

EMAN2 and EMEN2: Flexible Python-based platforms for electron microscopy

SciPy 2013
June 27, 2012

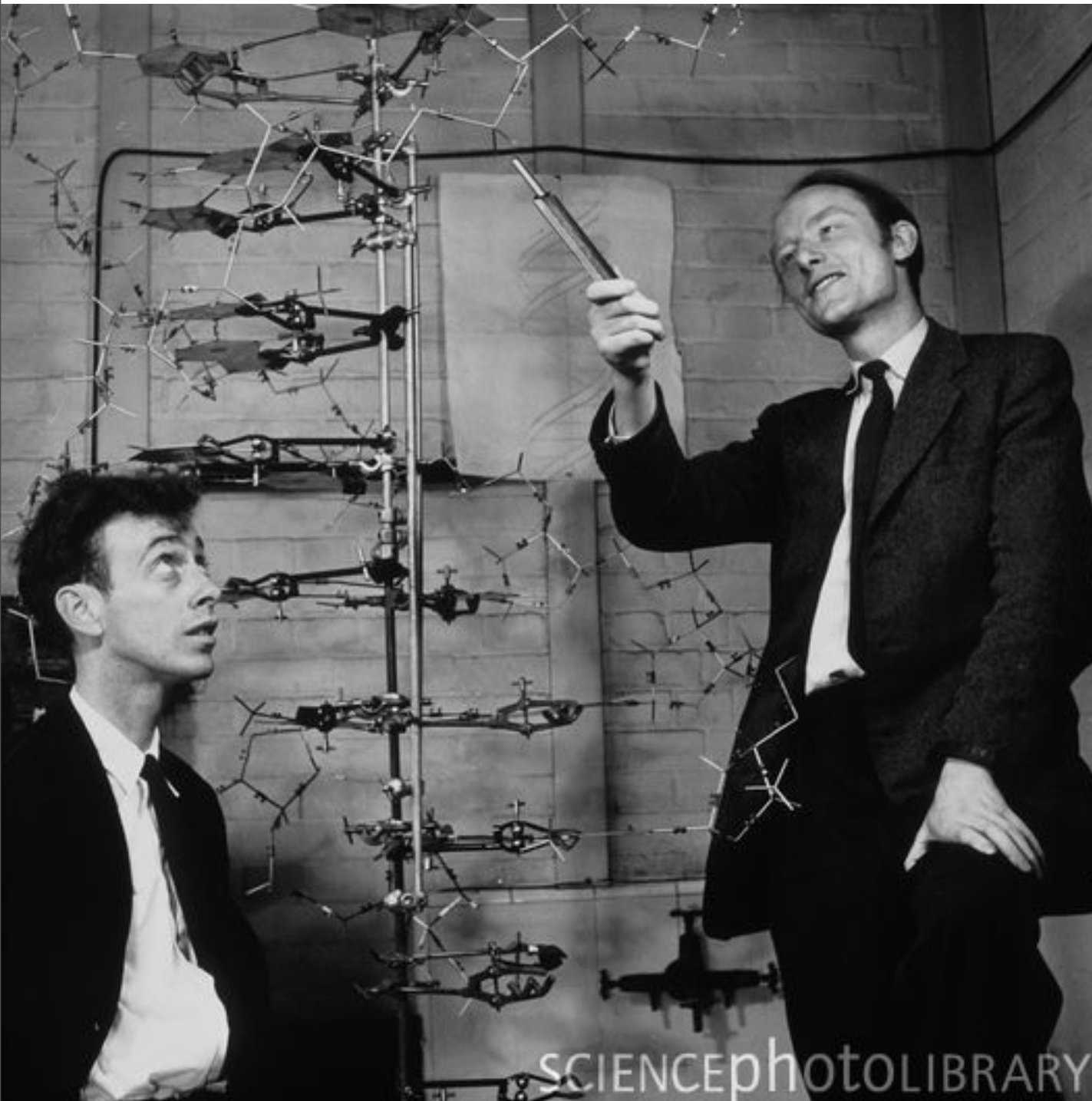
Ian Rees

National Center for Macromolecular Imaging
Baylor College of Medicine
Houston, TX
ian.rees@bcm.edu
ian@ianrees.net

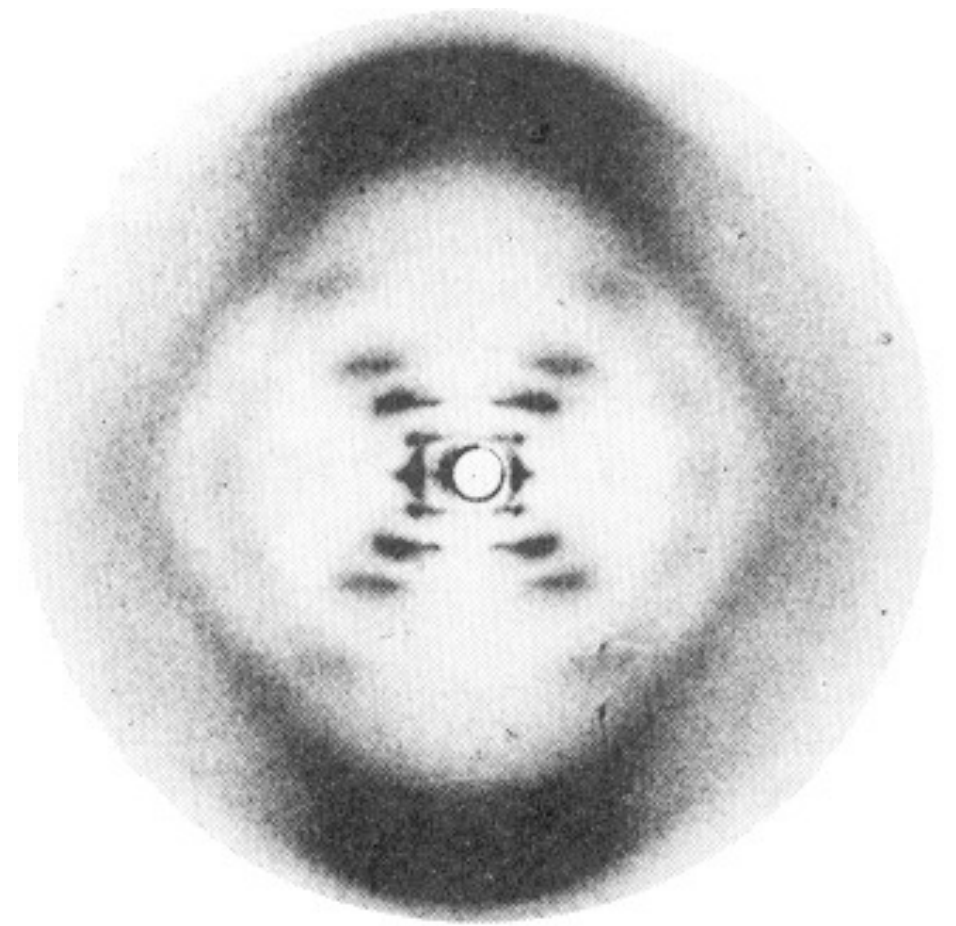
Overview

- National Center for Macromolecular Imaging
- EMEN2 Database

Structure!



<http://www.sciencephoto.com/media/222783/enlarge>

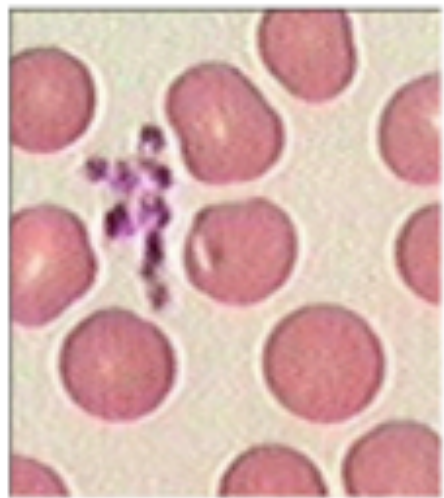


http://en.wikipedia.org/wiki/John_Kendrew

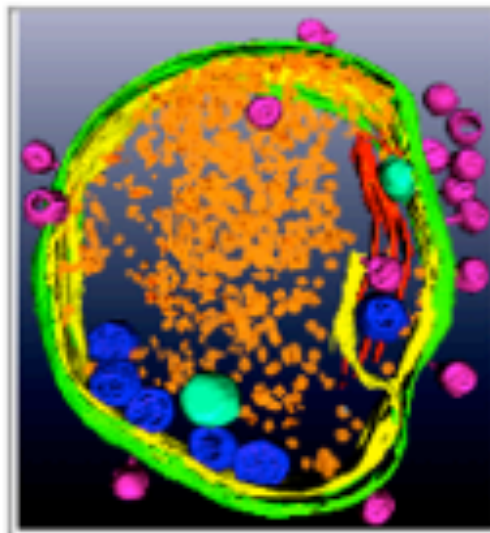
Franklin & Gosling 1953

Imaging macromolecules

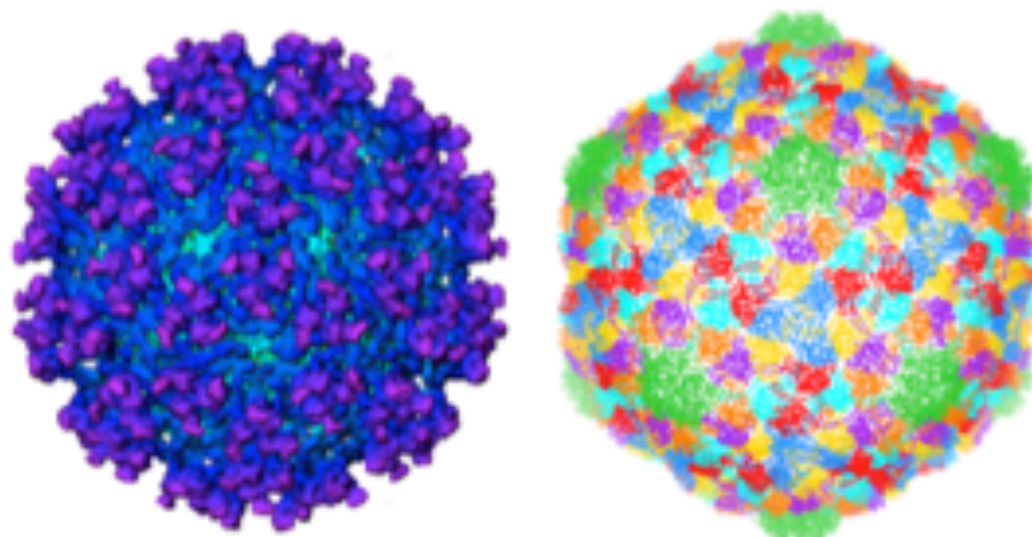
Optical
microscopy



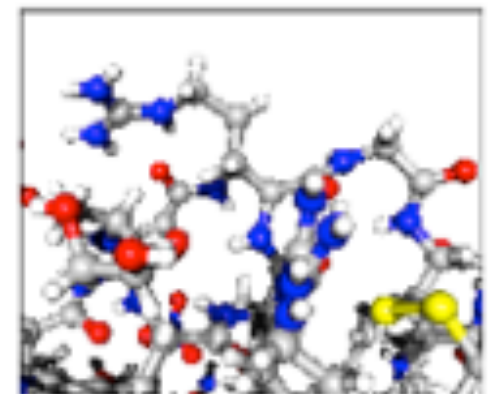
Electron
tomography



Single particle
reconstruction



Crystallography
NMR



2000 Å

60 Å

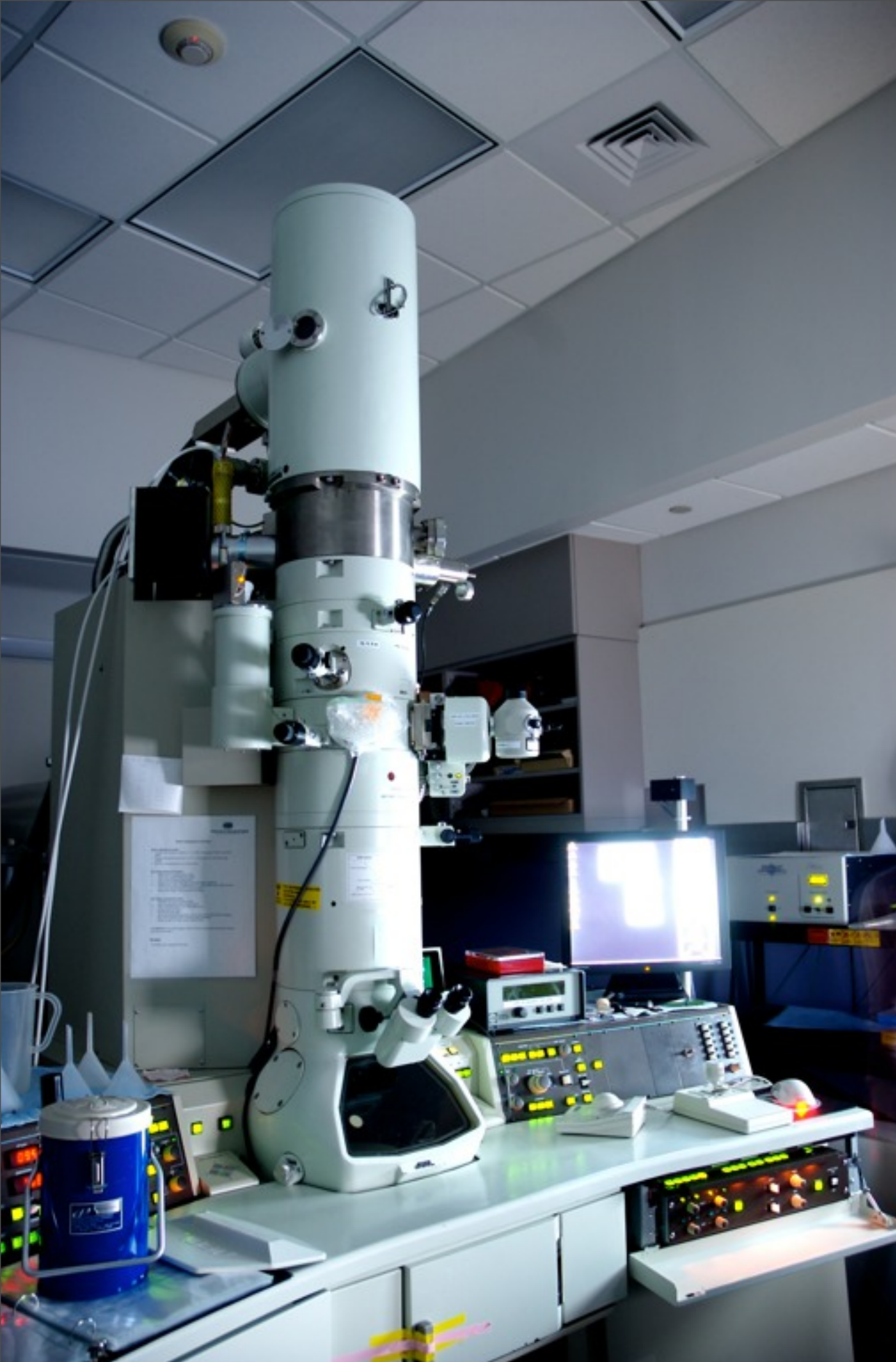
10 Å

4 Å

1 Å

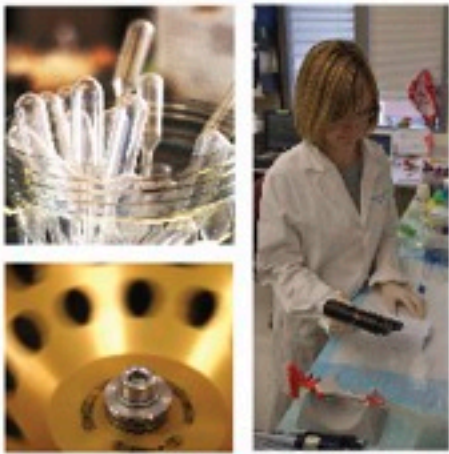
Cryo-EM

- No crystals
- Near-native solvent environment
- Large complexes
- Tomography: 20-40 Å
- Single-particle: 3-10 Å

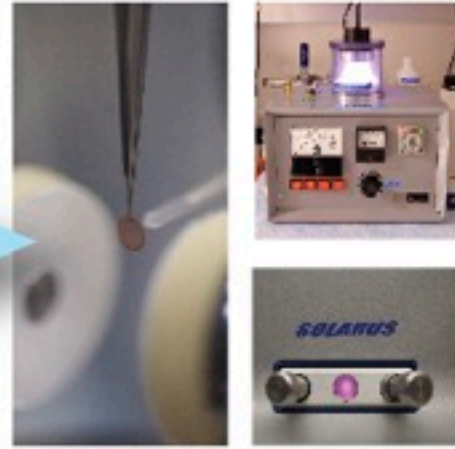


Cryo-EM pipeline

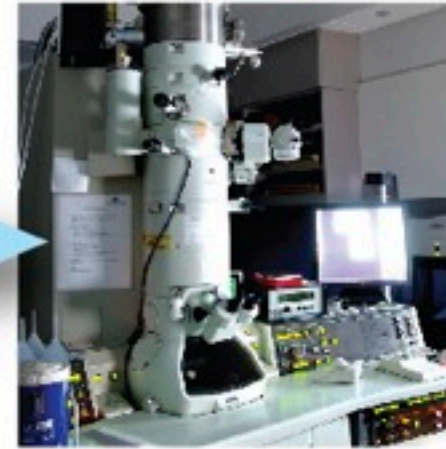
Biochemical Prep



Cryo-EM Prep



Screening



Data Collection

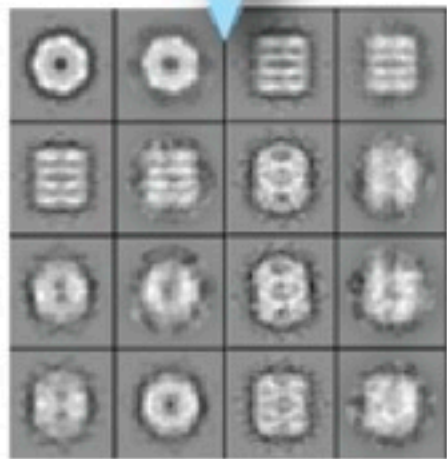
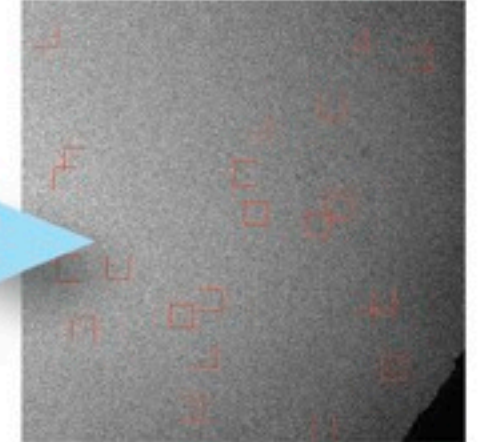
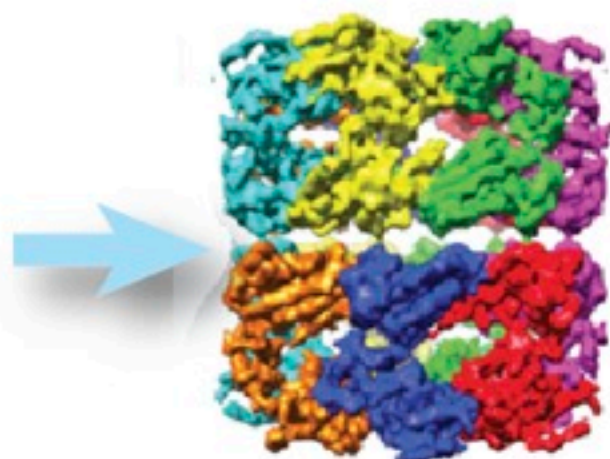
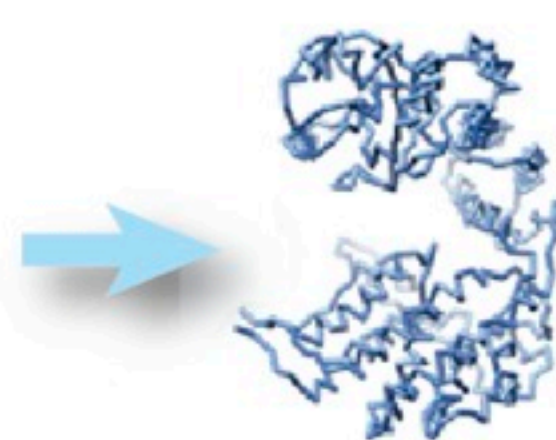


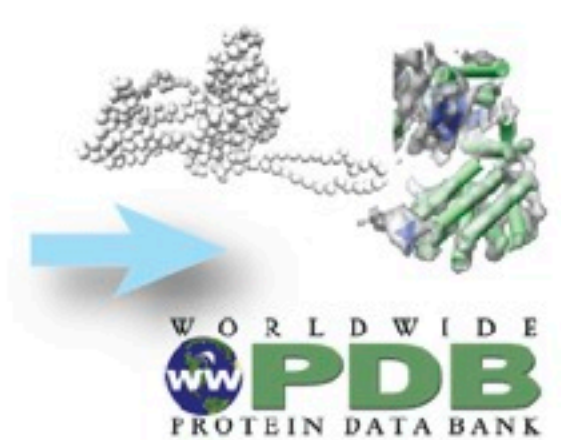
Image Processing



Reconstruction



Structural Analysis



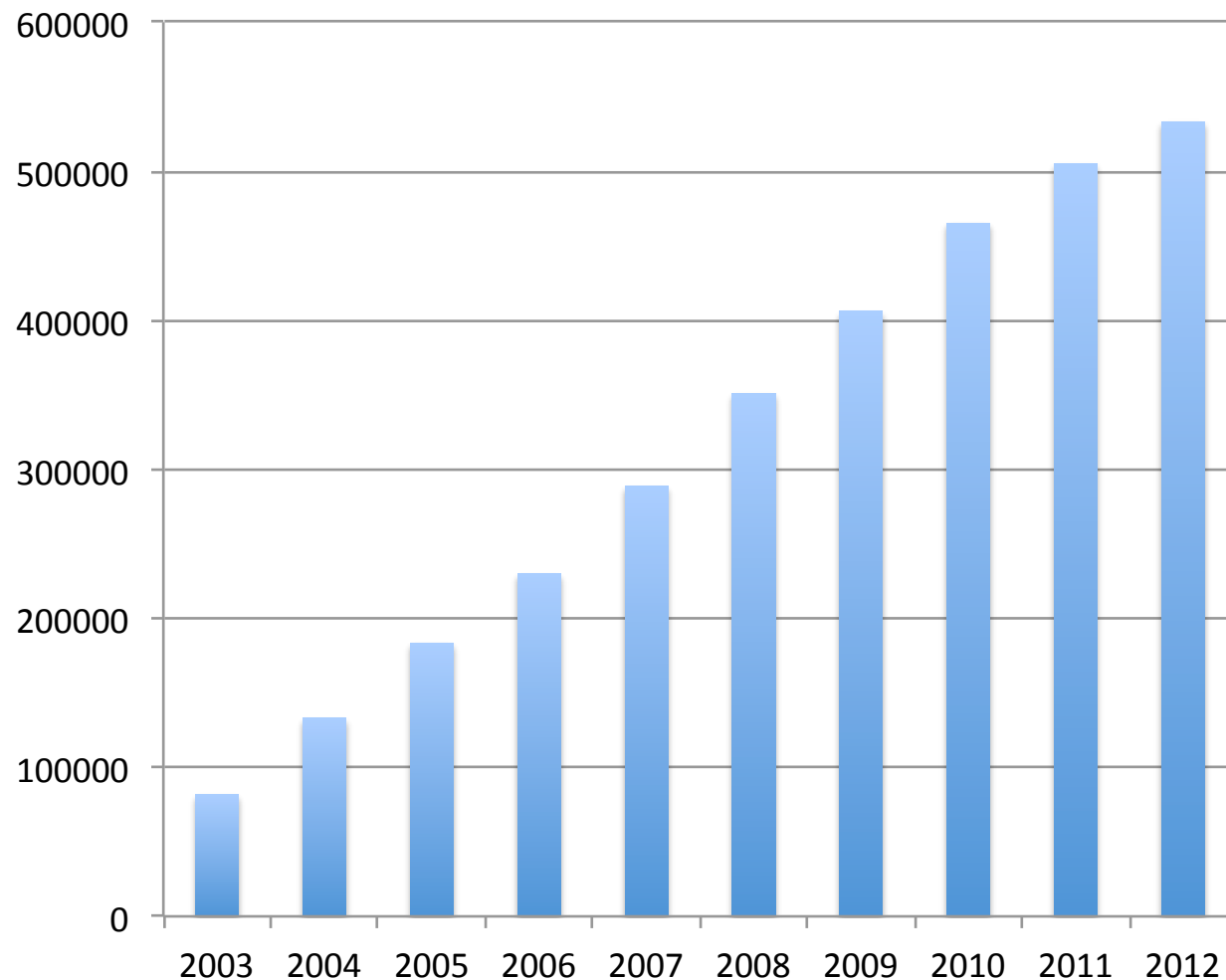
Annotation & Deposition

Cryo-EM pipeline

- “Garbage in, garbage out”
- Optimize each stage of the pipeline
- A Big Investment!
 - ▶ Time
 - ▶ Microscopes and other equipment
 - ▶ Computational resources
 - ▶ Skilled microscopists (and students...?)

Large and growing data

NCMI Data



- 300+ projects
- 800+ users
- ~5TB / month
- Variety of hardware and software

Beyond just archival...

- Encourage good record keeping (automation)
- Find things after people leave the lab
- Reconstruct an experimental protocol refined over years
- Share with collaborators
- Instrument usage accounting

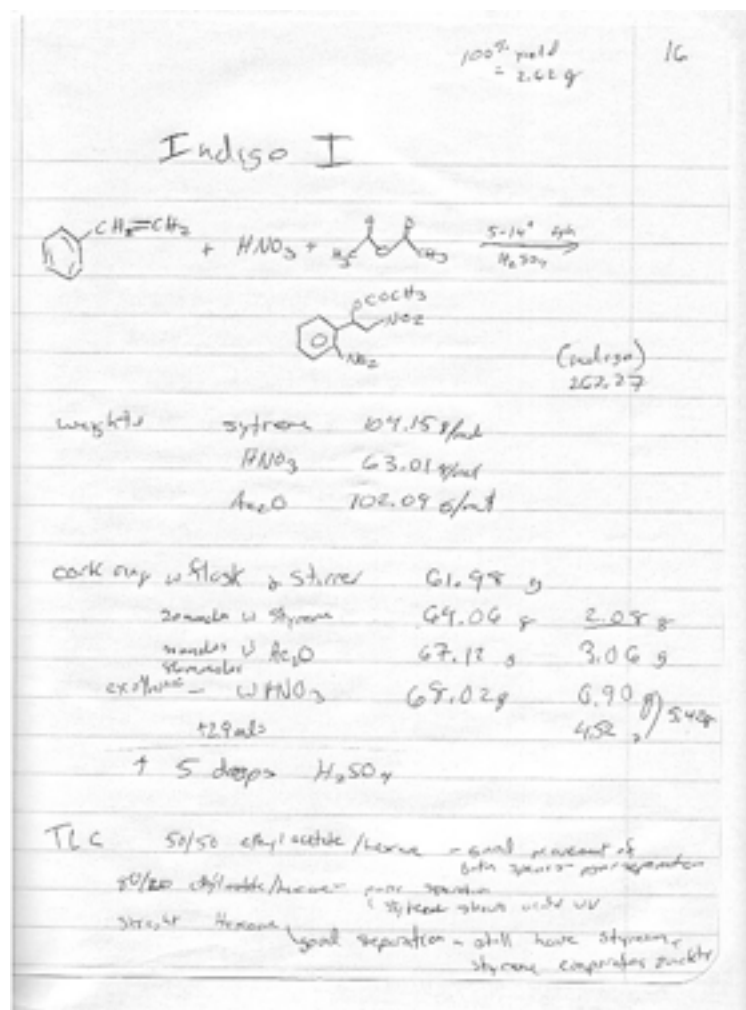
Experimental protocols?

- Hard to establish standards...
- Differences between investigators and labs
- Difficult to anticipate future needs

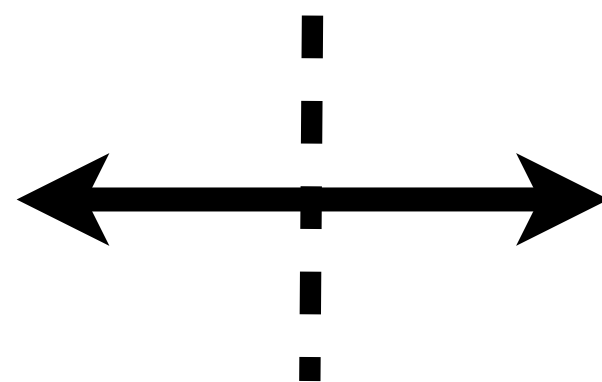
Protocols evolve...

- Protocol variations and customizations
- Sometimes a dead end!
- History of a protocol is itself important

How to store?



Film/Frame Id	Defocus	Mag	Total Dose	ExpTime
ccd_20040314 #1	0.8 um	138.44k	20.0	1.0 s
ccd_20040314 #2	2.5 um	138.44k	20.0	1.0 s
ccd_20040314 #1	0.8 um	138.44k	20.0	1.0 s
ccd_20040314 #2	2.5 um	138.44k	20.0	1.0 s
ccd_20040314 #1	0.8 um	138.44k	20.0	1.0 s
ccd_20040314 #2	2.5 um	138.44k	20.0	1.0 s
ccd_20040314 #1	0.8 um	138.44k	20.0	1.0 s
ccd_20040314 #2	2.5 um	138.44k	20.0	1.0 s
ccd_search1 #1	0.8 um	138.44k	20.0	1.0 s
ccd_search2 #2	2.5 um	138.44k	20.0	1.0 s
ccd_search3 #1	0.8 um	138.44k	20.0	1.0 s
ccd_search4 #2	2.5 um	138.44k	20.0	1.0 s
ccd_search5 #1	0.8 um	138.44k	20.0	1.0 s
ccd_search6 #2	2.5 um	138.44k	20.0	1.0 s



Our Needs

Human readable Unstructured Easy to change

Machine readable Structured Hard to change



Electronic Microscopy Electronic Notebook

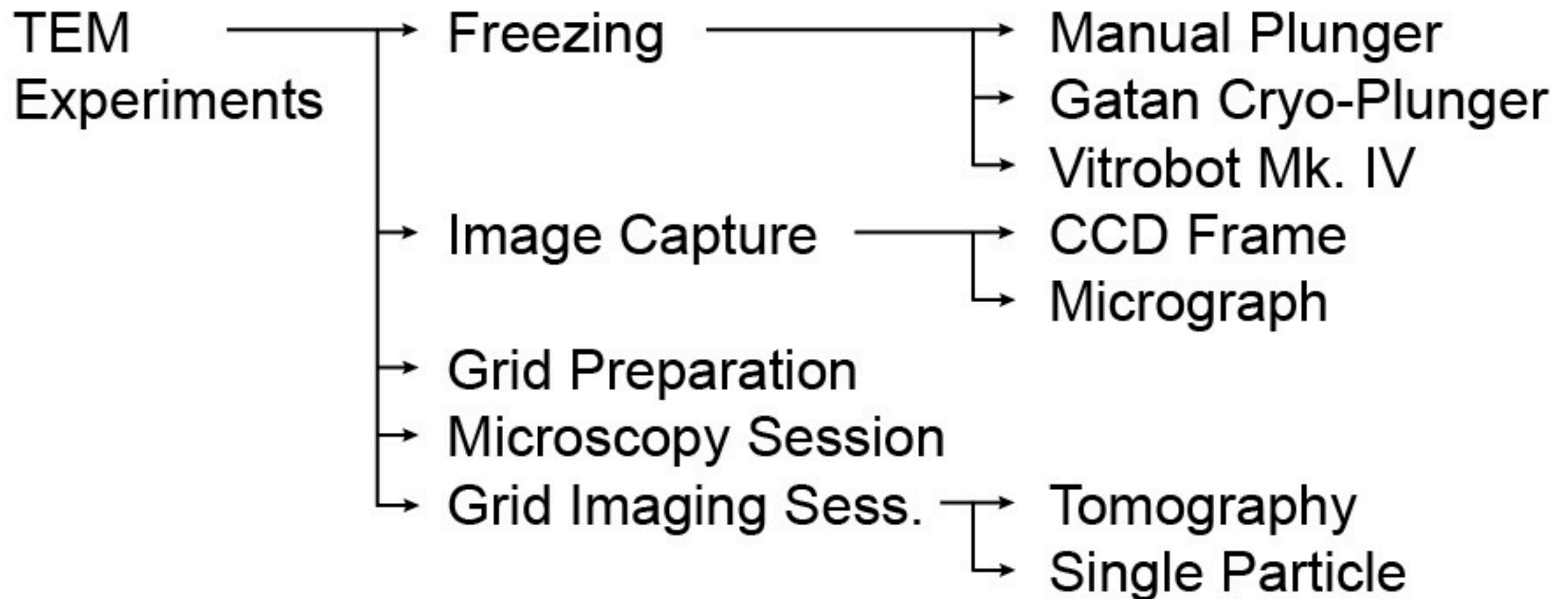
- BerkeleyDB key-value backend
- Flexible, end-user defined schema
- Originally designed for cryo-EM, but adaptable to other domains
- Extensions and custom applications

Protocols

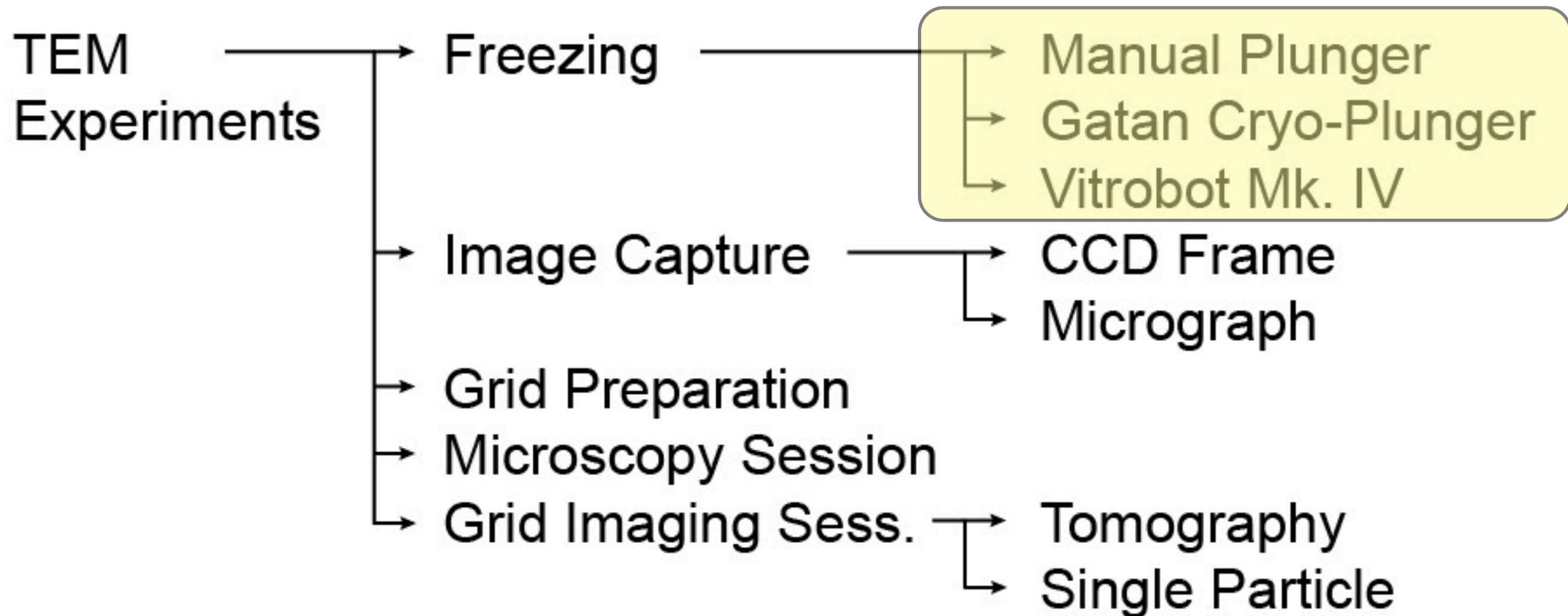
- Plain text description of experiment
- Embedded parameters

*A preprepared grid from batch **\$grid_batch_id** was placed in a pair of forceps and loaded into the plunger. **\$cryogen** was preprepared below the plunger.....*

Protocol ontology



Protocol ontology



Parameters

- Description of the parameter and intended use
- Data type (string, integer, list, etc.) and units
- Constraints and validation

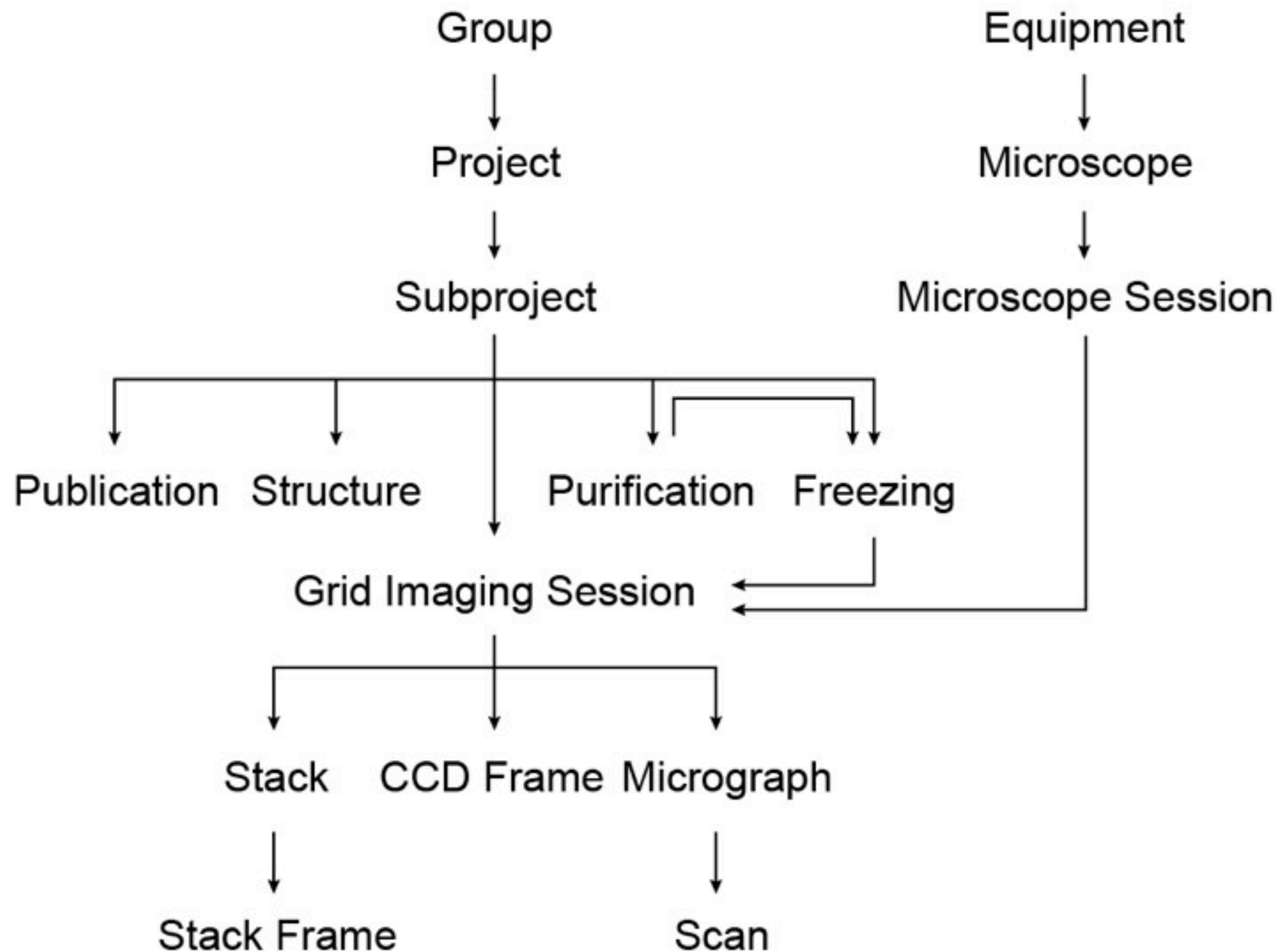
\$aperture_objective

The aperture of the objective lens

Integer, default unit is micrometer

0 μ m, 20 μ m, 50 μ m, 70 μ m, 150 μ m.

Flexible record organization



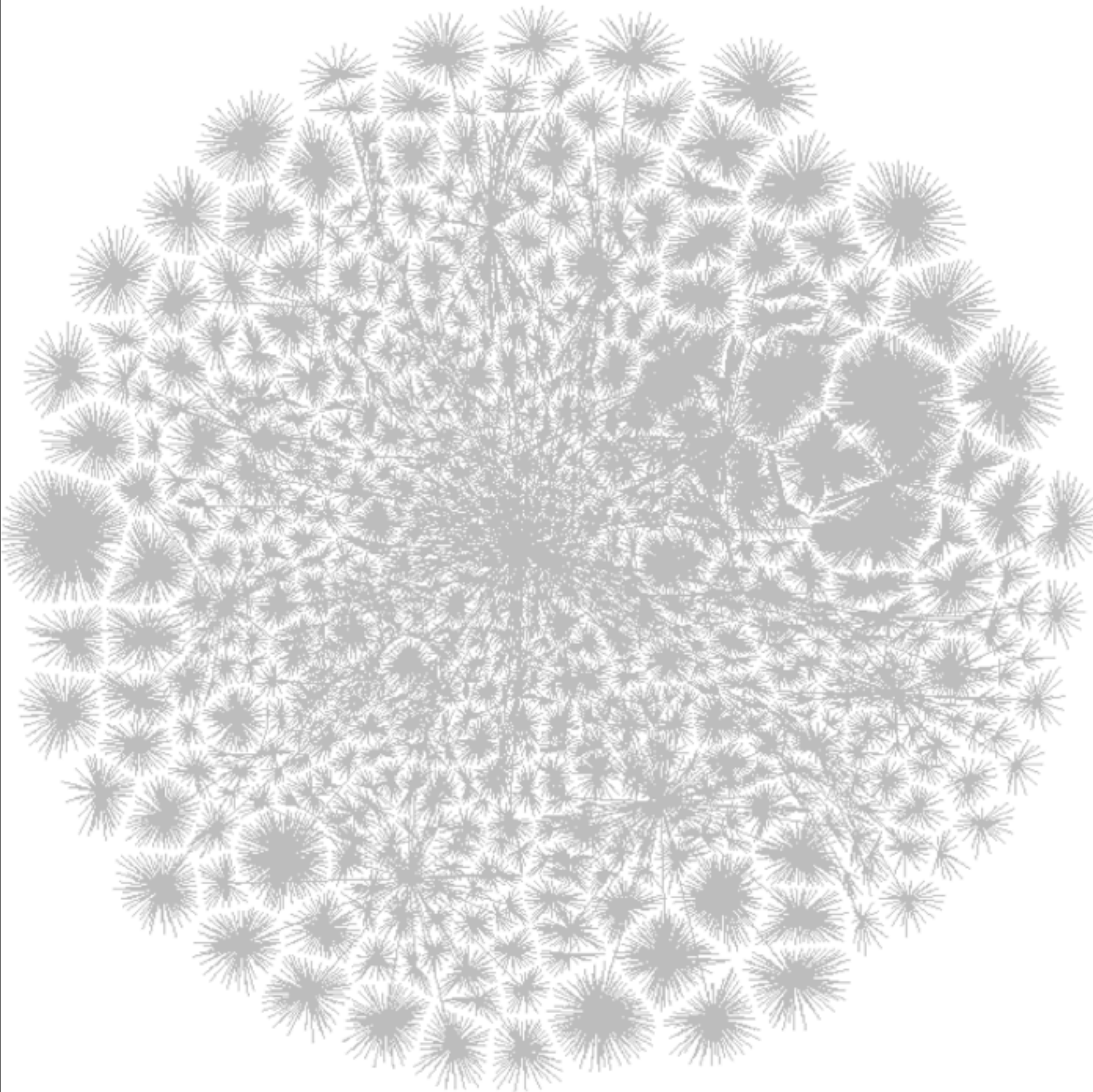
GroEL

10 years

22 users

15,500 records

- ▶ 18 subprojects
- ▶ 6,000 micrographs
- ▶ 5,000 ccd frames
- ▶ 14 purifications
- ▶ 34 freezings
- ▶ 170 grids
- ▶ 102 notes



```
>>> print db.record.get('46605')
{
  'rectype': 'project',
  'name_project': 'High resolution GroEL',
  'name_specimen': 'GroEL',
  'description_goals': 'We have found previously that during the assembly....',
  'mass_specimen': 800.0,
  'project_status': 'Complete',
  'project_type': 'Core',
  'project_investigators': ['jj', 'chrisb', 'matt', ...],
  'name_pi': ['davidchuang'],
  'file_binary': ['bdo:2009112400000'],
  'name': '46605',
  'children': set(['268417', '294994', '294995', ...]),
  'parents': set(['136']),
  'keytype': 'record',
  'creator': 'root',
  'creationtime': '2001-10-03T05:00:00+00:00',
  'modifyuser': 'mikeschmid',
  'modifytime': '2010-09-21T18:21:35+00:00',
  'groups': set('public'),
  'permissions': (('(', ), ('jj', 'matt', 'chrisb'), ('davidchuang')),
  'comments': [],
  'history': [['mikeschmid', '2010-10-21T20:08:48+00:00', 'project_status', None]],
  'uri': 'http://ncmidb.bcm.edu/record/46605/'
}
```

Security & logging

- Per-record, with four levels of privilege:
 - ▶ Read, read and comment, edit values, change permissions
- Groups and roles
- All changes are logged
- History log is integral to record

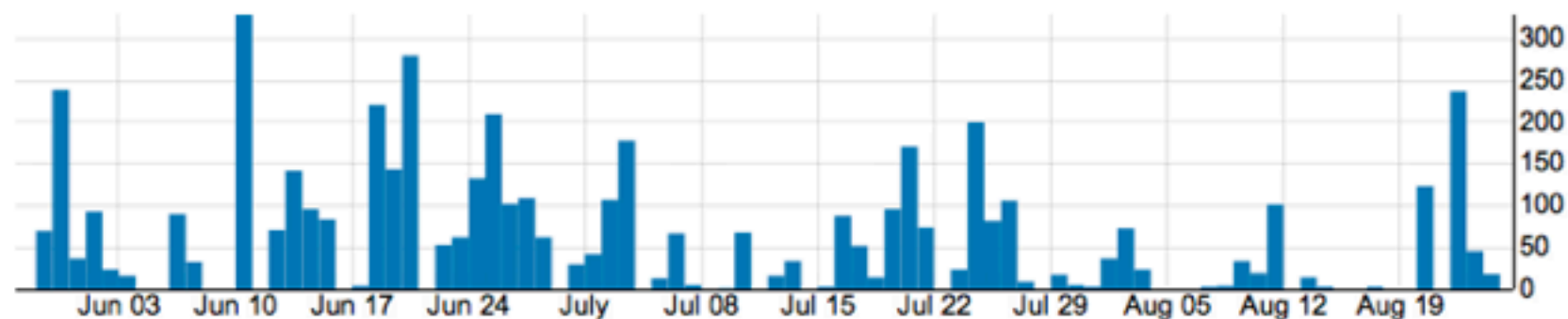
Open-source

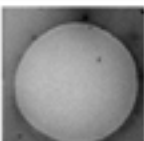
- Dependencies:
 - Python, BerkeleyDB, bsddb3, dateutil
 - Twisted, Mako Templates, Markdown, JSONRPC
 - EMAN2, ImageMagick, pyOpenSSL

 New group

A ginger cat is the central focus, sitting and looking towards the left. The background is dark and out of focus, featuring several bright, circular bokeh lights that suggest an outdoor night setting. The cat's fur has a distinct orange and white striped pattern.

Record tree



recname	thumbnail	Protocol	Object Name	Creation time	Created by
Lab notebook: Current status 8/24/2012		labnotebook	524968	2012/08/24 18:16	Chang, Juan
CCD		ccd	524967	2012/08/24 14:59	Dillard, Rebecca

NCMI

Project GroEL (GroEL)

Subproject High resolution GroEL

Record: Subproject High resolution GroEL

Visualization (1)

Publication (2)

Reference (10)

Purification (7)

Grid imaging session (105)

Lab notebook entry (34)

Structure (1)

Record: Subproject High resolution GroEL

 Edit New

Permissions

 Attachments

Relationships

Views

1 Comments

🕒 4 Edits

Steven J Ludtke
2010/09/21 13:21

Children

Visualization

Publication

Reference

Purification

Grid imaging session

Lab notebook entry











Structure

105 records (0.88s) [Modify query](#) ▾

New grid imaging

Rows

1/2 ›

Set Magnification	Specimen temp	Purpose	parentvalue title_freezing	# ccd	# ddd	# micrograph	# scan	Creation time	Created by
									
80	3.7 K	collecting data		49	0	0	0	2007/03/28 00:00	Admin
80	3.7 K	collecting data		108	0	0	0	2007/03/27 00:00	Admin
80	3.71 K	collecting data	GroEL G8 G9	205	0	0	0	2007/03/27 00:00	Admin
80	3.71 K	collecting data	GroEL G8 G9	133	0	0	0	2007/03/27 00:00	Admin
80	3.71 K	collecting data	GroEL G8 G9	182	0	0	0	2007/03/27 00:00	Admin
80	4.18 K	collecting data	HR GroEL 2005	202	0	0	0	2006/03/24 00:00	Admin
80	4.17 K	collecting data	HR GroEL 2005	112	0	0	0	2006/03/23 00:00	Admin
80	4.17 K	collecting data	HR GroEL 2005	92	0	0	0	2006/03/22 00:00	Admin
80	4.17 K	collecting data	HR GroEL 2005	208	0	0	0	2006/03/21 00:00	Admin
80	4.16 K	collecting data	HR GroEL 2005	101	0	0	0	2006/03/20 00:00	Admin
60	4.18 K	collecting data	GroEL G8 G9	0	0	100	100	2005/07/21 00:00	Admin
60	4.17 K	collecting data	GroEL G8 G9	0	0	80	80	2005/07/19 00:00	Admin
60	4.17 K	collecting data	GroEL g1 g2	0	0	100	100	2005/07/18 00:00	Admin

NCMI Database: Record: CCD x

ncmidb.bcm.edu/record/56969/

NCMI National Center for Macromolecular Imaging

Home Query Bookmarks Admin

Ian Rees

Record marked as published data

Microscopy: JEOL 3000SFF by Donghua Chen @ : collecting data

Subproject High resolution GroEL

08 00:00 Vitrobot: GroEL G8 G9 by Donghua Chen @ 2005/03/11 00:00

Imaging: on JEOL 3000SFF by Admin @ 2007/03/27 00:00: 205 images

CCD ccd_3160

Record: CCD ccd_3160

Record: CCD ccd_3160

Edit

New

Permissions

1 Attachments

Relationships

Views

0 Comments

3 Edits

Admin

2010/09/21 23:15

Children

No children

Image

- +

Center

Download

Convert

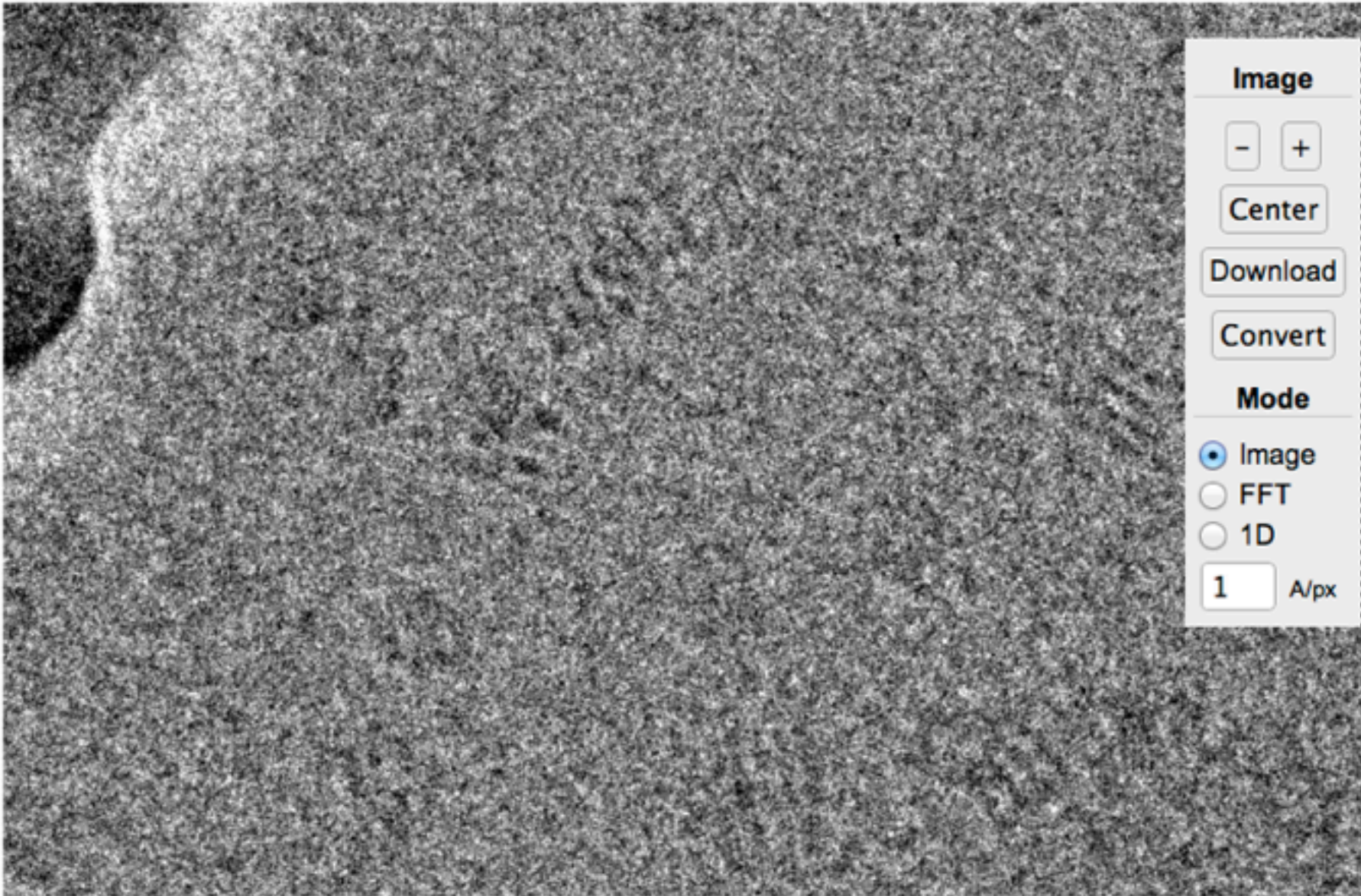
Mode

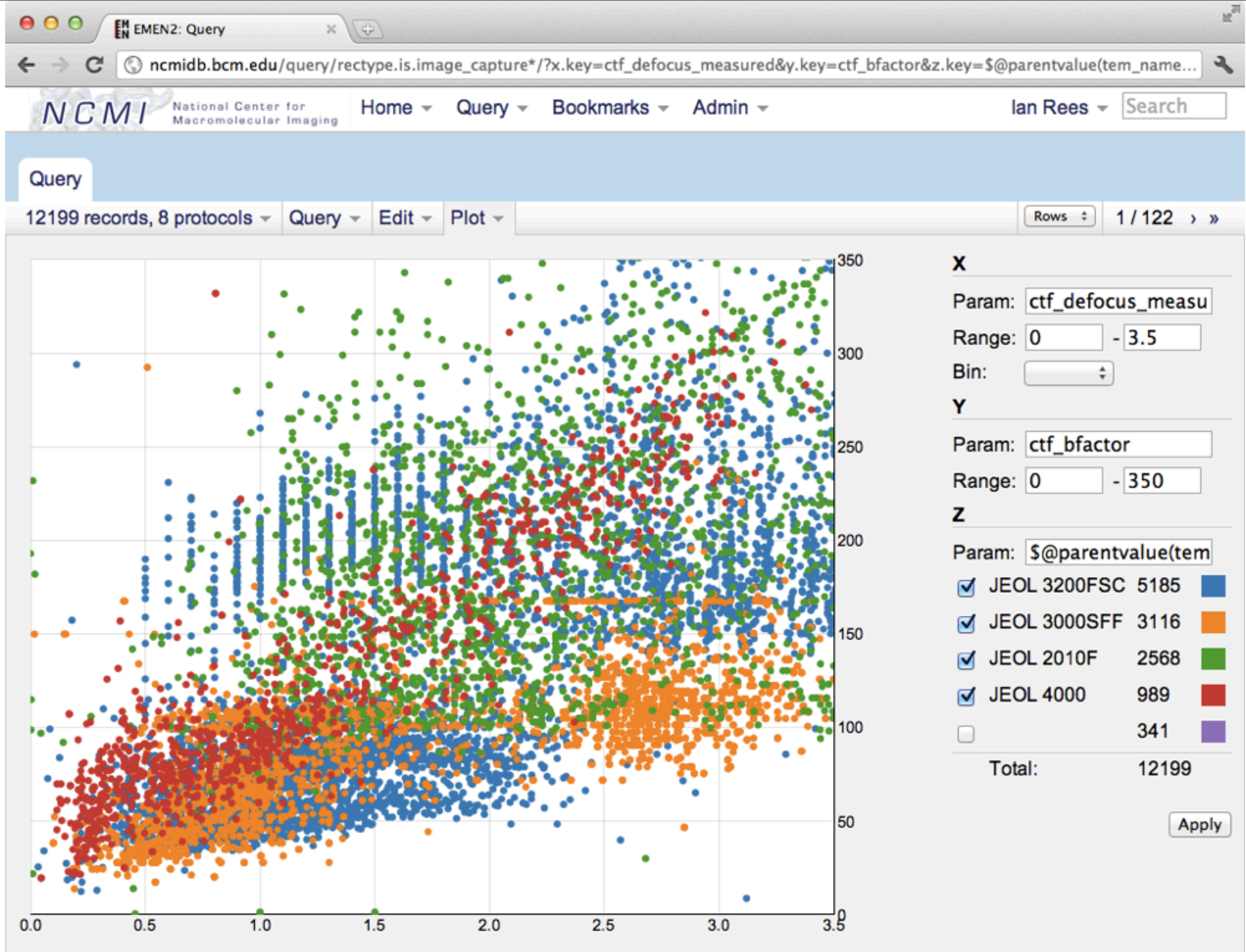
☒ Image

☐ FFT

☐ 1D

1 A/px





Data upload

The screenshot shows the EMDash web interface. At the top, there are several fields: Session (0:29:20 root (root)), Grid Imaging (Imaging: on by root @ 2005/01/14: 71 images), Browse (/Users/irees/workshop/emen2/micrographs), Project (Subproject Data for 4 A structure of GroEL), and Grid Prep (Grid: Test by root @ 2011/03/16 08:54:32). Below these is a large empty text area and an 'Add Comment' button. A 'Settings' button is also present. The settings section includes: Ice Conditions (Good), Ice Thickness (Perfect), Intended Mag (60.0 x 1000), Defocus (1 uM), Exposure (1.0 s), and Dose (10.23 e/A2/s). At the bottom, there is a table with columns: Name, Mag, Defocus, Dose, Exposure, Quality, and Status. The table shows two rows of data for Grid: 2110.

Name	Mag	Defocus	Dose	Exposure	Quality	Status
Grid: 2110						(view)
172371.dm3	60	1	10.23	1	★★★	13894
20011.dm3	60.0	1	10.23	1.0	★★★	

- EMDash
- Runs on microscope computer
- Manages sessions, uploads data

Extensible architecture

- EMEN2 Public API using JSON-RPC
- Extensions:
 - ▶ Data types, units, macros
 - ▶ File format handlers
 - ▶ Web interface
- Extend existing functionality, or entirely new applications

EMEN2 API

```
>>> import jsonrpc.proxy
>>> db = jsonrpc.proxy.JSONRPCProxy("http://localhost:8080")
>>> db.login("ianrees", getpass.getpass())
Password:

>>> children = db.rel.children('201364', recurse=-1)
>>> len(children)
63627

>>> q = db.query(['children', '==', '201364*'], ['rectype', '==', 'image_capture*'],
['creationtime', '>', '2012'])
>>> len(q['names'])
5015

>>> r = db.record.new(rectype='folder', inherit=['201364'])
>>> r['name_folder'] = "Presentations"
>>> db.record.put(r)
{u'name': u'563581', u'creator': u'ianrees', u'keytype': u'record', u'creationtime':
u'2013-06-27T20:47:43+00:00', u'comments': [], u'rectype': u'folder', u'name_folder':
u'Presentations', ....}
```

EMEN2 Extensions

```
from emen2.web.view import View

@View.register
class TestView(View):
    @View.add_matcher(r'^/test/view/(?P<name>[^/]*)/$')
    def main(self, name, **kwargs):
        self.title = 'Test view'
        self.template = '/test/testview'
        # do stuff here.
        self.ctx['name'] = name
        self.ctx['value'] = 'Test!'
```

```
<%inherit file="/page" />
```

```
<h1>Test page</h1>
```

This uses Mako-style templates. The page name was \${name}
and the value was: \${value}

Ext.: Mark public data

NCMI Database: Record: Sub: X

ncmidb.bcm.edu/record/46605/publish/

NCMI National Center for Macromolecular Imaging

Home Query Bookmarks Admin Ian Rees

Record: Subproject High resolution GroEL

Visualization (1) Publication (2) Reference (10) Purification (7)

Grid imaging session (105) Lab notebook entry (34) Structure (1)

Record: Subproject High resolution GroEL

Edit New Permissions Attachments Relationships Views 1 Comments 4 Edits

Steven J Ludtke 2010/09/21 13:21

Children

Visualization	1
Publication	2
Reference	10
Purification	7
Grid imaging session	105
Lab notebook entry	34
Structure	1

Manage public data — 7581 records selected Save

Records marked in "orange" will be marked as public data when this form is saved. The number of selected records is shown above.

Click on a record to select or deselect it. You can also hold down "shift" while clicking to select or deselect all the children of that record.

—Subproject High resolution GroEL

- Imaging: on JEOL 2010F by Admin @ 2002/04/22 00:00: 36 images
- Imaging: on JEOL 2010F by Admin @ 2002/04/26 00:00: 36 images
- Imaging: on JEOL 2010F by Admin @ 2002/04/26 00:00: 76 images
- Imaging: on JEOL 2010F by Admin @ 2002/05/01 00:00: 73 images
- Imaging: on JEOL 2010F by Admin @ 2002/05/07 00:00: 93 images
- Imaging: on JEOL 2010F by Admin @ 2002/05/09 00:00: 137 images
- Imaging: on JEOL 2010F by Admin @ 2002/05/11 00:00: 67 images
- Imaging: on JEOL 2010F by Admin @ 2002/06/12 00:00: 62 images
- Imaging: on JEOL 2010F by Admin @ 2002/07/18 00:00: 10 images
- Imaging: on JEOL 2010F by Admin @ 2002/10/15 00:00: 12 images
- Imaging: on JEOL 2010F by Admin @ 2002/11/04 00:00: 0 images

Ext.: Grant reporting

```
<?xml version="1.0"?>
<P41_Progress_Report xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://sis.ncrr.nih.gov"
xsi:schemaLocation="http://sis.ncrr.nih.gov http://APRSIS.NCRR.NIH.GOV/XML/p41_progress_report.xsd">
  <Grant_Info>
    <Serial_Number>002250</Serial_Number>
    <Fiscal_Year>2013</Fiscal_Year>
    <Reporting_To_Date>2012-10-31</Reporting_To_Date>
    <Reporting_From_Date>2011-11-01</Reporting_From_Date>
    <Project_Title>3-DIMENSIONAL ELECTRON MICROSCOPY OF MACROMOLECULES</Project_Title>
    <Recipient_Institution_Name>Baylor College of Medicine</Recipient_Institution_Name>
    <Activity_Code>P41</Activity_Code>
    <Director_Person_ID>271657</Director_Person_ID>
    <Patent_Or_Copyright_Award>N</Patent_Or_Copyright_Award>
  </Grant_Info>
  <Person Person_ID="271657">
    <Last_Name>Chiu</Last_Name>
    <First_Name>Wah</First_Name>
    <Full_Name>Wah Chiu</Full_Name>
    <Academic_Degree>PHD</Academic_Degree>
    <Phone_Number>+17137986985</Phone_Number>
    <Fax_Number>+17137988682</Fax_Number>
    <Email_Address>wah@bcm.edu</Email_Address>
    <Department>the National Center for Macromolecular Imaging</Department>
    <Non_Federal_Funding>
      <Source_Type>FDN</Source_Type>
      <Sub_ID>273871</Sub_ID>
      <Organization_Name>NSF</Organization_Name>
      <Grant_Or_Contract_Number>IIS-0705474</Grant_Or_Contract_Number>
      <Total_Support_Funds>60000</Total_Support_Funds>
    </Non_Federal_Funding>
    <Non_Federal_Funding>
      <Source_Type>FDN</Source_Type>
      <Sub_ID>273871</Sub_ID>
      <Organization_Name>NSF</Organization_Name>
      <Grant_Or_Contract_Number>EIA-0325004 </Grant_Or_Contract_Number>
      <Total_Support_Funds>0</Total_Support_Funds>
    </Non_Federal_Funding>
    <Federal_PHS_Funding>
      <Organization>NIH</Organization>
      <Sub_ID>273835</Sub_ID>
      <Sub_ID>273871</Sub_ID>
      <Grant_Or_Contract_Number>5PN2EY016525</Grant_Or_Contract_Number>
      <Total_Support_Funds>5110000</Total_Support_Funds>
    </Federal_PHS_Funding>
  </Person>
</P41_Progress_Report>
```

Simple ext.: Event registration

BMB/Pharm Retreat: Registrat

blake.grid.bcm.edu/bmbretreat/

**The Verna & Marrs McLean Department
of Biochemistry & Molecular Biology
and
The Department of Pharmacology
Research Conference 2012**

October 11 & 12, 2012
The Tremont House, Galveston TX

Ian Rees [Edit](#)

Email: ian@ianrees.net

Institution: Baylor College of Medicine

Department: BCM - Biochemistry and Molecular Biology

Registration [Edit](#)

I am: Student

Primary PI: Ludtke, Steve

Secondary PI: Chiu, Wah

I plan to attend: 2012-10-11, 2012-10-12

Presentation: I would like to present a poster.

Accommodations: I am a faculty member and will have my own hotel a room.

Meal preference:

T-shirt: Men's XL

Install

- Install dependencies, or EMAN2 binary package
- `easy_install emen2`
- `python -m emen2.db.create -h test.db`
- `python -m emen2.web -h test.db`
- `http://localhost:8080`

EMEN2 next steps

- Protocol sharing system
- Additional documentation:
 - ▶ tutorials, sphinx, example extensions
- New instruments and software

Acknowledgments

- Steven Ludtke
 - Wah Chiu
 - Mike Schmid
 - Irina Serysheva
 - Kendal Hirschi
 - NCMI staff
 - P41 GM103832
 - R01 GM080139
 - R01 GM079429
 - PN1EY016525
- NIH Training Grant:
- T15LM007093

NCMI

- <http://ncmi.bcm.edu>
- <http://blake.grid.bcm.edu/emanwiki>
- Feel free to contact me to discuss:
 - ian@ianrees.net