

Integrating of in-house and commercial LIMS databases: 4D and Finch

Jan Kieleczawa

Wyeth Research/ BT

Cambridge

ABRF Satellite Meeting, February 11

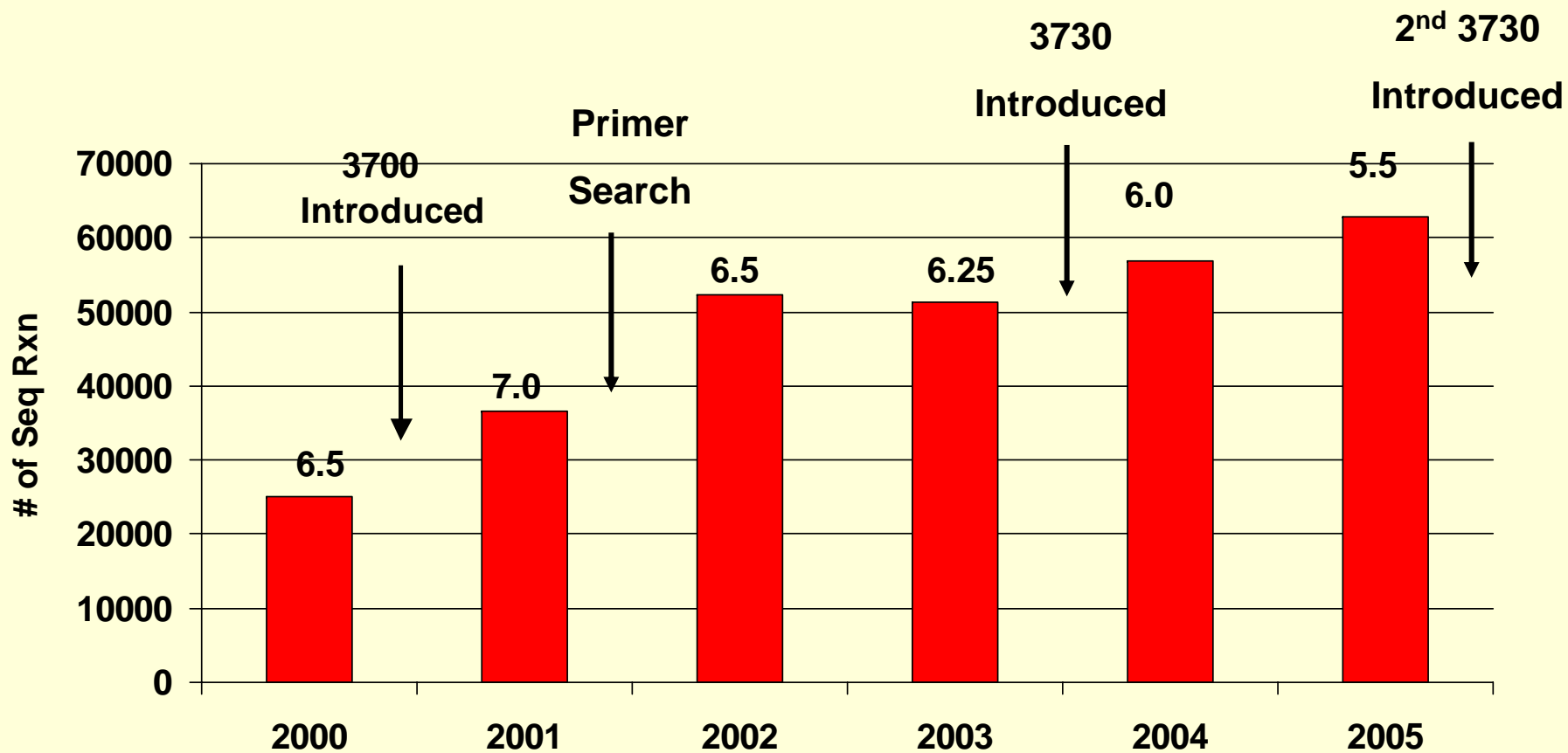
Long Beach, CA, 2006

Wyeth
Research

Current Status

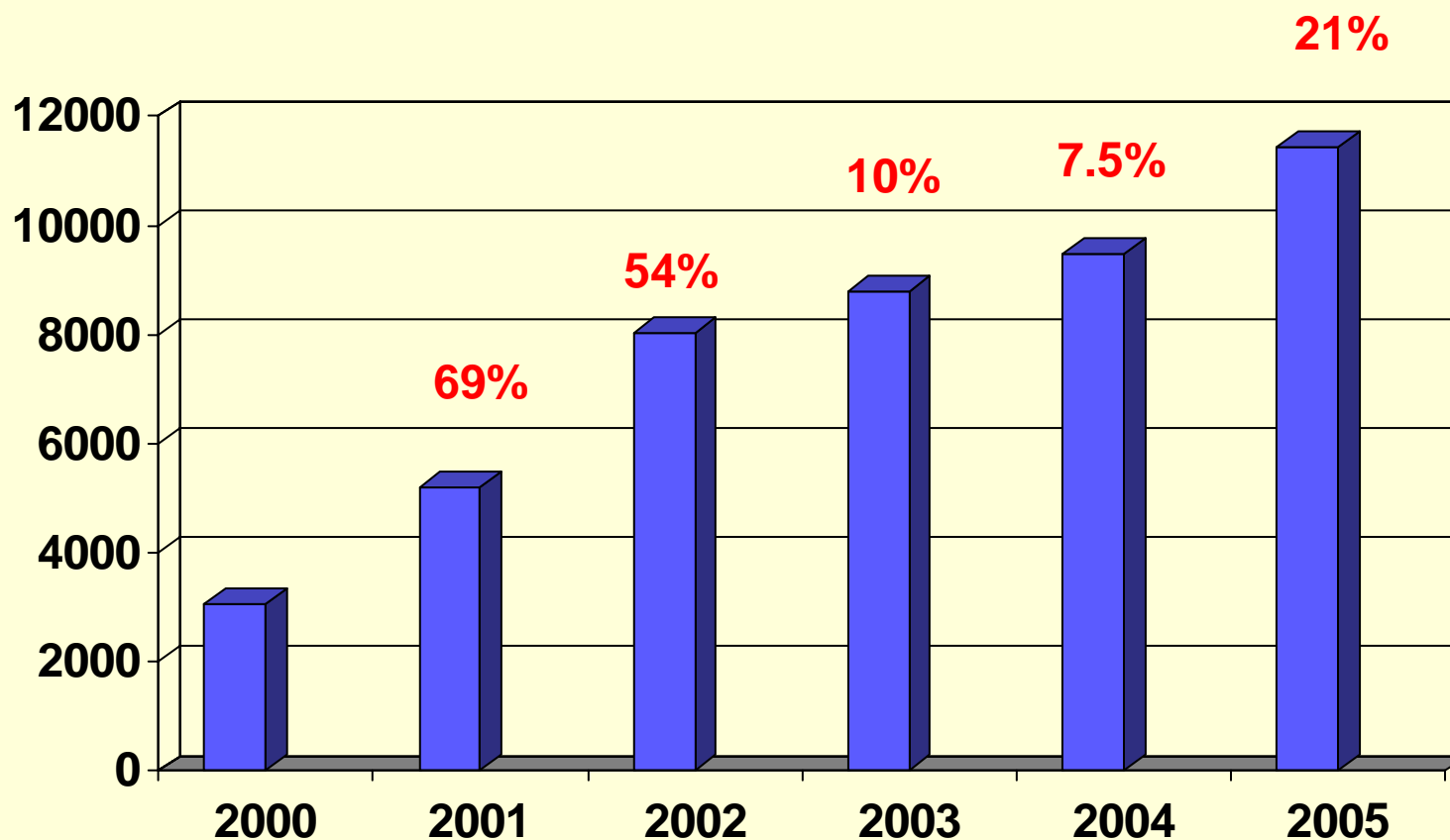
- **6 FTEs-all finishers**
- **ABI Sequencers:**
 - ▶ 2 ABI3730
 - ▶ 1 ABI3130xl
 - ▶ 3 ABI3100-not used currently
- **Robots:**
 - ▶ Beckman's NX-for magnetic cleanup
 - ▶ Qiagen's BioRobot 8000-DNA preps
- **Instruments needed:**
 - ▶ REMP-like storage system
 - ▶ Robot for assembly of sequencing reactions

Cumulative Sequencing Demand: 2000-2005



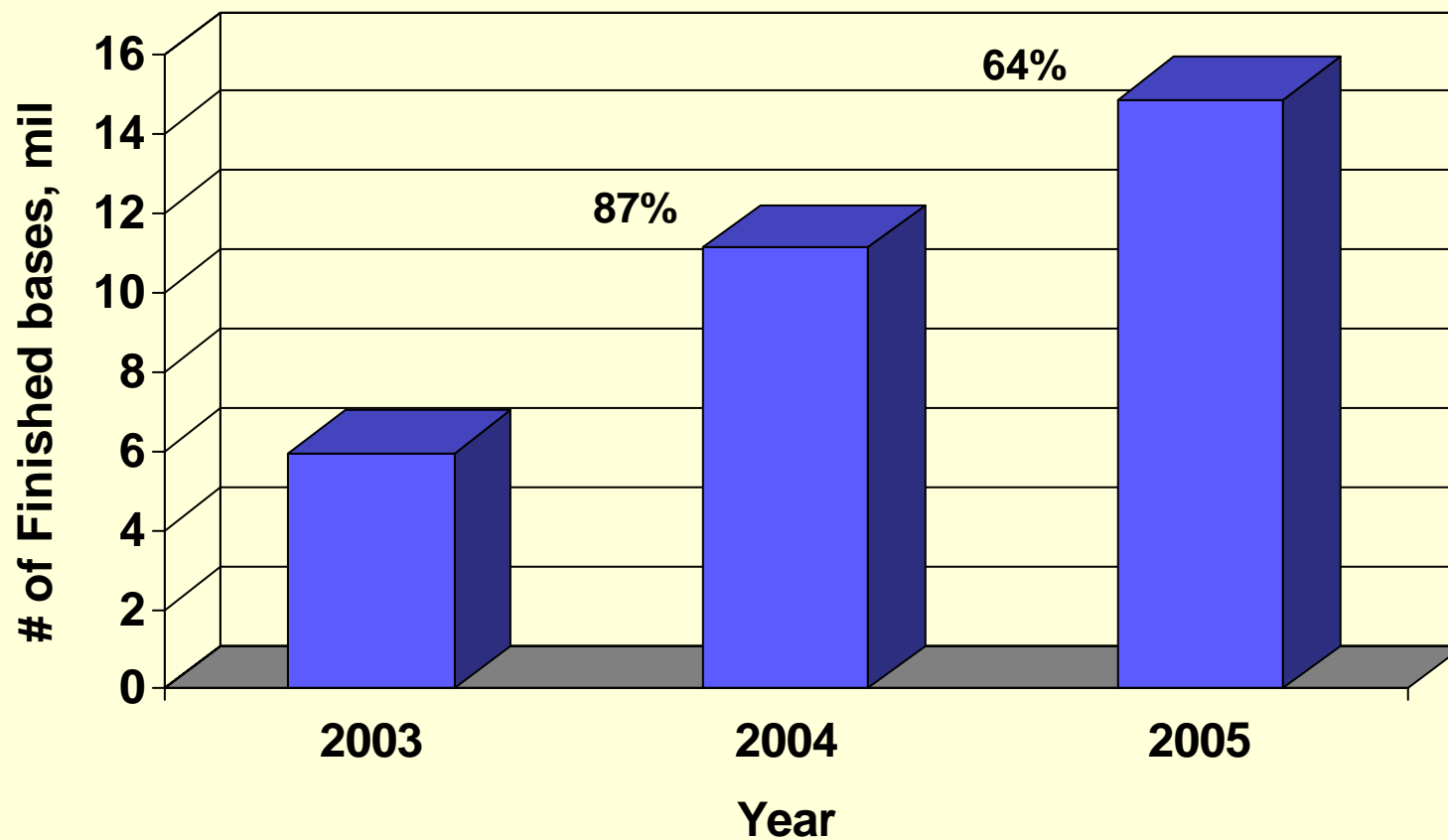
Number above the bars represent number of staff at the time

Average number of reactions per lab member

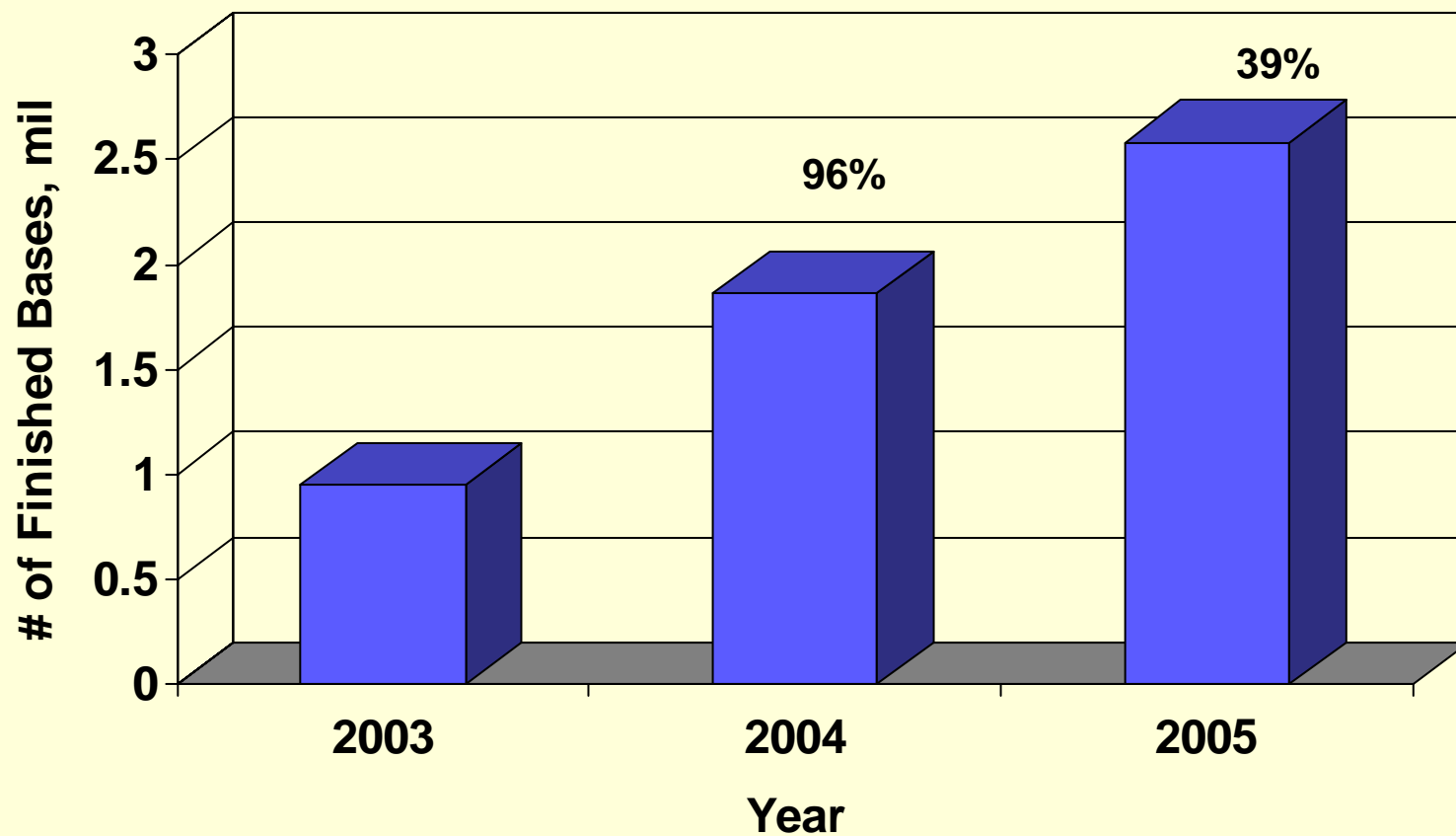


% numbers over bars=Increase over the previous year

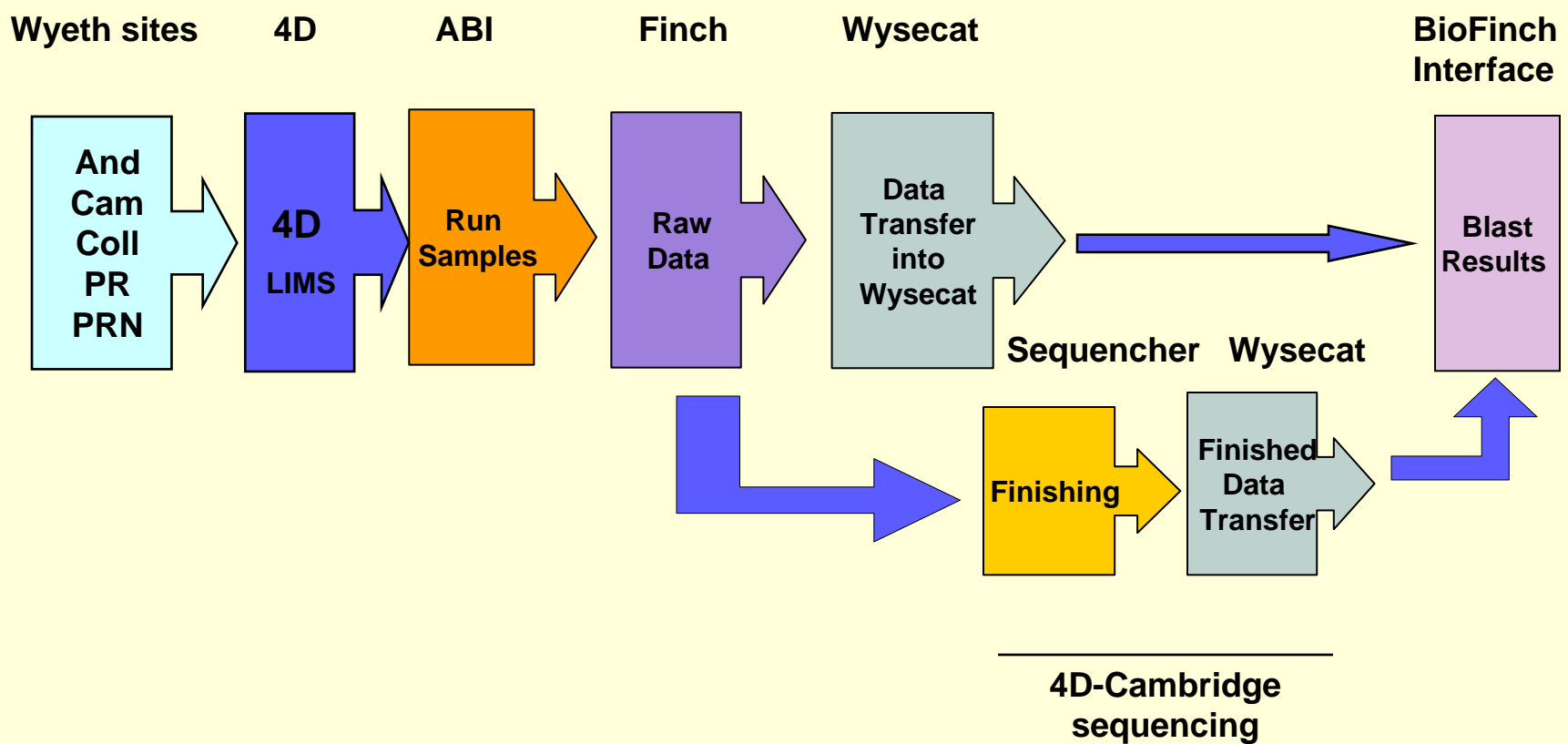
Number of Finished Bases: 2003-2005



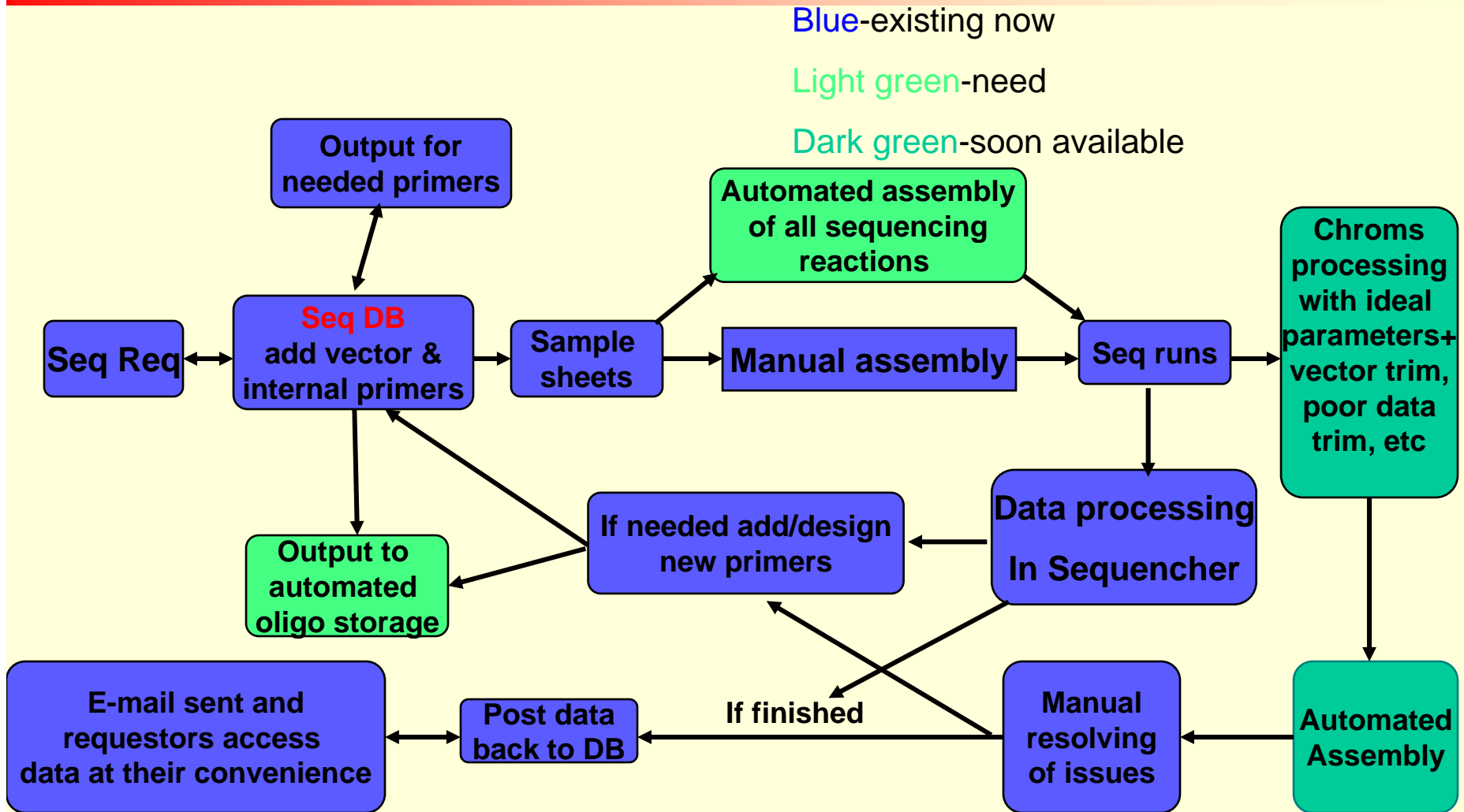
Number of Finished Bases per Lab Member



4D/Finch LIMS/BioFinch Pipeline at Wyeth



Workflow in the Wyeth finishing DNA sequencing lab: samples are shipped or delivered to Cambridge from all 5 locations



Request screen in 4D

4D Client
 File Edit Path Special Help

First Prev Next Last Find Print Save Cancel

Entry for Cambridge * = page has data Status: PND 01/11/2006

Requestor: E-mail Notes Seq Input
 New Request - Scientist: JanK TUBE Format Results: BLAST_NONE Result Type: Finish

Request #: Assigned To: Jan
 Super Group: Biological Technologies Seq. Project:
 Group: Biological Technologies Date Req'd: 01/12/06
 Wyeth Project: Biological Technologies Discov Notebook: 0
 Email: jkieleczawa@wyeth.com Page: 0
 Extension: 531 8318

Comments: This is just a test JK

Tube Plate by Col Plate by Row

Clones New Clone Add Clone Delete Clone Get Chromatograms

Clone #	* Clone Name	Prep Meth	* Conc. (ug/ul)	Conc. Obtained By	Insert (kb)	Type	Vector	5' site	3' site
_x	testpGem3zf-001	Qiagen Q-tips	0.25	Agarose Gel+EtBr	1.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-002	Qiagen Q-tips	0.25	Agarose Gel+EtBr	1.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-003	Qiagen Q-tips	0.25	Agarose Gel+EtBr	1.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-004	Qiagen Q-tips	0.25	Agarose Gel+EtBr	1.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-005	Qiagen Q-tips	0.25	Agarose Gel+EtBr	1.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-006	Qiagen Q-tips	0.25	Agarose Gel+EtBr	3	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>
_x	testpGem3zf-007	Qiagen Q-tips	0.25	Agarose Gel+EtBr	3.5	<input type="checkbox"/>	pHTOP	<input type="checkbox"/>	<input type="checkbox"/>

0.1
0.25
0.5
0.75
1
1.5
2
2.5
3
3.5
4
4.5
5
>5

data entry/edit a value
 * shift-double click in cell
 ** click on cell, click title

Request screen on the lab side

4D Client

Edit Path Special Help

First Prev Next Last Find Print Save Cancel

Entry for 8913

Lab User: **Collegeville** Status: BLD 01/12/2006

Request #: 8913 TUBE Format

Super Group: Women Health & Bone Assigned To: Jan All

Group: Women's Health and Musculos Seq. Project: 8913-Ror1EC-billiardj

Wyeth Project: Ror2 Date Recvd: 1/11/2006

Scientist: billiardj Date Req: 01/16/06

Email: billiaj@wyeth.com DNA Recvd: 01/12/06

Extension: 865 5-8030 Notebook: 0

Page: 0

Xtra Oligos Get Chromatograms Get CAF file

Clones New Clone Add Oligo Delete Oligo Order New Split Dilute Action... Expand

Results: BLAST_NONE Type: Finish

Comments:

Process Steps: data entry/edit a value
* shift-double click in cell
** click on cell, click title

Clone #	Clone Name	* Oligo #	Status	Coverage	Vector	5' site	3' site	DNA Type	* Conc. [ug/ul]	Insert (kb)	Conc. Obtained By	Priority
8913_1	Ror1EC-001	122149	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
		116086	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
		136584	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
		20208	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
		20931	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
		20234	RUN	Full Length [ds]	pENTR-1A	Hind III	Xba I	Construct	0.2	1	Spectro-UX	High
8913_2	Ror1EC-002	122149	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High
		116086	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High
		136584	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High
		20208	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High
		20931	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High
		20234	RUN	Full Length [ds]	pET-15b	EcoR I	BamH	Construct	0.2	1	Spectro-UX	High

Examples of various features/reports in 4D

The screenshot displays the 4D software interface with several key components:

- Special Menu:** A vertical list of options including 'Users & Groups...', 'List Editor...', 'Connection Values...', 'Load Oligo DB Lists...', 'MAP File Server to PC Volume', 'Update Wyeth Projects', 'Import Wyeth Projects', 'Edit Wyeth Projects', 'Terminate Wyeth Projects', 'Primer Inventory Maintenance', 'Sample Sheet Maintenance', 'Save Lists...', 'Load Lists...', 'Fix Gremlins...', 'Designate Mac Server', 'Test Connecting to Oracle DB', 'Test Connecting to Wysecat host', 'Fix CE Run Xfr to Finch...', 'Control CE Run Xfr to Finch', 'Fix CE Run Chromat IDs', 'Start Finch ChronJob', 'Start WyseCat ChronJob', 'Fix Run Xfr to E1a on FinchDev', 'Count Scientist Reactions', 'Sum Bases in Period's Results', 'Clone Job Duration Report', and 'Manage Maintenance Shutdown'.
- Report Menu:** A sub-menu with options: 'Labels...', 'Staff Effort for Period', 'Weekly Finishing & Lab', and 'Custom...'.
- Special Menu (Secondary):** A sub-menu with options: 'Send Requests', 'Finished Clone Results', 'Make Requests Complete', 'Make Requests Incomplete', 'ReSend EMail Notification', and 'Oligo Designer'.
- Main Window:** Contains a table with columns: Plate Loc, Clone Name, Oligo #, Special Instruct, Inst File, DNA ul, and O. The table lists various clones and their associated reagents and DNA amounts.
- Change Special Dialog:** A dialog box for selecting 'Special Instructions' from a dropdown menu. The menu is open, showing options like 'Betaine', 'Reagent A', 'Reagent B', 'Reagent C', 'Reagent F', 'Reagent G', 'DMSO', 'x DNA', 'dGTP V3.0', and 'dGTP3.0 & Rea A'. The 'DNA Factor' is set to 1.
- Control Panel:** Includes buttons for 'Change to GEL run', 'Assign to Group', 'Create File', 'Notebook Report', 'Comment', 'Big Dye 3', '# Lanes Occupied: 8', 'Duplicate Reaction', 'Apply Special', 'Clear and Move Up', 'Create Control', 'Insert Space', and 'Expand'.

Plate Loc	Clone Name	Oligo #	Special Instruct	Inst File	DNA ul	O
A01	pENTR221_furin	118102	Reagent A	<input checked="" type="checkbox"/>	0.5	
B01	pENTR221_furin	137364	Reagent A	<input checked="" type="checkbox"/>	0.5	
C01	119_mmp_02	137511		<input checked="" type="checkbox"/>	0.8	
D01	119_mmp_02	137512		<input checked="" type="checkbox"/>	0.8	
E01	119_mmp_02	137513		<input checked="" type="checkbox"/>	0.8	
F01	119_mmp_02	137514		<input checked="" type="checkbox"/>	0.8	
G01	HAGPAT6	142287	Reagent C	<input checked="" type="checkbox"/>	0.2	
H01	EmGFP_S2_miRPCR	105911		<input checked="" type="checkbox"/>	0.1	
A02				<input checked="" type="checkbox"/>		

Find Primers, Examine Repeats and GC Modules

The following thresholds will be used in the analysis. Please confirm or edit them.

Repeats	10	Palindromes	8
Dinucleotides	12	Trinucleotides	7
Homopolymers	10	Dinucleotides - non-repeats	40

Cancel OK

Region	Dir	%GC
1	-->	57
201	-->	92
401	-->	90
601	-->	78

Sequence	Length	GC%	Dir	Check
47527	100	75	92 -->	<input type="checkbox"/>
18110	0	75	92 -->	<input type="checkbox"/>
14909	0	75	92 -->	<input type="checkbox"/>
37545	100	76	92 -->	<input type="checkbox"/>
42141	100	103	122 -->	<input type="checkbox"/>
31642	100	103	122 -->	<input type="checkbox"/>
49247	100	104	120 -->	<input type="checkbox"/>
139659	6	594	611 -->	<input type="checkbox"/>
140705	7	76	58 <--	<input type="checkbox"/>
123731	11	79	62 <--	<input type="checkbox"/>
117960	9	80	63 <--	<input type="checkbox"/>
25887	0	87	70 <--	<input type="checkbox"/>
107524	13	100	84 <--	<input type="checkbox"/>
139661	12	725	706 <--	<input type="checkbox"/>

Lookup Oligo # Print Sequencer Files

Primer Design Criteria: Limits:

Lower Tm °C	54.0	54°C Min	Matches at 3' End	<	3
Upper Tm °C	70.0		Hairpin separation	<	7
GC% Range	55 +/-	10	Base Runs	<	4
Stability (kcal/mole)	>	1.3	Adjacent Homol Bases	<	7
			Repeats: Di-nucleotide pairs	<	3

Pre-Select All Add Actions

Restore Defaults Examine Repeats

& Schedule Cancel OK

Don Koffman, Bharadh Lakshmanan, Aaron Kitzmiller

Examine Repeats Module

1	Type	Length	Count	Positions	Sequence
2	Direct	66	2	171,174	GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCA
3	Direct	49	2	1369, 1372	GGCGGCGGCG GCGGCGGCGG CGGCGGCGGC GCGGCGGCG GCGGCGGCG
4	Direct	19	18	#####	GCAGCAGCAG CAGCAGCAG
5	Direct	15	2	27,612,764	CACCACCACC ACCAC
6	Direct	13	2	253,612	AGGCAGCAGC AGC
7	Direct	12	2	19,402,757	CCAGCACCAC CA
8	Direct	11	2	3,471,314	CTTCACAGCC G
17	Invert	21	2	161,162	TGCTGCTGCT GCAGCAGCAG C
18	Invert	13	3	134,927,632,766	GTGGTGGTGG TGG
19	Invert	13	2	160,228	TTGCTGCTGC TGC
20	Invert	12	4	1,349,276,127,642,760	GTGGTGGTGG TG
21	Invert	12	21	#####	GCAGCAGCAG CA
22	Invert	11	2	24,072,408	CAGGAATTCC T
23	Invert	11	2	16,981,969	AGCTTCTGGG T
24	Invert	11	25	#####	GCTGCTGCTG C
25	Invert	11	2	7,452,750	CTGGGTGTGG A
32	Palind	22	2	161,182	TGCTGCTGCT GCAGCAGCAG CA
33	Palind	20	2	162,181	GCTGCTGCTG CAGCAGCAGC
34	Palind	18	2	163,180	CTGCTGCTGC AGCAGCAG
35	Palind	16	2	164,179	TGCTGCTGCA GCAGCA
36	Palind	14	2	165,178	GCTGCTGCAG CAGC
37	Palind	12	2	24,072,418	CAGGAATTCC TG
38	Palind	12	2	166,177	CTGCTGCAGC AG
48	Trinucleotide (TN)	69	1	171	GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCA
49	Trinucleotide (TN)	66	1	173	AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGC
50	Trinucleotide (TN)	66	1	172	CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAG
51	Trinucleotide (TN)	51	1	1369	GGCGGCGGCG GCGGCGGCGG CGGCGGCGGC GCGGCGGCG GCGGCGGCGG C
52	Trinucleotide (TN)	51	1	1370	GCGGCGGCGG CGGCGGCGGC GCGGCGGCG GCGGCGGCGG CGGCGGCGGC G
53	Trinucleotide (TN)	48	1	1371	CGGCGGCGGC GCGGCGGCG GCGGCGGCG CGGCGGCGGC GCGGCGG
54	Non-repeat DN	52	1	1369	GCGGCGGCGG GCGGCGGCGG CGGCGGCGGC GCGGCGGCG GCGGCGGCGG CG

Integrated E-mail module

Entry for 8874

Lab User: **Collegeville** Status: **CMP** 01/12/2006

ViewResults WEB Interim Save Clear Apply to All

Clone	WAN#	Completed	Status Comment
PSPDE11A4D1		01/12/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PSPDE11A4D2		01/12/06	Fully ds between indicated cloning sites. 4 muts. Mostly on both ends
PSPDE11A4D4		01/12/06	Fully ds between indicated cloning sites. 6 muts. Mostly on both ends
PSPDE11A4D5		01/12/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PSPDE11A4D6		01/12/06	Incomplete coverage - will update. 4 mutations
PSPDE11A4D7		01/12/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PCPDE11A4D1	WAN03425M.1:WAR	01/10/06	Incomplete coverage - will update
PCPDE11A4D2	WAN03425N.1:WAR	01/10/06	Incomplete coverage - will update

Email Type: **Partially Completed** Comment for Biweekly Report: **All done. PCPD clones may need new vector.**

Body of E-mail

Please find some clones' results for Request # 8874 in the Results module (on the Files float Palette) in the DNA Sequencing 4D database.

Hi Dharmesh,

All end reads are done. They all look the same to me. Region about base 50-60 is of lower qual to the purification. It will be corrected when using the other strand.

Jan

Append to E-mail: **Hi Dharmesh,**
All end reads are done. They all look the same to me. Region about base 50-60 is of lower quality due to the purification. It will be corrected when using the other strand.

Sequencer Conclusions for Results

OK

- Data delayed - ABI or other technical problems
- Difficult template DNA - requires special conditions
- DNA concentration is incorrect
- Edited end reads
- Fully ds between indicated cloning sites or region
- Fully ss between indicated cloning site or region
- Incomplete coverage - will update
- Insert not in the indicated position
- Long poly A tail
- Long poly T tail
- Multiple mutations compared to refseq
- Need more DNA
- No insert
- No mutation compared to refseq
- One mutation compared to refseq
- Please reply if more info is needed
- Please reply if more sequencing is needed
- Poor quality or not enough DNA, need another prep
- Questionable vector info or vector primers did not work
- Single stranded region - good quality reads
- Traces contain high background
- Sequence does not match refseq
- Sequence matches refseq but cannot see cloning sites
- Sequence matches refseq but is in reverse direction
- Wrong orientation

Email received by a scientist: Clicking on WAN# takes scientist to blasted data

From: <jkieleczawa@wyeth.com> 1/10/20
To: <pateld@wyeth.com>
CC: <jkieleczawa@wyeth.com>
Subject: Some DNA Sequencing results for Request # 8874 ready!

Please find some clones' results for Request # 8874 in the Results module (on the Files floating Palette) in the DNA Sequencing 4D database.

Hi Dharmesh, All end reads are done. They all look the same to me. Region about base 50-60 is of lower quality due to the purification. It will be corrected when using the other strand. Jan Hi agian, PSPDA4 clones are doen (# 6 has a gap-one primer was short-can repeat). For PCPD clones most (I used 4 internal) primers worked and it assembles to refseq. You may consider to take another batch (or from soeone else) this pCDNA3.1 vector as it may be not right one. PS It looks that we have a not perfect batch of Edge plates and I see some poorer quality data., but you have good coverage so it may be OK. We are getting new batch of plates. I am completing this req. Please let me know if you want me to do anythink else. Jan



CLONE	WAN#	COMPLETED	STATUS COMMENT
PSPDE11A4D1	WAN03425G.1:WAR	01/10/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PSPDE11A4D2	WAN03425H.1:WAR	01/10/06	Fully ds between indicated cloning sites. 4 muts. Mostly on both ends
PSPDE11A4D4	WAN03425I.1:WAR	01/10/06	Fully ds between indicated cloning sites. 6 muts. Mostly on both ends
PSPDE11A4D5	WAN03425J.1:WAR	01/10/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PSPDE11A4D6	WAN03425K.1:WAR	01/10/06	Incomplete coverage - will update. 4 mutations
PSPDE11A4D7	WAN03425L.1:WAR	01/10/06	Fully ds between indicated cloning sites. 5 muts. Mostly on both ends
PCPDE11A4D1	WAN03425M.1:WAR	01/10/06	Incomplete coverage - will update
PCPDE11A4D2	WAN03425N.1:WAR	01/10/06	Incomplete coverage - will update

Click the Results button to open the Results list window. Use the Search menu and the Search menu item For Request Number... to find your results records for the finished clones or scroll through the list. Your results records will contain: 1-

Example of a report for a specific TA

Project Effort

Wyeth Project | Super Group | Therapeutic Area | Convert Hours to % Effort

Date From: 12/01/05 | Belonging To: ALL | Req Type: ALL

Date to: 12/31/05 | TA: ALL | Search

	Raw Data	Finished	SS Trace	Total
# Reactions	1715	4284	404	6403
Hours	120	639	32	791

Staff	Therapeutic Area	Hours	Type
ALL	Biological Technologies	215.5	ALL
ALL	Biopharma	1.7	ALL
ALL	Cardiovascular and Metabolic Diseases	135.1	ALL
ALL	Chemical and Screening Sciences	17.4	ALL
ALL	Inflammation	155.2	ALL
ALL	Neuroscience	198.3	ALL
ALL	Oncology	17.7	ALL
ALL	Women's Health and Musculoskeletal Biolo	43.8	ALL
ALL	Women's Health and Musculoskeletal Biology	6.8	ALL

Neuroscience Details



Requestor	SuperGroup	Project	Reactions	Hours
atkinsp2	Neuroscience	SHh Agonist	64	9.5
A/Widom	Biological Technologies	AAB-001 BU	62	4.3
bardj	Neuroscience	Neurodegeneration	168	25.0
benderc3	Neuroscience	Depression & Anxiety	16	2.3
chandap	Neuroscience	NAV1.8 Channel Blocker	128	19.1
chengk	Neuroscience	NEUROSCIENCE RESEARCH	50	7.4
huy1	Neuroscience	Gamma Secretase Inhibitor BU(Oral)	6	0.8
jiangl	Neuroscience	Schizophrenia & Bipolar	128	19.1

Export File | Print | Help | Done

Example of lab report for individual sequencer

1	Weekly Report for Finishing & Lab										
2	Finishing Work: Jan Kieleczawa										
3	Date: 12/01/05 to 12/31/05										
4	Requestor	Req#	Req Type	# of cln	Act Cln	Sizes	Cov	C	D-to-C/A	A	Comments
5	AWidom	8865	Raw Data	26	0	0.5	5' End Read [s	1	3		
6	BapatA	8850	Finish	16	0	0.5	Full Length [ds	1	1		Compound 116073 failed on two and was short on 3 others. 3'SNP
8	camardr	8802	Finish	2	0	1	Full Length [ds	1	2		Fully ds between indicated cloning sites. 7 muts
9	DQian	8717	Raw Data	96	0	0.5	Full Length [ds	1	1		Needed just raw data. All worked
10	DXUAN	8863	Finish	4	0	1.5	Full Length [ds	1	3		Only 221 clone Ok. Rest NG
19	fengg	8814	Finish	8	0	0.75	Full Length [ds	1	2		All fully ds.
20	fengg	8833	Finish	16	0	2	Full Length [ds	1	3		All done
21	haltlib	8740	Finish	4	0	0.75 to 1.5	Full Length [ds	1	3		Incomplete coverage. Strange clones
24	haow	8683	Finish	1	0	2.5	Full Length [ds	1	2		Lots muts. Done
25	hlaken	8848	Finish	2	0	2.5	Full Length [ds	1	1		OK, fully ds-Bill edited
31	jansoj	8640	Raw Data	17	0	1.5 to >5	Other	1	2		It was a FINISHED req but I had to switch to Raw-Error
32	jansoj	8797	Finish	1	0	1.5	Full Length [ss	1	4		Quite poor
33	jansoj	8817	Finish	10	0	0.5 to 1.5	Full Length [ds	1	2		All fine
35	keeneyd	8779	Finish	2	0	1	Full Length [ds	1	2		OK. No mutations compared to refseq
36	kimberm	8722	Finish	2	0	0.25	Other	1	2		One clone Ok one not
38	KMarquett	8864	Finish	6	0	0.5	Full Length [ds	1	1		All done. One clone does not have muts. Rest >10 or 1-6 deletion
39	kmmccartl	8739	Finish	2	0	2.5	Full Length [ds	1	2		Fully ds between indicated cloning sites or region
40	liuyb	8830	Finish	8	0	1	Full Length [ds	1	2		All don
41	mastror	8735	SS Trace	4	0	1 to 2.5	5' and 3' Ends	1	1		
45	PatelD	8874	Finish	8	0	3	5' and 3' Ends	1	2		ALI done. PCPD clones may need new vector.
47	PWu	8841	Finish	2	0	>5	Full Length [ds	1	1		
48	qinp	8772	Finish	3	0	1.5	Full Length [ds	1	2		
49	qyao	8861	Finish	5	0	3.5	Full Length [ds	1	1		Fully ds between indicated cloning sites or region
51	ritaccf	8816	Finish	2	0	1.5	5' and 3' Ends	1	1		OK
52	ruzina	8769	Finish	5	0	1	Full Length [ds	1	1		Some clone (72/73) OK. Rest NG or very poor
53	SBenard	8721	Finish	19	0	1.5	Full Length [ds	1	1		Bunch of muts on 1 end + 1 to 5 internal
54	tangx2	8785	Finish	24	0	2.5	Full Length [ds	1	1		Overall poor data and tons of muts. Poor DNA
55	tanw	8800	SS Trace	10	0	0.5	5' End Read [d	1	1		All Ok except for one read
56	tuckmam	8771	Finish	7	0	1	Full Length [ds	1	1		Some clones are good some either no inser or very short
57	VDaesety	8775	Finish	4	0	1	Other	1	1		One clone possibly has needed mutation. 3 do not have
58	Summary: al reqs: 53			Total cmp reqs: 50							
59	Total clones: 588			Total actv reqs: 3							
60											
61	ve clones, 'Cov' = coverage, 'C/A' = completed/active, 'D-to-C' = days to complete										
62											

Finch's new request page

 Cambridge Login: jkieleczawa - Jan 11, 6:37 2006 

[Home](#) > [Sequencing Requests](#) > [New Request](#)

New Sequencing Request Step 1 of 2

Request Information


Request Label: <input type="text" value="jkieleczawa_2006-01-11"/>	Location: <input type="text" value="<none>"/>
DNA Type: <input type="text" value="<none>"/>	DNA Source: <input type="text" value="Homo sapiens"/>
Service: <input type="text" value="BLAST_NONE"/>	Priority: <input type="text" value="Standard"/>
"Bill To": <input type="text" value="<none>"/>	Notebook: <input type="text" value=""/>
Comment: <input type="text" value=""/>	Page: <input type="text" value=""/>

Request Type *cont ...*

<input type="button" value="Plate Request"/>	Use an interactive plate diagram and several fields to assign sample information.
<input type="button" value="Tube Request"/>	Use an interactive tube diagram and sample fields to assign sample information.
<input type="button" value="Batch Request"/>	Register multiple plates in a single step.
<input type="button" value="Upload Request"/>	Upload sample information via a tab-delimited file.

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Finch's tube request screen

 Cambridge Login: jkieleczawa

Home > Sequencing Requests > New Request

New Tube Sequencing Request Step 2 of 2

Sample Information

All	1	2	3	4	5	6	7	8	9	10	11	12
1-12												
13-24												

Select Mode: Single Multi

Template: Folder:

Primer: Chemistry:

Comment:

Vector: Direction: Insert Size: (Kb)

Label:

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Finch LIMS-Status Page for Completed Runs

Search Favorites History

etics.com/Finch/CM/seqRunList?Page=9;PageSize=25

Cambridge Login: jkieleczawa - Jun 10, 4:4

Home > Sequencing Lab > Sequencing Runs

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[Folders](#)
[Pipeline Cleanup](#)
[Vector Databanks](#)

Instrument
[Runs](#)
[New Run](#)
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[New Gel Run](#)
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Reports
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[Sequencers](#)
[File Transfers](#)

Sequencing Runs

All Runs *Runs by Month* *Runs by Week* *Runs by Day*

Find: Label = GO

Items 201-225 of 4659 ([more](#) | [all](#)) Page 9 of 187 Go To: << [6](#) [7](#) [8](#) [9](#) [10](#) >>

Label	Sequencer	Avg(Q>20)	# Reads	% Passed	End Time
n/a	ABI3730-15105-014	978	48	100.0	2004-05-12 19:47:51
n/a	demo_3100	701	16	100.0	2004-05-12 18:41:59
n/a	demo_3100	573	16	100.0	2004-05-12 15:02:03
n/a	ABI3730-15105-014	933	47	100.0	2004-05-12 01:14:25
n/a	ABI3730-15105-014	983	47	100.0	2004-05-11 23:17:07
n/a	ABI3730-15105-014	693	32	87.5	2004-05-11 21:18:47
n/a	ABI3730-15105-014	728	39	84.6	2004-05-11 19:21:26
n/a	ABI3730-15105-014	977	48	100.0	2004-05-11 01:01:01
n/a	ABI3730-15105-014	978	48	100.0	2004-05-10 23:03:27
n/a	ABI3730-15105-014	663	35	88.6	2004-05-10 21:05:19
n/a	ABI3730-15105-014	682	40	95.0	2004-05-10 19:07:47
n/a	demo_3100	776	16	93.8	2004-05-08 09:33:56
n/a	demo_3100	739	16	100.0	2004-05-08 05:55:18
n/a	ABI3730-15105-014	980	38	100.0	2004-05-08 05:29:47
n/a	ABI3730-15105-014	977	39	100.0	2004-05-08 03:32:15
n/a	demo_3100	717	16	100.0	2004-05-08 02:16:45
n/a	ABI3730-15105-014	526	31	58.1	2004-05-08 01:34:06


Finch LIMS-Instrument Capillary Usage

Items 91-120 of 504 ([more](#) | [all](#))

Page 4 of 17

Cap	2004-05-21 02:37:28	2004-05-21 01:39:54	2004-05-20 22:41:49	2004-05-20 20:44:15	2004-05-20 18:46:10	2004-05-20 16:32:34	2004-05-20 10:50:43	2004-05-20 08:53:11	2004-05-20 06:55:10	2004-05-20 04:57:37	2004-05-20 02:59:36	2004-05-20 01:02:01	2004-05-19 23:03:58	2004-05-19 21:06:25	2004-05-19 19:08:24	2004-05-19 16:54:46	2004-05-18 18:06:06	2004-05-18 15:52:47	2004-05-18 03:52:02	2004-05-18 01:54:31	2004-05-17 23:56:28	2004-05-17 21:58:57	2004-05-17 20:00:56	2004-05-17 17:47:55	2004-05-14 23:33:50	2004-05-14 21:36:21	2004-05-14 19:38:21	2004-05-14 17:26:18	2004-05-13 23:12:25	2004-05-13 21:14:53
1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
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7	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
8	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
9	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
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25	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
26	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
27	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
28	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	

Finch LIMS-Chromatogram Details

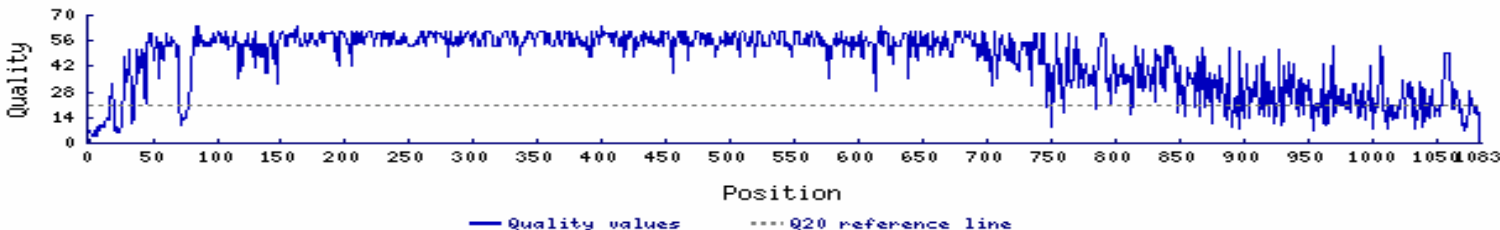
 Cambridge Login: jkieleczawa - Jun 10, 4:54 2004

Home > Sequencer Runs > Details > Chromats > Chromat Details

Chromatogram Details

Label:	zpzGem3-008_116060_00	Format:	ABIF
Folder:	000_DEFAULT	Sample ID:	n/a
Sample Name:	zpzGem3-008_116060_00	Plate Label:	n/a
Instr. Model:	3730	Instr. Name:	ABI3730-15105-014
Run Start:	2004-06-10 01:27:00	Run Stop:	2004-06-10 03:24:15
Lane:	1	# Lanes:	48
Spacing:	16.38	Signal Strs:	A=48,C=49,G=48,T=51
Mobility:	KB_3730_POP7_BDTv3.mob	Matrix:	n/a
Comment:	4D1100002649794D		

Quality Graph



— Quality values - - - Q20 reference line

Read Length 1084 b **Trimmed Length** 1084 b (pos. 1-1084) **Q20** 954 b

Comparison Between 4D and Finch LIMS Systems

#	Feature	4D	Finch
01	Primer Match/Design/Order	Yes	N/N/Y
02	No. of Primers/clone	∞	One
03	No of clones/request in tubes	∞	24
04	Plate Submission	Yes	Yes
05	Effort Reporting	Yes	N/Y
06	Special Conditions	Yes	No
07	Stat. data analysis & Display	No	Yes
08	Storage of Chromatograms	No	Yes
09	Storage of Results	Yes	No
10	Contig Assembly	No	In Dev

Acknowledgments

DNA Sequencing Group

Ait-Zahra, Mostafa

Bajson, Katarzyna

Haines, Lori

Li, Tony

Ulmer, Bill

ERD/PGx

Bernard, Jacob

Sawicky, John

M & A

Projan, Steve

Sookdeo, Hemchand

McColgan, Flo

Travesi, Kathy

All Our Requestors

Andover, Cambridge, Colledgeville

Pearl River and Princeton (>300)

4D Development

Koffman, Don

Lakshmanan, Bharadh

Bioinformatics

Atnoor, Deven

Cannon, Tom

George, Jones

Howes, Steve

Kitzmiller, Aaron

Lakshmanan, Bharadh

Lang, Wayne

Morris, John

Geospiza Team

(Eric, Joe, Rob, Scott, Todd..)