.
Exosome quantification	RNA	$45/sample (1-6 samples) $40/sample (7-12 samples) $30/sample (13-24 samples)	$50/sample (1-6 samples) $45/sample (7-12 samples) $35/sample (13-24 samples)	Total Exosome RNA Protein Isolation Kit (Life Technologies).
	Protein	$35/sample (1-4 samples) $30/sample (5-12 samples) $20/sample (13-24 samples)	$40/sample (1-4 samples) $35/sample (5-12 samples) $25/sample (13-24 samples)	Pierce™ BCA Protein Assay Kits (Thermo Scientific).
Exosome Characterization		$25/sample	$30/sample	NTA analysis (NanoSight NS300, Malvern Panalytical).
Exosome Surface Marker Analysis	1 marker	$40/sample	$45/sample	Western blot.
	2 markers	$50/sample	$55/sample	
Exosome miRNA Isolation & Sequencing		Inquire.	Inquire.	
Functional Studies: Exosome-induced inhibition of inflammatory cytokines; Exosome-induced cell proliferation; Exosome-induced cell migration and invasion; Exosome-induced *In vitro* wound healing (scratch assay).		Inquire.	Inquire.	

Instrumentation

Sorvall LYNX 4000 Superspeed Centrifuge

Thermo Scientific™ Sorvall™ LYNX 4000 superspeed centrifuge has a 4L capacity and centrifuagation speeds up to 68,905 x g. Advanced rotor innovations including Thermo Scientific™ Auto-Lock™ rotor exchange, Thermo Scientific™ Auto-ID™ instant rotor identification and lightweight and durable Thermo Scientific™ Fiberlite™ carbon fiber rotors that shorten run set-up time and increase rotor security.

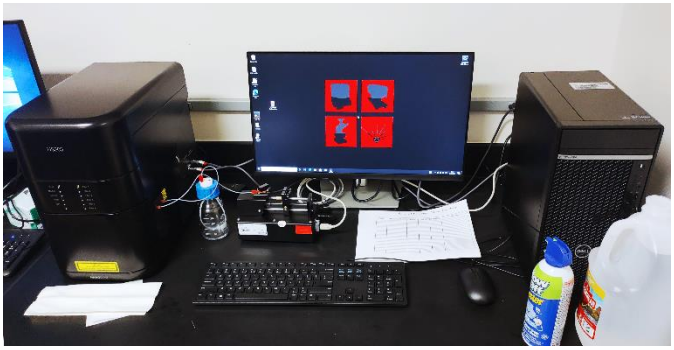
Sorvall™ WX+ Ultracentrifuge Series

Thermo Scientific™ Sorvall™ WX+ ultracentrifuge can reach 100,000 rpm. It features lightweight and fatigue-resistant Thermo Scientific™ Fiberlite™ carbon fiber rotors that do not need to be derated over time, and an intuitive, easily accessible touch screen interface and imbalance tolerance to accelerate run set-up.

Malvern NanoSight NS300

This instrument uses unique Nanoparticle Tracking Analysis (NTA) technology to detect and visualize populations of nanoparticles (10nm to 2000nm) on a particle-by-particle basis. The technique uses the properties of both light scattering and Brownian motion to calculate

particle size and concentration. The random movement of each particle in a fluid (Brownian motion) is tracked by capturing the light scattered by the particles when illuminated by a laser. A digital camera and specially designed software capture the light scattered by the particles and track their motion frame by frame. The rate of movement is related to particle size, which is calculated by using the Stokes-Einstein equation to give hydrodynamic diameter. Labeled or naturally fluorescent particles can also be detected with a choice of laser wavelengths and a motorized fluorescence disc. NTA provides high-resolution particle size distribution concentration, and measurements for individual nanoparticles, while a fluorescence mode allows differentiation of fluorescing particles, protein aggregation, and viscosity results, independent of particle density and refractive index. Events such as aggregation and dissolution can be monitored as they occur.



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