Research Council
June 2, 2014

- **Please open all wrapped or sealed items in your lunch before the presentations begin.**
- **Please silence your cell phones & pagers. Thank you!**

UPCOMING PROGRAMS

Management 101 for Scientists: Communication as a Key to Leading People
Monday June 9, 2014, 4:00 – 5:30 pm
Speaker: Joanne Kamens, PhD
Sponsored by the Mass General Postdoc Association (MGPA)

Grant Writing Series: Mock NIH Study Section
Monday June 16, 2014, 12:00 – 1:30 pm
Speakers: Dennis Brown, PhD, Darlene Dartt, PhD, Bakhos Tannous, PhD
RCR credit-eligible

Academic Career Advancement Series: Instructor to Assistant Professor
Tuesday, June 10, 2014, 4:30 – 6:00 pm
Speakers: Carol Bates, MD, Isaac Schiff, MD, Markella Zanni, MD
Moderator: Nancy Rigotti, MD

To register for any program, email orcd@partners.org

Save Money on Software

ERIS

You can now purchase MATLAB & Stata licenses for individual machines at considerable savings year-round.

- New annual subscription service model

CORE

See the Research Computing Core Fee Table for details
http://rc.partners.org/core/catalog *Internal link

- Available for Mac & Windows systems
- Partners Network Connection Required

To sign up: email rcc@partners.org with # of licenses & Research fund # for chargeback.

Access to MATLAB & Stata software is also available via the ERIS HPC Infrastructure.

HPC

For more information, read this KnowledgeBase article http://rc.partners.org/kbase?cat_id=45&art_id=268 and contact hpcsupport@partners.org with any questions.

Academic Software Licenses

Software	What is it?	Partners Network	Fee Type	Subscription Term
GraphPad	Scientific graphing/ stats	Not required	License/year	Aug 29 - Aug 29
MATLAB	Numerical computing/ stats	Required	License/year	365 days upon activation
Safari Books Online	Online library database: IT	Not required	License/year	365 days upon activation
Stata	Data analysis/ stats package	Required	License/year	365 days upon activation
Freezerworks	Freezer inventory system	Required	Initial cost + License/year	July 1 - June 30

How does it work?

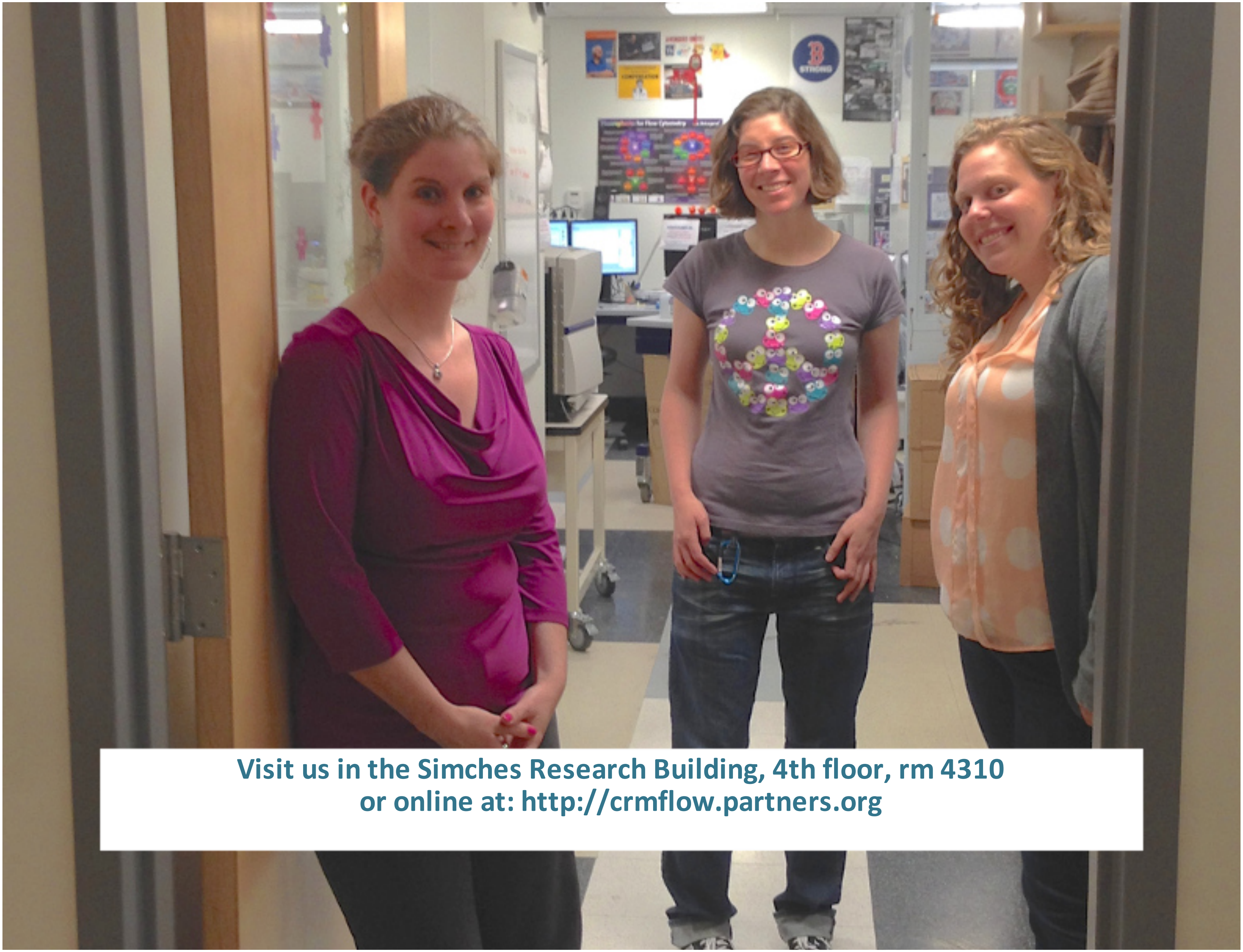
- Researchers reimburse the core for the cost of the software, upgrades and maintenance.
- Both Windows and Mac systems are fully supported.
- Visit the website for full description and pricing: http://rc.partners.org/core_SoftwareLicenses.
- Contact rcc@partners.org with any questions.

HSCI
HARVARD STEM CELL INSTITUTE

MASSACHUSETTS GENERAL HOSPITAL
CENTER FOR REGENERATIVE MEDICINE

Research Council Meeting
Tools and Technologies
Monday, June 2, 2014

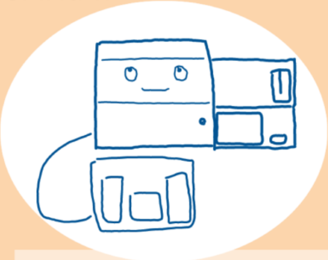
HSCI-CRM Flow Cytometry Core Facility
Presented by Core Director: Hanno Hock, MD, PhD



Visit us in the Simches Research Building, 4th floor, rm 4310
or online at: http://crmflow.partners.org

A2 FACSAria II

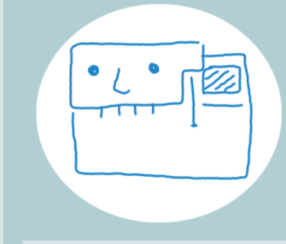
Name: *Lethe*
Occupation: *Sorter*
Lasers: *UV, violet, blue, green, red*
Tell us about yourself:
I love self run users!! If you can sort by yourself, you will sort with me! Plus I'm great at cell cycle analysis.



Anything else?
I don't have a biosafety enclosure, so I can't sort human cells.

Miltenyi AutoMACS

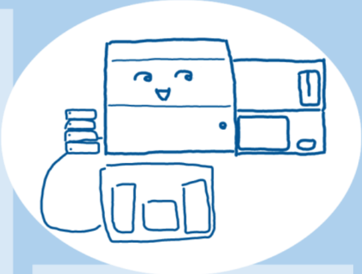
Name *Otto-Max*
Occupation *Magnetic Cell Sorter*
Tell us about yourself
Label your cells with magnetic beads and bring them to me! I can do positive selection or negative selection.



Anything else?
I am great for all cell types no matter how big or fragile.

AL FACSAria II Loaner

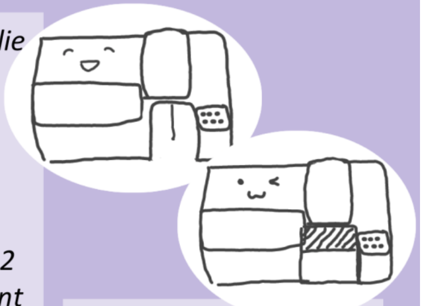
Name *The Loaner*
Occupation *Sorter*
Lasers *UV, violet, blue, yellow-green, red*
Tell us about yourself
I'm great at looking at small particles. Plus, I have a yellow-green laser, perfect for mCherry and other red fluorescent proteins.



Anything else?
I don't have a biosafety enclosure, so I can't sort human cells.

FACSCalibur 1 and FACSCalibur 2

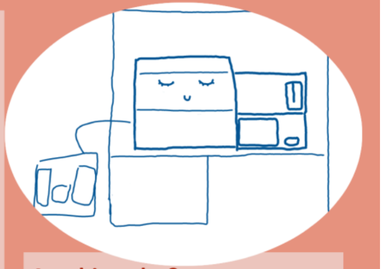
Names *Callie 1 and Callie 2*
Occupation *Analyzer*
Lasers *blue, red*
Tell us about yourself
We are the Calibur Twins! We each have 2 lasers and 4 fluorescent channels. Sign up for self run training to use us!



Anything else?
Callie 1 has a plate reader, called a High Throughput Sampler.

A1 FACSAria IIu with Hood

Name: *Persephone*
Occupation: *Sorter*
Lasers: *UV, violet, blue, green, red*
Tell us about yourself:
I can sort human cell lines and human primary cells! But please test for HIV, HepB, and HepC first.



Anything else?
I'm the first 5-laser Aria ever made. But I can still keep up with the new kids!

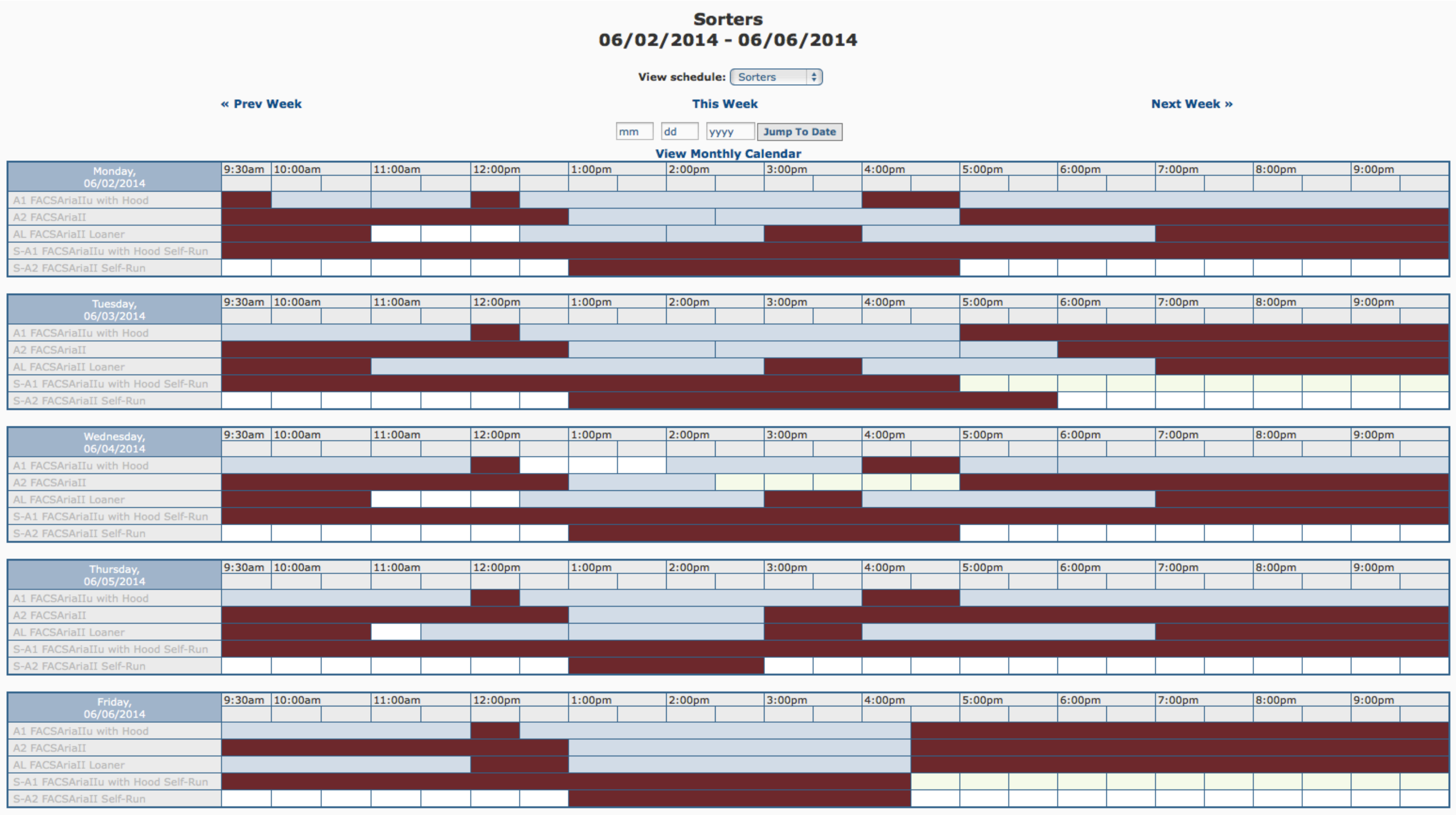
LSR II

Name: *Eurydice*
Occupation: *Analyzer*
Lasers: *UV, violet, blue, red*
Tell us about yourself
I have 4 lasers and 14 fluorescent channels!! Sign up for self run training to use me!

Anything else?
Fix your human cells before analysis. I don't have a biosafety enclosure.

User Biosafety Information

Principal Investigator:



Sorters
06/02/2014 - 06/06/2014

View schedule: Sorters

« Prev Week
This Week
Next Week »

mm dd yyyy Jump To Date

View Monthly Calendar

Monday, 06/02/2014
- A1 FACSAriaIIu with Hood
- A2 FACSAriaII
- AL FACSAriaII Loaner
- S-A1 FACSAriaIIu with Hood Self-Run
- S-A2 FACSAriaII Self-Run

Tuesday, 06/03/2014
- A1 FACSAriaIIu with Hood
- A2 FACSAriaII
- AL FACSAriaII Loaner
- S-A1 FACSAriaIIu with Hood Self-Run
- S-A2 FACSAriaII Self-Run

Wednesday, 06/04/2014
- A1 FACSAriaIIu with Hood
- A2 FACSAriaII
- AL FACSAriaII Loaner
- S-A1 FACSAriaIIu with Hood Self-Run
- S-A2 FACSAriaII Self-Run

Thursday, 06/05/2014
- A1 FACSAriaIIu with Hood
- A2 FACSAriaII
- AL FACSAriaII Loaner
- S-A1 FACSAriaIIu with Hood Self-Run
- S-A2 FACSAriaII Self-Run

Friday, 06/06/2014
- A1 FACSAriaIIu with Hood
- A2 FACSAriaII
- AL FACSAriaII Loaner
- S-A1 FACSAriaIIu with Hood Self-Run
- S-A2 FACSAriaII Self-Run

Online Scheduler available at:
http://crmflow.partners.org

Open Hours and Fees

Maximum available sorting time:

-Assisted hours per week: 99.0
-Non-assisted hours per week: 38.5 during facility open hours

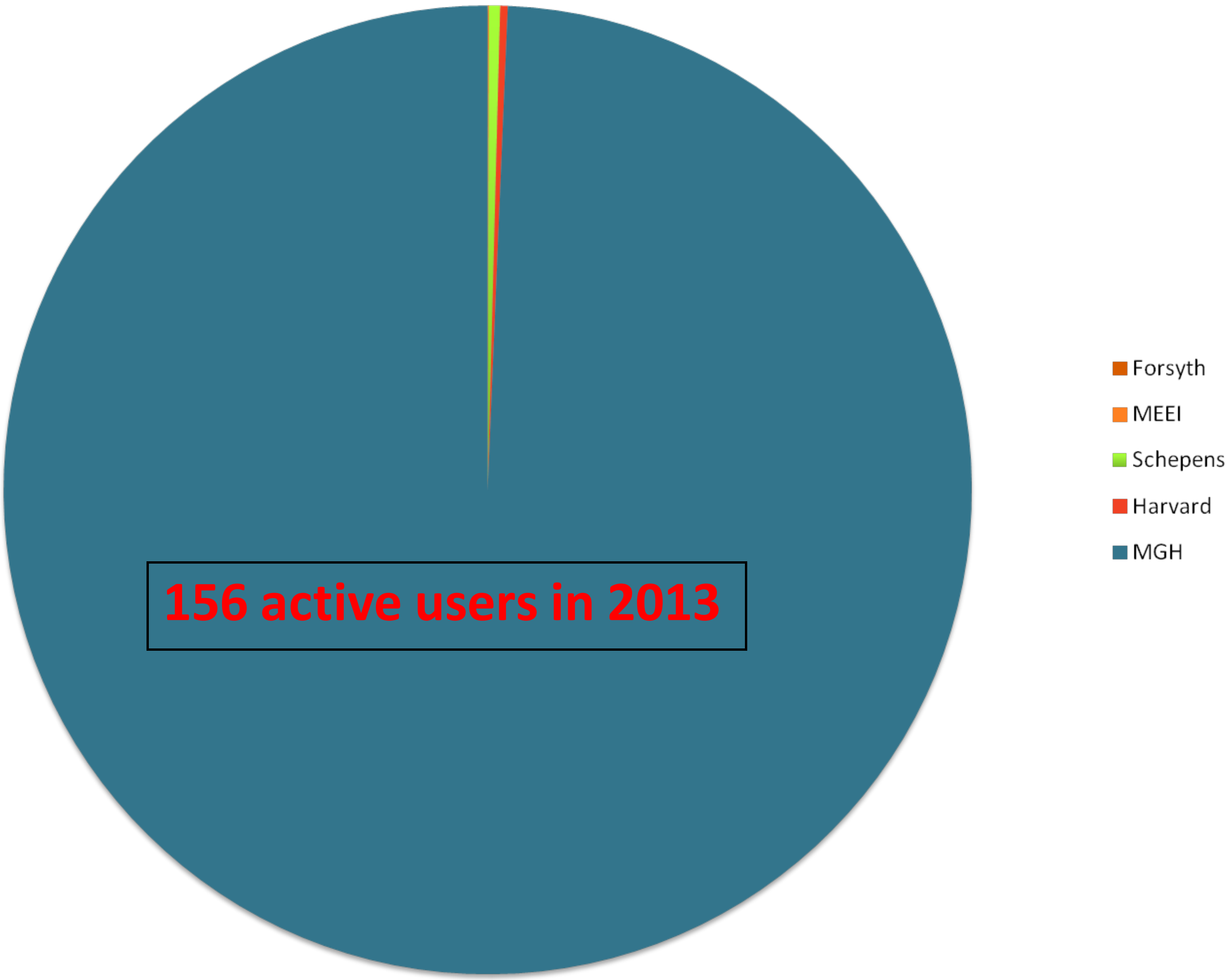
Maximum available cell analysis time:

- Each analyzer is available for self-run use 24 hours a day, 7 days a week
- Core staff are available to assist during open hours

Rates:

	HSCI	MGH	Other Academic	For Profi
Sorting, Assisted	$50.00	$60.00	$171.10	$188.92
Sorting, Self-Run	$35.00	$35.00	$145.70	$160.88
FACSCalibur, Training	$30.00	$48.00	$70.47	$77.81
FACSCalibur, Self-Run	$20.00	$20.00	$46.23	$51.05
LSRII, Training	$50.00	$60.00	$196.25	$216.69
LSRII, Self-Run	$50.00	$60.00	$125.87	$138.99
Assisted Data Analysis	$25.00	$25.00	$52.26	$57.70

2013 - Total Users



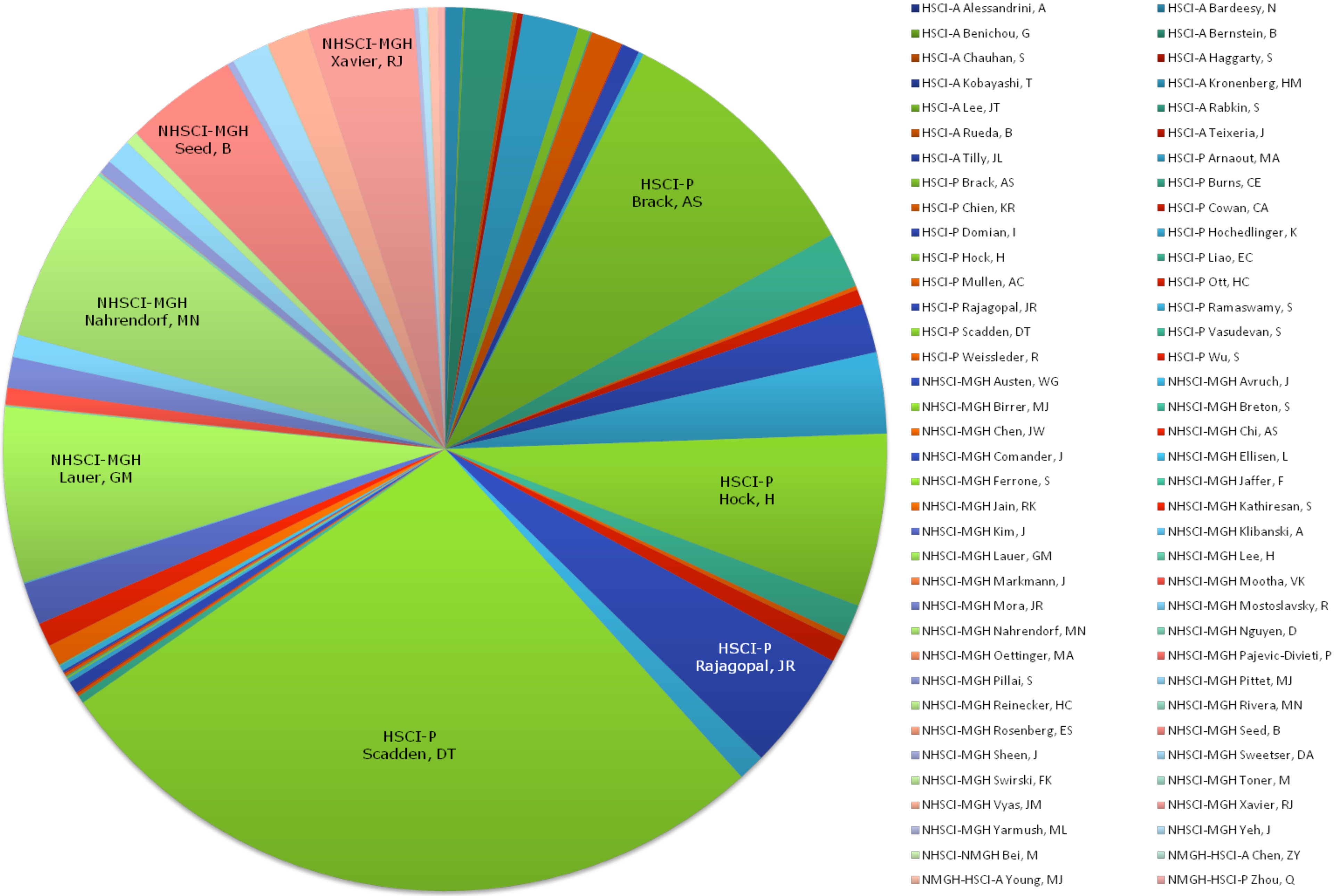
156 active users in 2013

HSCI
HARVARD STEM CELL
INSTITUTE

2013 - Total Users

MASSACHUSETTS
GENERAL HOSPITAL

CENTER FOR
REGENERATIVE MEDICINE



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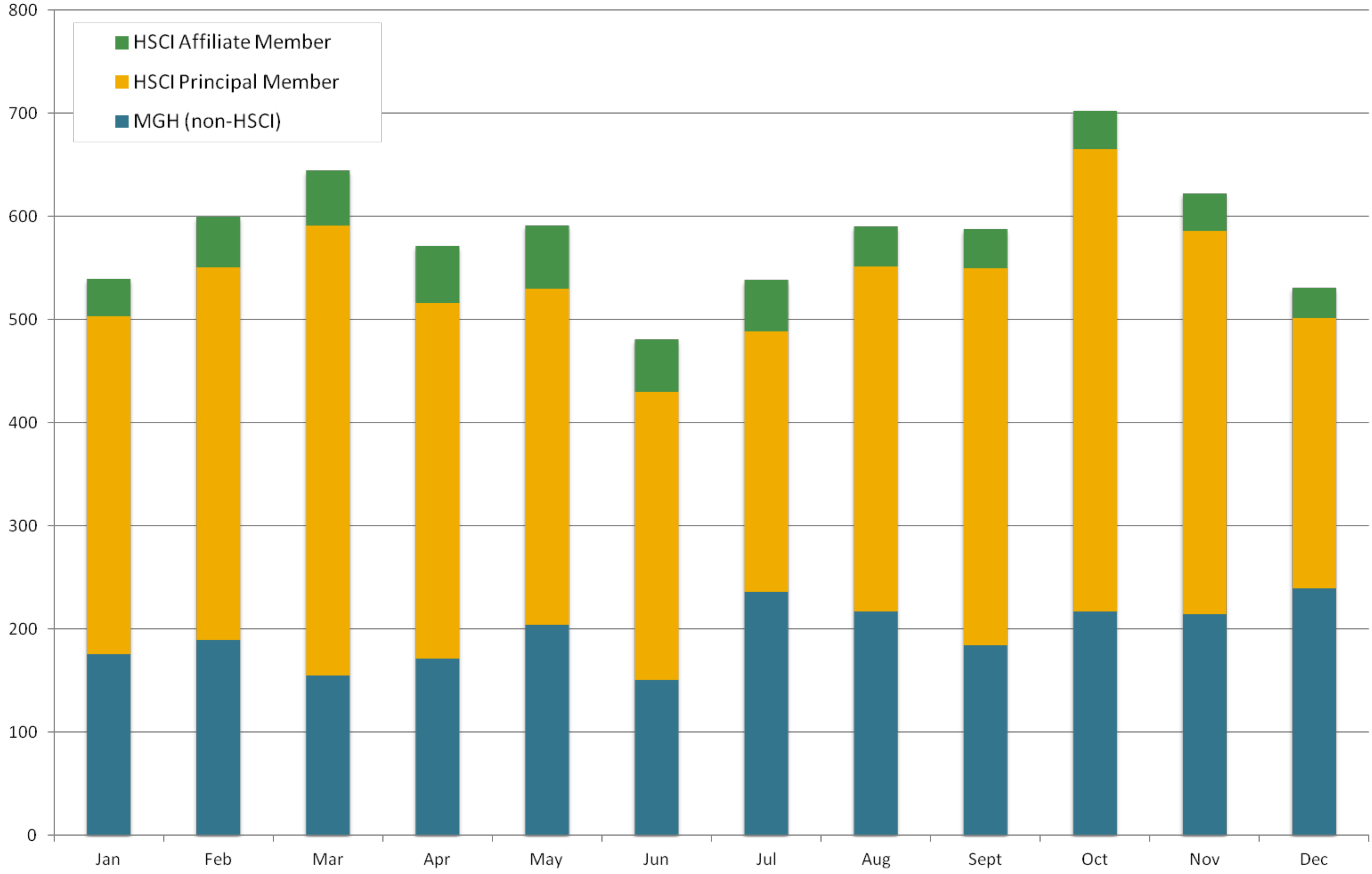
2013 Overall Usage

MASSACHUSETTS GENERAL HOSPITAL
CENTER FOR REGENERATIVE MEDICINE



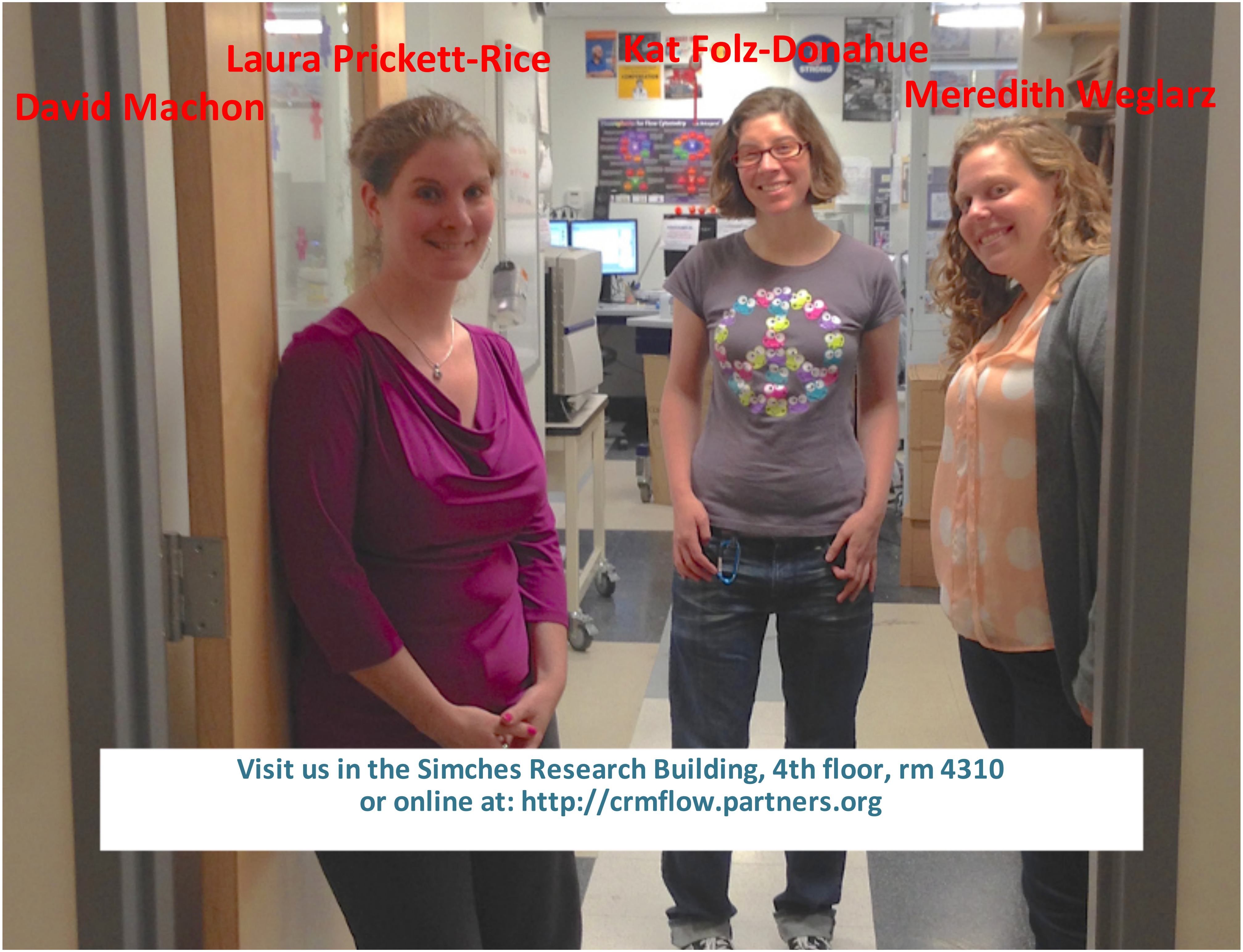
Publications

	2007-2012	2013	Total
Aging	1		1
AmJRespirCellMolBiol		1	1
AmJTransplant	1		1
Blood	5	1	6
CalcifTissueInt	1		1
CancerCell	1		1
CancerLett		*1	1
CancerRes	1		1
Cell	4	*2	5
CellCycle	2		2
CellRes	1	1	2
CellStemCell	12	*1	13
CircRes	2	*1	3
ClinCancerRes	1		1
CurrBiol	1		1
CurrentBiology	1		1
CurrProtocStemCellBiol	1		1
Development		*1	1
DevelopmentalCell	2		2
Gastroenterology	1		1
Gut		1	1
IntegrBiol(Camb)	1		1
Intravital		*1	1

*** Core/Staff Acknowledged**

	2007-2012	2013	Total
JBiolChem	2	1	3
JCellMolMed	1		1
JCellSci	1		1
JClinInvest	1	*1	2
JExpMed	1		1
JVisExp	1	1	2
MolCell		*2	2
MolCellBiol	1		1
NatBiotechnol	2		2
NatCellBiol	1	*1	2
NatGenet	2		2
NatMed	1		1
NatMethods	1		1
Nature	10	*1	11
Neoplasia		*1	1
PLoSOne	3	2	5
ProcNatlAcadSciUSA	3	*1	4
ReprodBiolEndocrinol	1		1
ReprodSci		*2	1
Science	2		2
SciTranslMed	1		1
StemCells	2		2
Transplantation	1		1
Grand Total	**77**	**22**	**99**

Financial support:
HSCI
Center for Regenerative Medicine
Cancer Center
Department of Medicine
ECOR



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Overview of MGH next-generation sequencing core

Ruslan Sadreyev

Director of Bioinformatics
Department of Molecular Biology, MGH
Department of Pathology, MGH, HMS

Next-generation sequencing core and Bioinformatics team at Molecular Biology

My groups:

Next-generation sequencing core

Website: nextgen.mgh.harvard.edu
Email: nextgen@research.mgh.harvard.edu

Bioinformatics team

Website:
molbio.mgh.harvard.edu/department/bioinformatics
Email: bioinfo@molbio.mgh.harvard.edu

Major NGS applications: examples

- Whole Genome Shotgun Sequencing (WGS)
- Targeted/exome sequencing
- RNA-seq
- ChiP-seq
- Metagenomics (targeted region/ whole genome sequencing)
- MANY more

sadreyev@molbio.mgh.harvard.edu

Basic workflow

DNA Prep	Randomly shear DNA + end repair + size select
Library Prep	Append sequencing adapters
Chip Prep	Layout of library on sequencing slide or wells (e.g. C-Bot)
Sequencing	For each library fragment, determine the first N bases at one or both ends of the fragment
Raw Analysis	Image processing + base calling -> bases and quality (FASTQ)

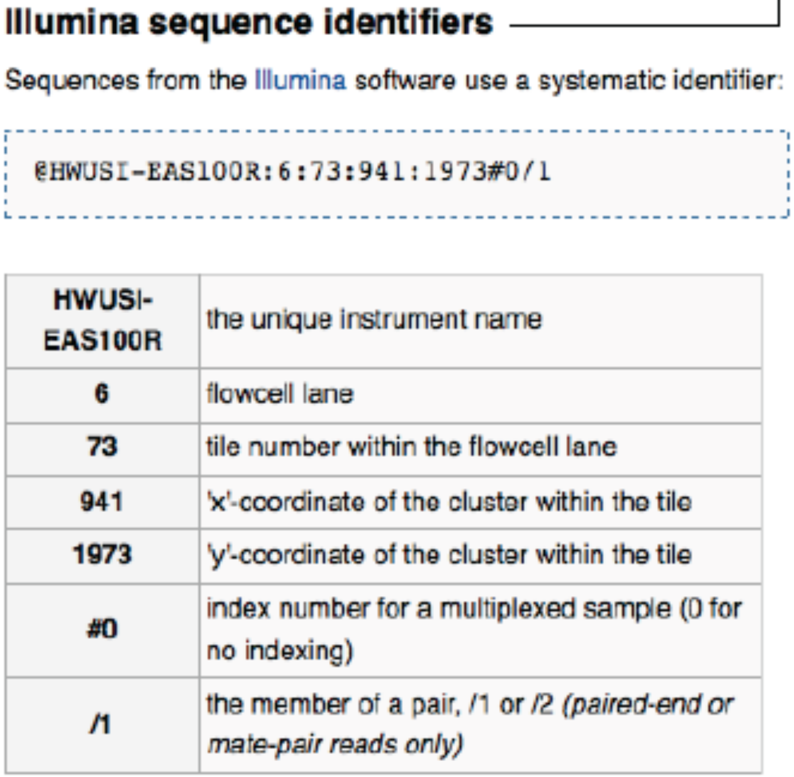
From: Thomas Keane

FASTQ format for NGS sequences

```
@HWUSI-EAS582_157:6:1:1:1501/1
NCACAGACACACACGAACACACAAAGACATGCCCATATGAAGAT
+
%.7786867:778556858746575058873/347777476035
@HWUSI-EAS582_157:6:1:1:1606/1
NCTGGCACCTTGATTTTGGACTTCCCAGCCTCCAGAACTGTGAG
+
%194898888879898836689888864899878889888588
@HWUSI-EAS582_157:6:1:1:453/1
NCTGCTTGCACCCCTGAAGTCACTGATCACATTTCAGGGTCACC
+
%/86899898888886766888898664478898841348885
@HWUSI-EAS582_157:6:1:1:1844/1
NGATTGACATTGGCAAAGAGGACAACTGATTGCAAACTTCACAC
+
%-7;:::::;86499;75574586::635:62687666887879
@HWUSI-EAS582_157:6:1:1:1707/1
NAGGCTCAGGCGCACGGCCTACATCGTCGCTGTCGGCCAAGGGG
+
```

"Read" (sequence)

Quality scores (phred-33)



Illumina sequence identifiers

Sequences from the Illumina software use a systematic identifier:

```
@HWUSI-EAS100R:6:73:941:1973#0/1
```

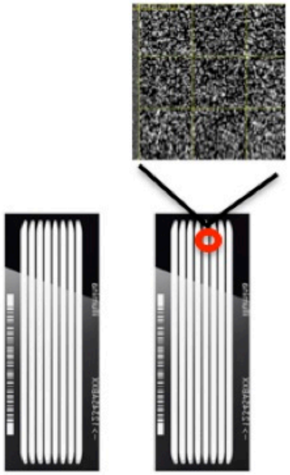
HWUSI-EAS100R	the unique instrument name
6	flowcell lane
73	tile number within the flowcell lane
941	'x'-coordinate of the cluster within the tile
1973	'y'-coordinate of the cluster within the tile
#0	index number for a multiplexed sample (0 for no indexing)
/1	the member of a pair, /1 or /2 *(paired-end or mate-pair reads only)*

http://en.wikipedia.org/wiki/FASTQ_format

Large-scale Illumina instruments: HiSeq2000, HiSeq2500

Illumina HiSeq2000

c-Bot
(automated cluster generation)



Cluster density
750-800K/mm^2

HiSeq Flow Cells

High-output mode: 8 lanes, 150-200 M reads per lane
(runs for a few days)

Rapid mode: 2 lanes, 100-150 M reads per lane
(runs for a few hours)

From http://www.qbi.uq.edu.au

Illumina MiSeq: desktop device

- Fast
- Flexible (can do longer reads, up to 500 bp)
- ~10x fewer reads than HiSeq
- Cheaper per run (but not per read)

Applications:

- Amplicon sequencing
- QC before large-scale runs
- Bacterial genomes
- …..

Our current output: 1 lane, 10-15 M reads per lane

www.illumina.com

Bioinformatics team provides creative collaborative data analysis

Four staff (after postdoc) bioinformaticians analyze data in different contexts to produce <u>hypotheses</u>

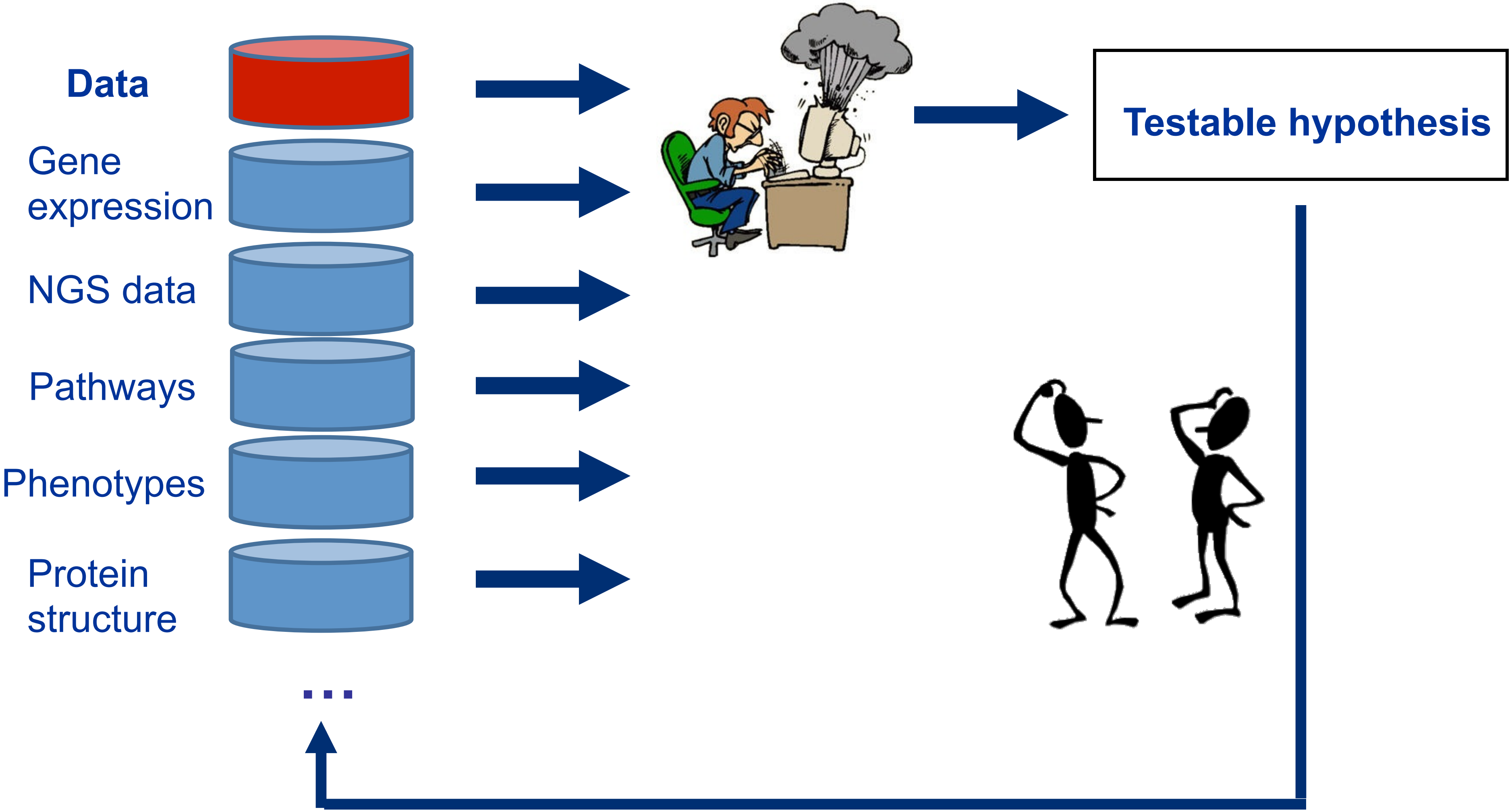
Less productive collaboration:

Data

Spreadsheet

Bioinformatics team provides creative collaborative data analysis

More productive collaboration:



Data

Gene expression

NGS data

Pathways

Phenotypes

Protein structure

…

Testable hypothesis

Next-generation sequencing and Bioinformatics cores at Molecular Biology

My groups:

Next-generation sequencing core
Website: nextgen.mgh.harvard.edu
Email: nextgen@research.mgh.harvard.edu

Bring your libraries!

Bioinformatics team
Website:
molbio.mgh.harvard.edu/department/bioinformatics
Email: bioinfo@molbio.mgh.harvard.edu

Bring your data!