

LabKey Server: An open source platform for scientific data integration, analysis, and collaboration

Mark Igra Partner, LabKey Software marki@labkey.com

Presentation Topics



- Why Scientific Data Integration
- Examples of Usage
 - Common requirements for scientific data integration
- Architecture
- Future Directions

Why Scientific Data Integration



Data Volume

- Hundreds of millions of results from thousands of high throughput assay runs
- Data Variety
 - Clinical, Demographic, Assay & Specimen Data
 - Scientific data annotation
- Collaboration
 - Investigators aren't all in the same place
 - Need secure, selective data sharing
- Broad Range of Analyses
 - Queries, Reports, Domain Specific Tools
 - Custom Novel Applications

Evolution of LabKey Server



- Core team came from software industry, not bioinformatics
- Moved to Hutchinson Center to work on proteomics for biomarker discovery
- Expanded from there into
 - More assays
 - Study data management
 - Lab Data Management
 - Network Data Management

Proteomics.fhcrc.org



Problems Faced

- Number of reads from MS2-based proteomics assay were exploding & difficult to handle on existing tools
- Analysis Pipeline on cluster was difficult to optimize
- Solution
 - The original LabKey Server (CPAS)
 - Pipeline to run MS2 analysis jobs via web browser and load results into Database
 - Web based analysis tools to view, combine & share results
 - Lots of Data
 - More than 90,000 MS2 Runs
 - More than 700,000,000 peptide identifications
- Rauch et al, Journal of Proteome Research, 5/2006

Proteomics Examples





6

Flow Cytometry



Problem

- Lab using Flow Cytometry to measure intracellular cytokines in many samples
- Per-run quantity of data increasing
- Need consistent analysis within an experiment type
- Cross-run analyses
- Each experiment type may have different statistics
- Solution: LabKey Flow
 - High-throughput flow analysis engine
 - Loading of flow statistics
 - Adaptable data model for varying analysis types
 - Query tools for analyzing data
- Shulman et al, Cytometry A, Sep 8 2008

Flow Results



Flow Dashboard > labkey-analysis >

labkey-demo.xml analysis

Run Comment: Type to enter a comment

SHOW GRAPHS

OUERY *	VIEWS *	EXPORT *	PRINT	PAGE SIZE *

1 - 68 of 68

	Name	Flag	S:Count	S:%P	4+:Count	8+:Count	4+/(!IFNg+&!IL2+):Count	4+/(!IFNg+&!IL2+&IL4+&!TNFa+):Count	4+/(!IFNg+&!IL2+&IL4+&TNFa+):Count	4+/(!IFNg+&IL2+
DETAILS >	119142.fcs	M	9,764	97.64	3,713	1,917	3,711	1	0	
DETAILS	118813.fcs		9,770	97.7	2,357	1,888	2,357	1	0	
DETAILS	118981.fcs		9,807	98.07	2,338	1,848	2,337	47	0	
DETAILS	118947.fcs		9,555	95.55	2,065	1,703	2,065	2	0	
DETAILS	119199.fcs		9,728	97.28	2,336	1,907	1,977	0	0	
DETAILS	119154.fcs		9,545	95.45	2,541	1,629	2,541	0	0	
DETAILS	118836.fcs		9,496	94.96	504	466	503	0	0	
DETAILS	119010.fcs		9,817	98.17	3,804	1,824	3,801	0	0	
DETAILS	118762.fcs		9,743	97.43	5	131	5	0	0	
DETAILS	118756.fcs		9,753	97.53	0	0	0	0	0	
DETAILS	119171.fcs		9,662	96.62	2,200	2,196	1,661	5	0	
DETAILS	118801.fcs		9,706	97.06	2,251	2,087	2,251	2	0	
DETAILS	118754.fcs		9,787	97.87	1	0	1	0	0	
	110000 6		0.447	A 4 4 7	1 051	1 000	1 050			

View Graphs





9

Customize View



Flow Dash	board > labkey-analysis >				
labkev	/-demo.xml analysis				
labitoj					
Run Comm	nent: Type to enter a comment				
HIDE GRAPH	Is Large Graphs] [Medium Graphs] [Small Graphs]				
QUERY 🛎	VIEWS * EXPORT * PRINT PAGE SIZE *				1 - 68 of 68
Columns	Available Fields		Selected Fields		×
Filter	🗄 🗹 Flag		Name		
The	Created		Flag		
Sort	⊎ ⊂ Run		S:Count		
	Analysis Script		S:%P		
	Compensation Matrix		4+:Count		
			8+:Count		
			Lv/L(<pe cy55-a="">:<pe re<="" th="" tx=""><th>D-A>)</th><th></th></pe></pe>	D-A>)	
	$(\langle A e_X = 680-A \rangle)$		3+(<pe cy55-a="">:<fitc-a>)</fitc-a></pe>		
	<pre>(<fitc-a>)</fitc-a></pre>		4+(SSC-A: <apc-a>)</apc-a>		
	(<pe cv55-a="">)</pe>		4+(SSC-A: <alexa 680-a="">)</alexa>		
	(<pe cy7-a="">)</pe>		4+/(!IFNg+&!IL2+):Count		
			4+/(!IFNg+&!IL2+&IL4+&!TNF	a+):Count	
		Show Hidden Fields	4+//ITENa+&ITL2+&TL4+&TNE:	a+).Count	
	Editing an unsaved view.				×
	DELETE REVERT			VIEW GRID	SAVE
	Name Flag S:Count S:%P 4+:Count 8+:Count 4+,	/(!IFNg+&!IL2+):Count 4+/(!IFNg	+&!IL2+&IL4+&!TNFa+):Count	4+/(!IFNg+&!IL2+&IL4+&TNFa+):Count 4+,	/(!IFNg+&IL2+
DETAILS >	119142.fcs 9,764 97.64 3,713 1,917	3,711	1	0	
	S/Lv/L S/Lv/L/3+	S/Lv/L/3+/4+	S/Lv/L/3+/4+		

10

Atlas – SCHARP Data Portal



Problems faced

- Combine many data types for HIV Vaccine studies
 - Clinical Response Forms (CRF), Specimens, Many Assays
- Enable secure collaboration for scientists worldwide
- Allocate & distribute valuable specimens
- Solution
 - Secure web portal for HIV Vaccine Enterprise Data
 - Used by several networks to share data
 - CHAVI, CAVD, HVTN, HPTN (3000 Users Worldwide)
 - Core software was written by LabKey
 - SCHARP runs Atlas
 - Defines available data and relationships
 - Manages security and permissions
 - Manages data loading
 - Builds custom modules
- Nelson et al, BMC Bioinformatics, March 2011

Atlas Data Flows





Combining Data



Demographic	: Data	Assay D	ata	Specimen Data			
					-		
Participant	Gender	CD4+	Hemoglobin	Specimen	Available?		
249318596	Male	420	12.2	5390.204.36	Yes		
249320107	Female	344	13.2	2493.404.56	Yes		
249320127	Male	897	21.0	2493.323.33	Yes		
249320489	Male	234	16.4	2493.789.44	No		
249320897	Female	893	12.9	5266.440.61	Yes		

Study Page





Dataset



I 001 > Study Overview >

taset: Binding Antibody, All Visits

WS · P	ARTICIPAN	GROUPS *	EXPORT	PAC	SE SIZE *	VIEW	V SPECIMEN	IS							1	- 100 of	282 Nex
'articipant D 🔺	Sequence Num 🔺	Draw Date	Enrollment date	Assay ID	Isotype	Antigen	Coat Lot	Dilution	Concentration	Reading	St. Dev.	No Antigen	No Ant. St. Dev.	QC Titer 50	Plate ID	Network	Protocol
	101.0	20-Jun-06	20-Jun-06	JTL 61- 38	IgA	CONT 140 CF	#2	10		0.394	0.013			151450.0	3	CHAVI	1
	102.0	27-Jun-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.387	0.034			151450.0	3	CHAVI	1
	103.0	05-Jul-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.408	0.016			151450.0	3	CHAVI	1
	104.0	12-Jul-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.417	0.0070			151450.0	3	CHAVI	1
	105.0	20-Jul-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.436	0.014			151450.0	3	CHAVI	1
	106.0	14-Aug-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.52	0.0020			151450.0	3	CHAVI	1
	107.0	07-Sep-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.634	0.03			151450.0	3	CHAVI	1
	108.0	10-Oct-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.227	0.076			151450.0	3	CHAVI	1
	109.0	29-Nov-06		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.574	0.01			151450.0	3	CHAVI	1
	110.0	26-Feb-07		JTL 61- 38	IgA	CONT 140 CF	#2	10		0.413	0.084			151450.0	3	CHAVI	1
	101.0	20-Jun-06	20-Jun-06	JTL 61- 38	IgA	GP41	J15/6J13R	10		0.833	0.034			19790.0	4	CHAVI	1
	102.0	27-Jun-06		JTL 61- 38	IgA	GP41	J15/6J13R	10		0.531	0.024			19790.0	4	CHAVI	1
	103.0	05 1-1 00		JTL 61-	T - A	CD41	115/01100	10		0.531	0.015			10700.0		CUANT	

Participant View





Participant Specimen Summary



Study	Overview	> Dataset:	Binding	Antibody,	All Visits >
-------	----------	------------	---------	-----------	--------------



IPANT | SEARCH FOR

s	Specimen Timeline	Clinical Data	Requested Specimens	All Specimens	Binding Antibodies	Cytokines	

nformation: Available Vials \$

	Devive the Ture	Additive Trees	Envellerent	Week	Wee								
	Derivative Type	Additive Type	Enrollment	1	2	3	4	0	12	10	24	30	48
)	Blood (Whole)	Tempus	0	() (0	(J)		0	0
)	PBMC Cells, Viable	Acid Citrate Dextrose	5	2	2 !	5 :	L (5 2	2	7 3	3 4	4	4
)	Serum	Serum Separator	2		3 4	4 4	4 4	4 θ	5 4	4 4	4 4	4	4
)	Whole Blood Pellet, Specify Methodology	EDTA	0	() :	1							
)	Plasma	Acid Citrate Dextrose	24	1)	7 (5 !	5 1	1	L :	3 1	3 1	.3
)	Plasma	EDTA	2		1 :	1 2	2 :	1 1		4 :	L (D	1
	Tear Flo Strips	None	1	:	1 :	1 :	1			1		1	
hal	Cryopreserved primary cells from Non-Blood Spec Type, Viable	None	0	(0	0 (D			D		D	0
nal	Fluid Portion from a Non-Blood Specimen Type	None	0	:	1 :	1 :	L		:	3	:	3	5
nal		None	0	() (0 (D			D			

Lab Data Flows





Assays: upload example





Piehler et al, BMC Immunology, May 2011

Custom Applications



- Dozens of small applications needed for different groups
 - Most used data already in LabKey System
 - But custom workflows, reports & analysis required
- SCHARP has detailed knowledge of the requirements
- LabKey provided an API and simple application building tools

HVTN IQC



Internal Quality Control for Sample Processing



RV144 Followup Study Tracking System



Tools for tracking information about studies

Overview	Assay(s)	Team Members	SCHARP	Atlas Admin	Other Tools			
Stat T	ask Lis	t				LDO	Task List	
tudy T	asks					Assay	Tasks: Borrow Chemokine	
	Task Desc	ription		Date Comp	leted		Task Description	Date Completed
[edit]	Sampling F	Plan from SCHAR	Р	28-Dec-200	Ð	[edit]	Data Uploaded for Borrow Chemokine	
	Cot To ale	_				[edit]	Data Imported for Borrow Chemokine	
ampie	Set Task	5 c	ample Set/	e)		[edit]	Data QCd for Borrow Chemokine	
Task Description Sample Set(Used		3)		[edit]	Data Sent to Stat for Borrow Chemokine			
Sample Chemok	set(s) for Bo ine	orrow		Add	Sample Set	[edit]	Analysis Complete for Borrow Chemokine	
Sample	set(s) for Bo	orrow		bbA	Sample Set	Assay	Tasks: Borrow Cytokine	
Cytokine	1				Sumple See		Task Description	Date Completed
						[edit]	Data Uploaded for Borrow Cytokine	
						[edit]	Data Imported for Borrow Cytokine	
						[edit]	Data QCd for Borrow Cytokine	
						[edit]	Data Sent to Stat for Borrow Cytokine	
						[edit]	Analysis Complete for Borrow Cytokine	

Primate Electronic Health Record



Problem

- 30 years of daily data on thousands of animals
- Clinical staff & vets need health record
- Researchers need scientific data
- Colony Management is an ongoing problem

Solution

- EHR is a a specialized, ongoing "study"
- LabKey enhanced scalability of study solution
- LabKey enhanced API
- LabKey wrote tools to transfer data into new EHR within minutes of entry into old EHR
 - Now LabKey EHR is only one in use
- Wisconsin Primate Center built custom views & reports to analyze the data

Primate EHR



VIE	EWS * EXP	ORT 🔻	PRINT	PAGE SIZ	E * MOI	RE ACTIONS *				1 - 12 of	f 12
		Id	Current	Current	Problem	Date	Date Resolved	Category	Remark	C	Code
			Room	Cage	Number	Observed 🗸					
	DETAILS				12	2011-10-04	2011-10-07				
	DETAILS				11	2011-05-16	2011-05-20				
	DETAILS >				10	2010-11-22	2010-11-30				
	DETAILS >				9	2008-05-22	2008-05-23				
	DETAILS				8	2007-09-05	2007-09-07				
	DETAILS >				7	2007-06-05	2007-06-08				
	DETAILS >				6	2005-01-12	2005-01-26				
	DETAILS				5	2003-12-03	2003-12-03				
	DETAILS				4	2003-03-17	2003-04-10				
	DETAILS				3	2002-11-19	2002-11-19				
	DETAILS				2	2002-07-22	2002-07-22				
	DETAILS >				1	2002-03-07	2002-03-19				
VIE	EWS * EXP	ORT *	PRINT	PAGE SIZ	E * MOI	RE ACTIONS *				1 - 12 of	f 12



ITN Trial Share



Problem

- Sharing clinical trial amongst distributed teams
- Publish data in support of studies
- Solution
 - ITN TrialShare
 - Publish Study Capabilities
 - Support for point in time access to study data
 - Copy protected data
 - Interactive access to publication data
 - Improved Visualization

ITN TrialShare





Visualization with Participant Groups





nPOD – Network for Pancreatic Organ Donors

INFORMATION	TISSUE INVENTORY	
DEMOGRAPHICS	PanHead	3
	PanTail	3
Age/Gender 22 year old Male	PLN-A	1
Race White	PLN-C	1
^{BMI} 24.09	Serum	1
O DIABETES	Spleen	1
Donor Type T1D	PATHOLOGY IMAGES	
High Resolution HLA A*01/24, B*08/18, DR*03/06, DQ*01/02		
C Peptide Levels 0.025	A AND A	A DE CARACTER
Duration (Years) 14		Charles and the
INVESTIGATOR REPORTS		and the second s
Network for Pancreatic Organ Donors with Diabetes (nPOD): developing a tissue biobank	SAD SHA	1000
for type 1 diabetes Campbell-Thompson M. Wasserfall C. Kaddis 1. Albanese-O'Neill A. Staeva T. Nierras	ST 12 112	AVONCORE
C, Moraski J, Rowe P, Gianani R, Eisenbarth G, Crawford J, Schatz D,Pugliese A, Atkinson	36/2010/20	
M. Diabetes/Metabolism Research and Reviews, 2012	See Aller	Law man
PMID: 22585677		THE REPORT OF
Expression of the enteroviral capsid protein VP1 in the islet cells of patients with type 1	St. Van St.	
diabetes is associated with induction of protein kinase R and downregulation of McI-1 Richardson SJ, Leete P, Bone AJ, Foulis AK, Morgan NG	5-20	CARD-AD
Diabetologia, 2013 PMID: 23064357	ALC: THE REAL	
		TABLERGERAL VINIA
Paricreas organ weight in individuals with disease-associated autoantibodies at risk for type 1 diabetes	T. Star Werter	Constant State
Campbell-Thompson M, Wasserfall C, Montgomery EL, Atkinson MA, Kaddis JS.		22
PMID: 23232891	Contraction of the	
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
ACTIVE DROJECTS		
ACTIVE PROJECTS		
Anderson		

Investigator Dr. D Anderson Description Virus detection in pancreas and other tissues

Clark Investigator Dr. H Clark Description Non-Study Related Lab Processing LabKey Software

Ancillary Studies



Study Execution

- 4. Consent verification or acquisition
- 5. Retrieval of existing data
- 6. Delivery & analysis of specimens
- 7. Data integration

Nelson et al, Ancillary study management systems a review of needs BMC Med Inform Decis Mak Jan 2013

Results Sharing

- 8. Data/specimen repatriation
- 9. Publication

Study Initiation

- 1. Hypothesis generation
- 2. Proposal review
- 3. Creation of protocol or plan



Targeted Promeenics LabKey Software Repository

Admin 👻 | Help (default) 👻 | vsharma@uw.edu 👻

Targeted MS Folder					Targete	d MS Dashboard	
Targeted MS Runs >							
Study7				Targeted MS Folder			Targeted MS Dashboa
Document Summary				Targeted MS Runs > MRMer.zip > TNNPETLVALR			
-				Pentide Summary			
Peptide Group Count 7 Precursor Count 20	Peptide Count 10 Transition Count 60			File MRMer.zip Frotein YAL038W Sequence TNNPETLVALR NeutralMass 126.6619 Avg. RT 26.898569107055664 Precursors TNNPETLVALR - 614.3382	++ <u>Å</u>		
Precursor List -				TNNPETLVALR - 619.3423	++ (heavy) 🚣		
Transition List	PAGE SIZE V			Chart Width 400 Synchronize Y-axis ☑	Chart Height Synchronize X-a	400 xis €	
Protein / Label	Description						
				Chromatograms			
Peptide	Missed Neutral Cleavages Mass	Rank Precursor	Labe	silac_1_to_4 TNNPETLVALR		silac_1_to_4 TNNPETLVALR - 614.3382++	silac_1_to_4 TNNPETLVALR - 619.3423++ (heavy)
AGLCQTFVYGGCR	0 1487.6649	AGL <u>C</u> QTFVYGG <u>C</u>	R ligh	4,000		2,250	2,250
AGLCQTFVYGGCR	0 1487.6649	AGL <u>C</u> QTF <mark>V</mark> YGG <u>C</u>	R hea	3,500		2,000 n 1,750	n,750
□ ⊕ LEP -				9 2,500		1,500	1,500
□ MYO				2,000		1,250 52 1,000	1,250 1,000
□ □ MBP -				1,500 ·		1 750 -	1 750 ·
Peptide	Missed Neutral Cleavages Mass	Rank Precursor	Labe	1,000 - 500 -		500 - 250 -	500 - 250 -
HGFLPR	0 725.3973	HGFLPR	light	0 26.0 26.5 27.0	27.5 28.0		
HGFLPR	0 725.3973	HGFLPR	heav	Retention Tir	me	Retention Time	Retention Time
YLASASTMDHAR	0 1321.6085	YLASASTMDHAR	light	TNNPETLVALR - 614.3382++ TNNPETLVALR - 619.3423++ (heavy)		y9 - 1012.5786+ y8 - 898.5356+ y6 - 672.4403+	
YLASASTMDHAR	0 1321.6085	YLASASTMDHAR	heav				
D B PSA							

Q

Search LabKey Server

VIEWS * EXPORT * PRINT PAGE SIZE *

LabKey Server

1 - 7 of 7





User Requirements



Data integration is the unifying theme

- Samples to Assays
- Assays to Subjects
- Subjects to Studies
- Translational Medicine involves integrating data from "Molecules to Populations" (Kuhn et al 2008)
- Data types to integrate are constantly evolving
 - Both file and "structured data types"
 - Can't rebuild new systems for new data types
- Tools grow as fast as data types
- Scientists need to share data
 - Central lab doing work for distributed clients
 - Distributed group of labs contributing
 - Need to manage many users

Basic Connectivity





LabKey Data Connectivity





Major Feature Areas



- Data Model
- Security
- Extensibility
- File Handling
- Assays
- Data pipelines to get data in
- Reports & visualizations to get data out
- Auditing

Data Model Goals & Requirements



- User interface
- Reporting & Querying
- Seamless data integration
 - Select columns across study, assay, specimen data
- Extensible
 - Data types are dynamic & user defined
 - Existing data stored in external systems
- Rich Column Types
 - Concepts, Lookups, Formatting, URL, Validation
 - Out of Range (e.g. < 30), SAS-style missing values
- Secure: See security slide

LabKey Sof

LabKey Data Model



- Data Exposed via Relational Model
- Virtual Schema
 - Modules expose a "User Schema"
 - User Schema maps virtual tables/columns to queries on underlying database
 - User Schema depends on user's permissions
- Users typically query by editing grid views
 - Add columns from related tables
 - Filter, Sort
- Full SQL Queries Available
 - SQL translated to underlying relational database

Query Processing





Major Feature Areas



Data Model

Security

- Extensibility
- File Handling
- Assays
- Data pipelines to get data in
- Reports & visualizations to get data out
- Auditing

Security Model Requirements



Pervasive

- Applies to data no matter how you get at it
- Modules, Search, Reporting, Queries, API, Files
- Easy Partitioning of Data by security context
- Easy Administration
 - Uniform administration across applications
 - Integrates with existing authentication systems
- Easy implementation by custom modules
- Extensible where necessary

Folders, Files and Data



	Files	Proteomics	Flow
Folder 1			
Folder 2			

Data and files are visible in folders

Major Feature Areas



- Data Model
- Security
- Extensibility
- File Handling
- Assays
- Data pipelines to get data in
- Reports & visualizations to get data out
- Auditing

Extensibility: Developers, Admins & Users



- Users:
 - Create custom views of their data using graphical tools
- Administrators
 - Configure LabKey Server
 - Set up projects and security.
 - Customize schema via data sets, assays, etc.
 - Create SQL queries and reports
- Application Module Developers
 - Build Custom Modules solving particular problems
 - Modules may be private or shared, open source or not
 - File-based modules (HTML + Script + SQL + XML)
 - Java Modules (usually built by LabKey)
- Platform Developers:
 - Build the core LabKey Server and key modules
 - Java code that is distributed in the LabKey Server distribution.
 - LabKey Software employees with few exceptions

Reporting



- Needs to be available on all data in the system
- Need flexible reporting infrastructure
 - LabKey cannot predict reports needed
 - Integrate R
- Interactive reports are preferable
 - Grids are interactive now
 - R reports allow filtering/redisplaying data
 - Interactive graphs under development

File Handling Requirements



- Files are the fundamental unit of data exchange
 - Contain structured & unstructured data
 - Sometimes huge
 - Sometimes many little files
- Need to find the files
 - Full text search + properties
- Need rapid & flexible file transfer
- Need to analyze & load structured data within files
 - Extensible actions including "load data"





- Audit service available to all modules
- Modules responsible for auditing actions
 - Easy implementation for basic data auditing
 - Would be nice if this were automatic
 - Many modules have custom audit events
 - (e.g. login, password reset etc)
- Each audit event type can have custom associated data
 - E.g. list updates store old values in audit trail

Futures



- Data Integration Improvements
 - Data Loading
 - ID Management
 - Smart Union of related datasets
- Lab Data Management
- Data Integration for EMRs





- Data Integration is a common need across scientific endeavors
- LabKey Server is a platform for addressing these challenges
 - Secure
 - Built for specialized challenges of scientific data
 - Extensible
 - Open
- We continue to work hard to advance the platform capabilities and usability

Acknowledgements



- Partners & Funders
- Martin McIntosh (FHCRC)
 - NCI
 - Canary Foundation
- Steve Self (SCHARP)
 - CHAVI (NIH)
 - HVTN (NIH)
 - CAVD (Gates Foundation)
- David O'Connor (Wisconsin)
 - Primate EHR (ARRA)
 - Genotyping Tools (NIAID)
- Parag Mallick (USC)
- Michael Katze (UW)
- Immune Tolerance Network
- nPOD

- LabKey Development
 - Matthew Bellew
 - Adam Rauch
 - Britt Piehler
 - Josh Eckels
 - Kevin Krause
 - Brendan MacLean (now UW)
 - Nick Shulman (now UW)
 - Karl Lum
 - Nick Arnold
 - Cory Nathe
 - Ben Bimber
 - Alan Veniza
- Documentation
 - Elizabeth Nelson
 - Steve Hanson
- Test
 - Trey Chaddick
 - Elizabeth Van Nostrand
- Management & Operations
 - Britt Piehler
 - Kristin Fitzimmons
 - Peter Hussey
 - Ren Lis

Any questions?



Mark Igra <u>marki@labkey.com</u>



If you use LabKey Server for your research, please reference one of these publications about the platform:

General Use: Nelson EK, Piehler B, Eckels J, Rauch A, Bellew M, Hussey P, Ramsay S, Nathe C, Lum K, Krouse K, Stearns D, Connolly B, Skillman T, Igra M. <u>LabKey Server: An</u> <u>open source platform for scientific data integration, analysis and collaboration</u>. BMC Bioinformatics 2011 Mar 9; 12(1): 71.

Proteomics: Rauch A, Bellew M, Eng J, Fitzgibbon M, Holzman T, Hussey P, Igra M, Maclean B, Lin CW, Detter A, Fang R, Faca V, Gafken P, Zhang H, Whitaker J, States D, Hanash S, Paulovich A, McIntosh MW: <u>Computational Proteomics Analysis System</u> (CPAS): An Extensible, Open-Source Analytic System for Evaluating and Publishing <u>Proteomic Data and High Throughput Biological Experiments</u>. Journal of Proteome Research 2006, 5:112-121.

Flow Cytometry: Shulman N, Bellew M, Snelling G, Carter D, Huang Y, Li H, Self SG, McElrath MJ, De Rosa SC: <u>Development of an automated analysis system for data from</u> <u>flow cytometric intracellular cytokine staining assays from clinical vaccine trials</u>. Cytometry 2008, 73A:847-856.

