

ExRNA Virtual Biorepository





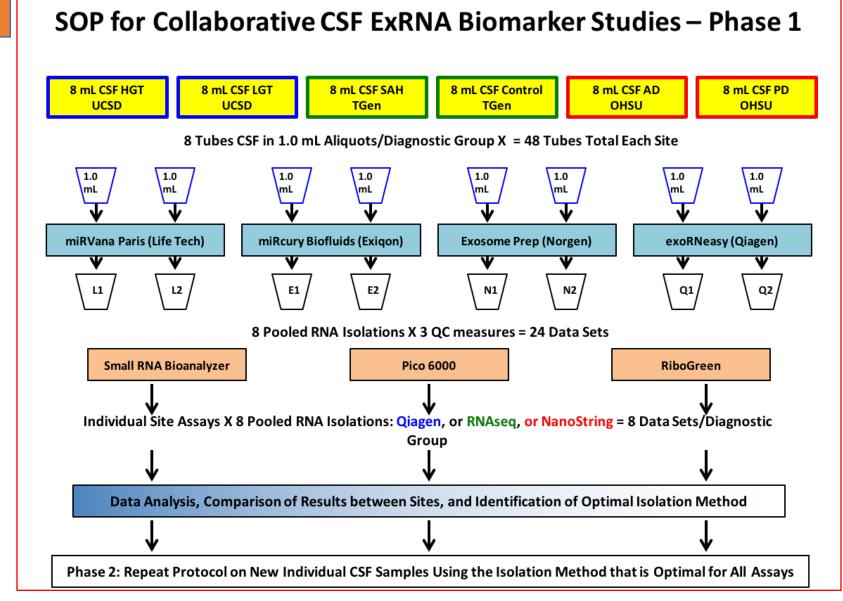
Rocco D. Lucero¹, Sai Lakshmi Subramanian¹, Bob Carter², Fred Hochberg², William Butler³, Matthew Huentelman⁴, Kendall Van Keuren-Jensen⁴, Theresa Lusardi⁵, Joseph Quinn⁵, Matthew E. Roth¹, Julie A. Saugstad⁵, **Aleksandar Milosavljevic¹**

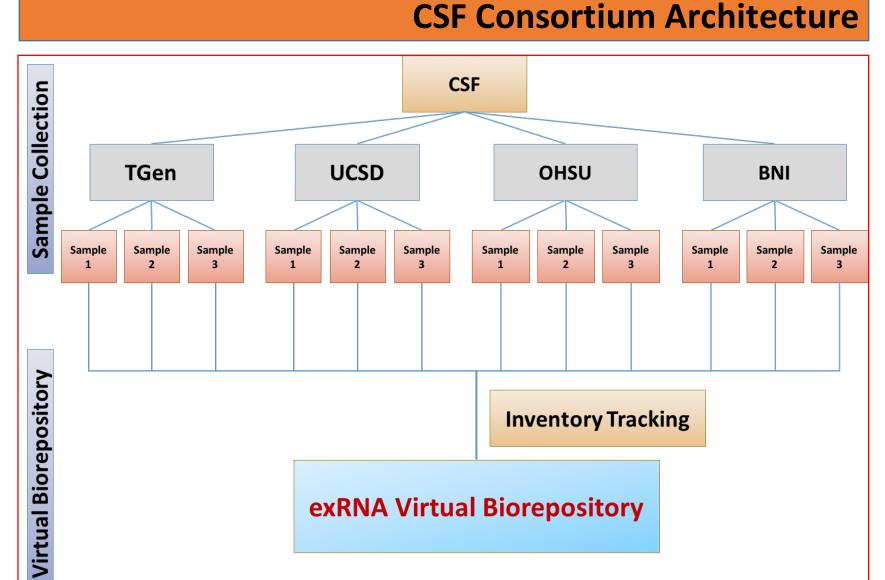
> 1 Baylor College of Medicine, Houston, TX; 2 University of California at San Diego (UCSD), San Diego, CA; 3 Massachusetts General Hospital, Boston, MA; 4 Translational Genomics Research Institute (TGen), Phoenix, AZ; 5 Oregon Health & Science University (OHSU), Portland, OR

The exRNA virtual biorepository (EVB), developed by the Resource Sharing Working Group and the Data Management and Resource Repository (DMRR) of the exRNA Communication Consortium (ERCC), facilitates tracking and sharing of biofluids. The shared EVB is key to discovery and validation of biomarkers while providing normative and experimental controls for specificity assessments.

Vision of the exRNA Virtual Biorepository

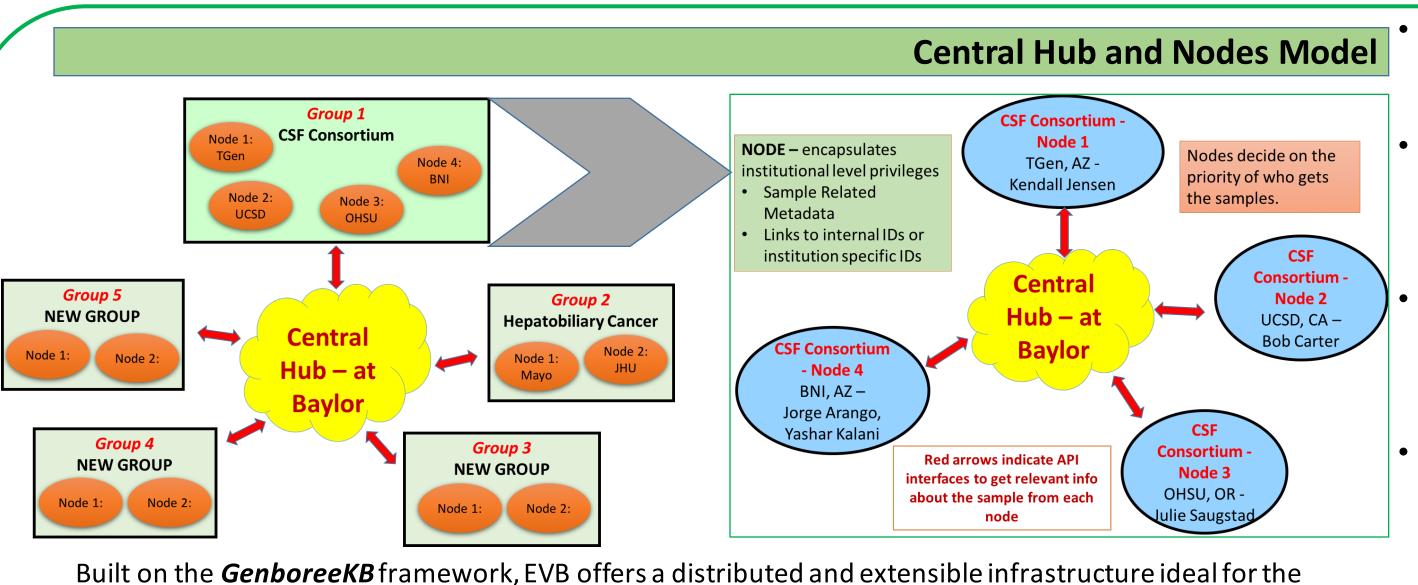
- Shared biofluid and tissue specimens for the ERCC and research community
- Resource for assessing and validating exRNA biomarkers for
- Disease diagnosis, prognosis, stratification, toxicity
- Providing normative and experimental controls
- Improving biomarker sensitivity and specificity
- United Common IRBs and uMTAs
- Optimized and stringent SOPs and site quality control
- Our operating philosophy is based upon the CSF consortium template
- Mindful of the need to determine long-term funding model and transition
 - Work with advocacy groups, commercial, non-profits
 - Guided by Advisory Board of stakeholders





The first 'use case' for the EVB involves the evaluation of CSF for the diagnosis of:

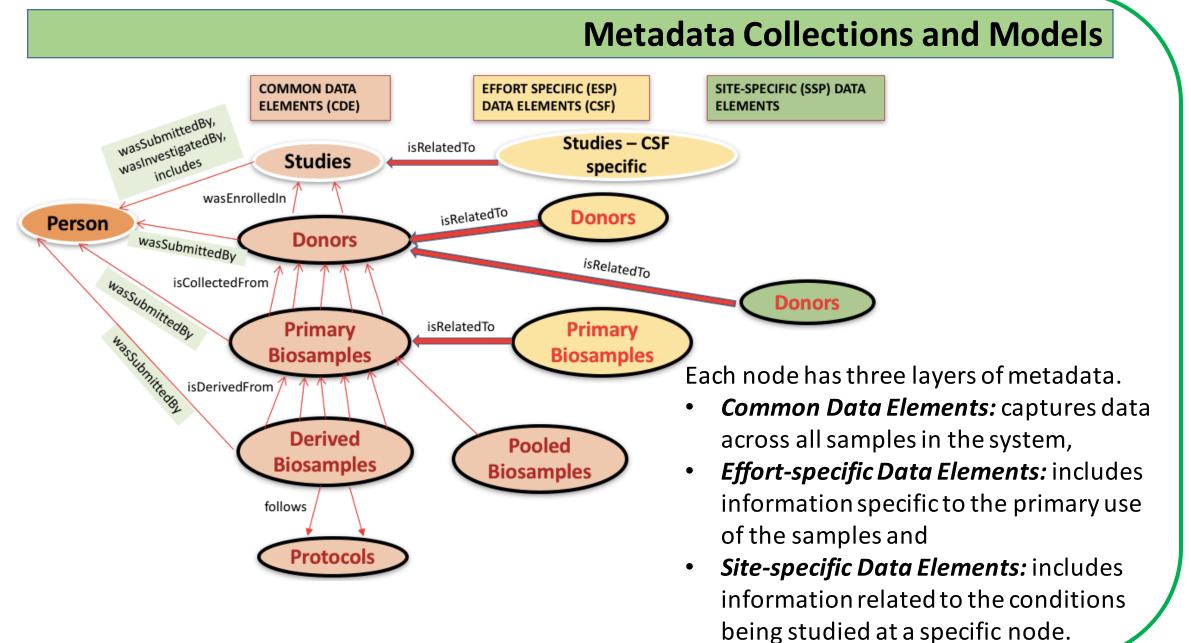
- Primary tumors of brain (UCSD);
- Subarachnoid hemorrhage (TGen);
- Alzheimer's & Parkinson's diseases (OHSU);
- EV profiles of normal CSF; EVB also stores CSF samples collected routinely from patients with various neurological conditions (Barrow Neurological Institute, BNI).

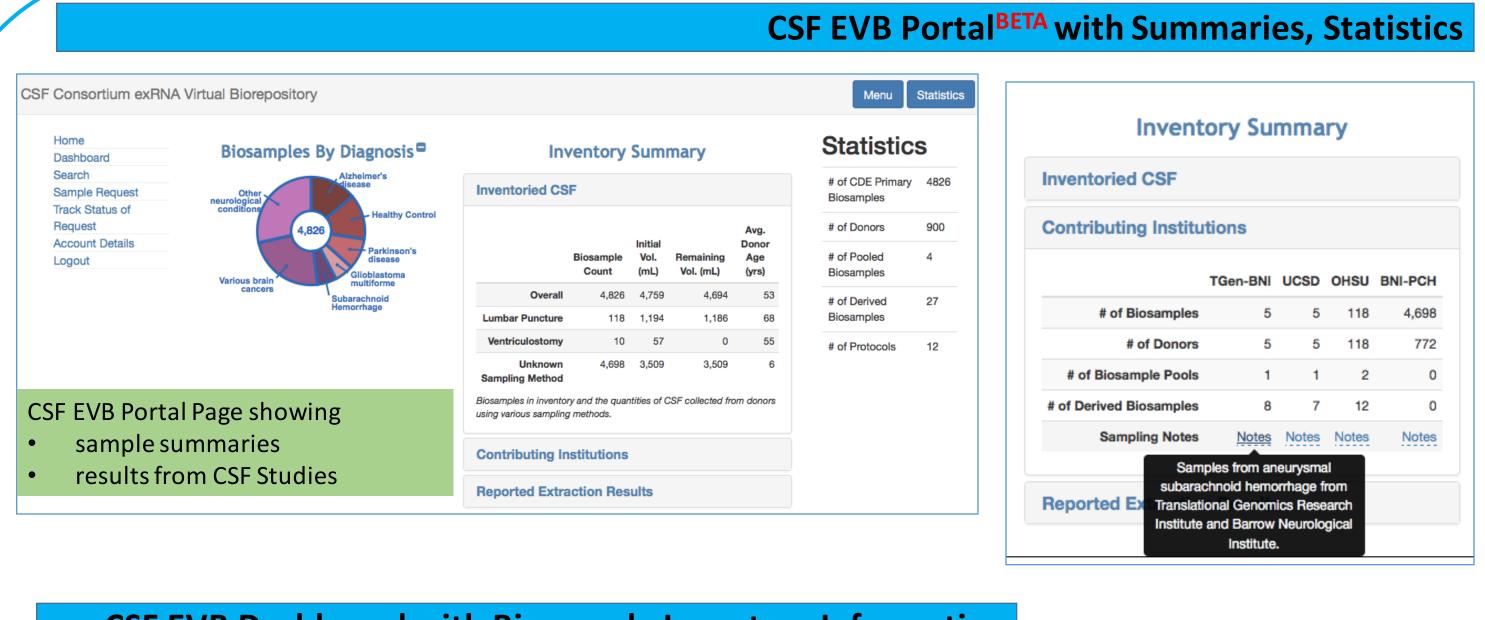


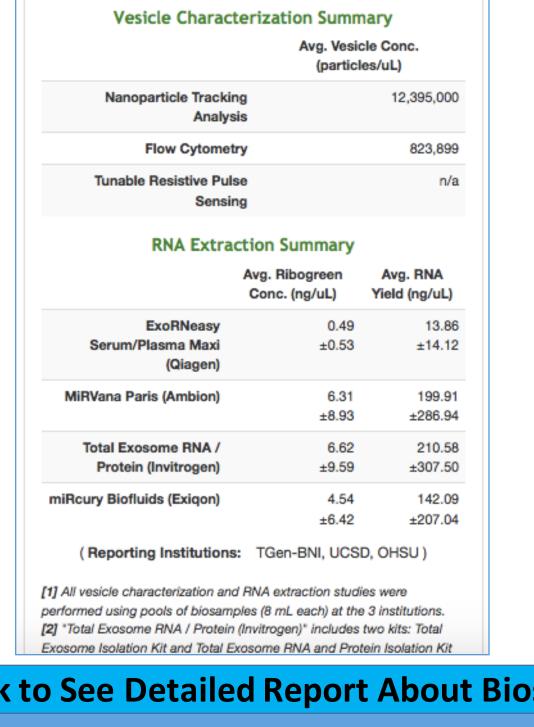
promotion of collaboration with controlled information sharing. Each institution participating in the EVB possesses a 'node' within the system.

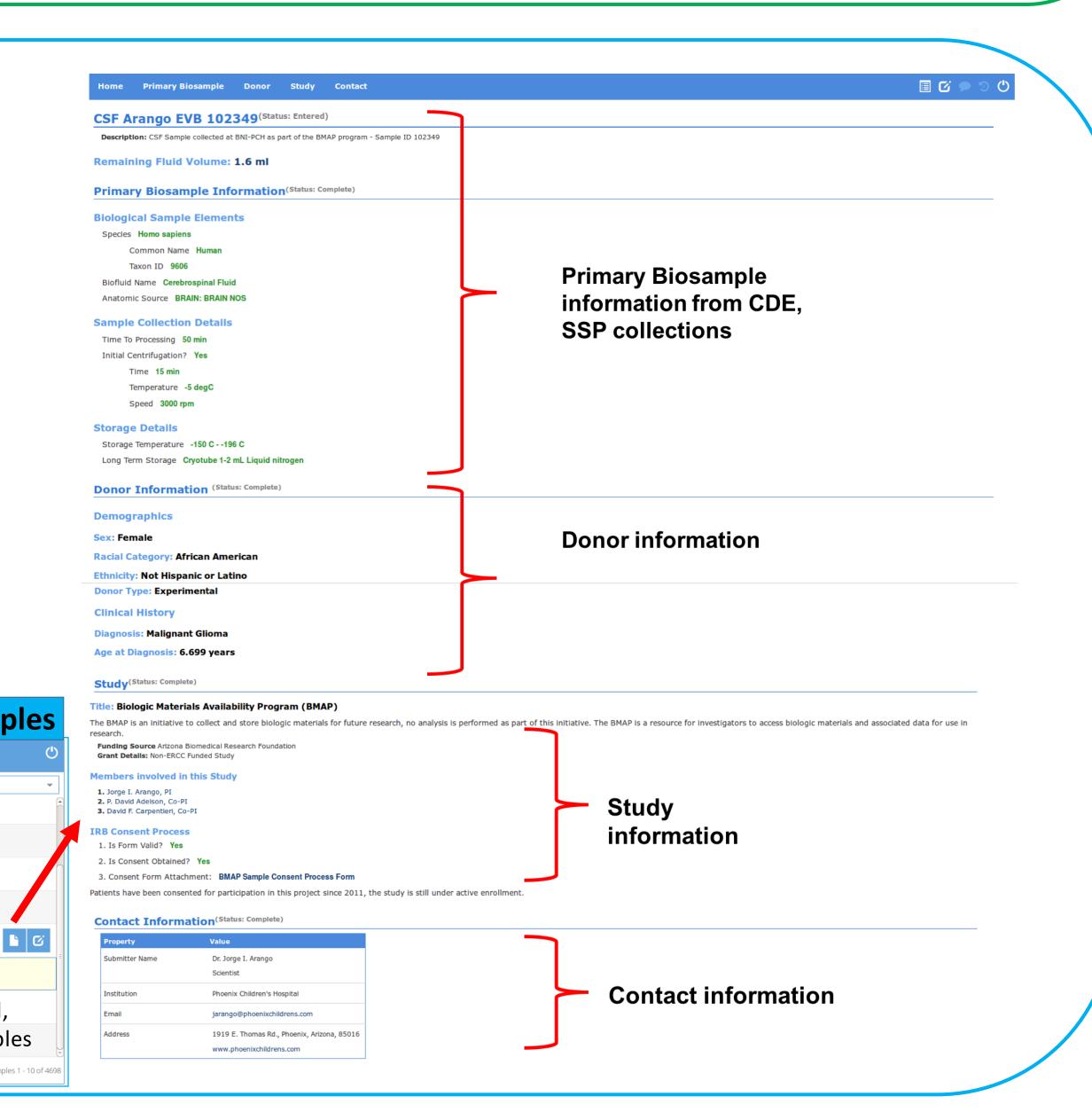
- The local nodes are configurable so that only a subset of non-identifiable data about samples may be shared outside of the collection site.
- For ease of installation, the nodes are pre-configured virtual machines (VMs) and may reside at participating institutions or may be hosted remotely at commercial or private clouds.
- The central EVB hub is a "web service broker" for data query, annotation, requesting and tracking samples and generating summary reports for samples available across the network of EVB nodes.
- Genboree REST Application Programming Interfaces (APIs) that enable standards-based data sharing across physically distributed nodes are projected to be fully compliant with W3C JSON-LD and RDF Linked Open Data standards, thus facilitating data interoperability with EHR and other IT systems.

Reported Extraction Results

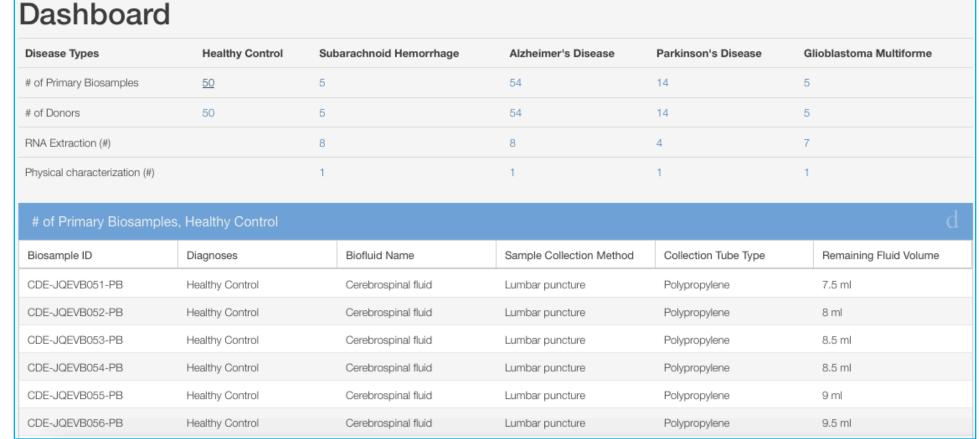


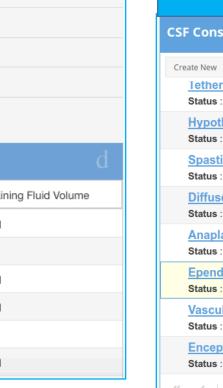


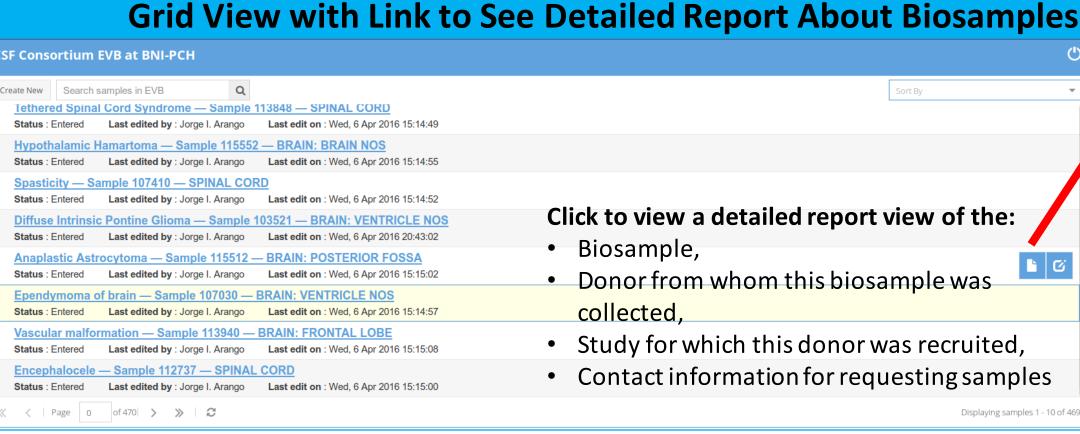




CSF EVB Dashboard with Biosample Inventory Information







Future Direction: The EVB will devise specimen tracking request policies, voting rules and prioritization rules for sample requests. The EVB as a model for collaborative EV studies will be expanded to hepato-biliary diseases and oro-pharyngeal fluids as the next series of 'use cases'.

Acknowledgements:

- Genboree Dev Team at Baylor: Andrew Jackson, Neethu Shah, Aaron Baker, William Thistlethwaite, Sameer Paithankar
- Contributors from various institutions: UCSD: Ryan Kim, Johnny Akers, Douglas Galasko; OHSU: Betty Lind; TGen: Rebecca Reiman, Ashish Yeri; Barrow Neurological Institute: Yashar Kalani, Jorge Arango
- This research is supported by the Supplement Grant 3U54DA036134-03S1 from the NIH Common Fund, through the Office of Strategic Coordination/Office of the NIH Director.