

Phenix Introduction

*Macromolecular Crystallography School
Madrid, May 2017*

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The Phenix Project

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*An NIH/NIGMS funded
Program Project*

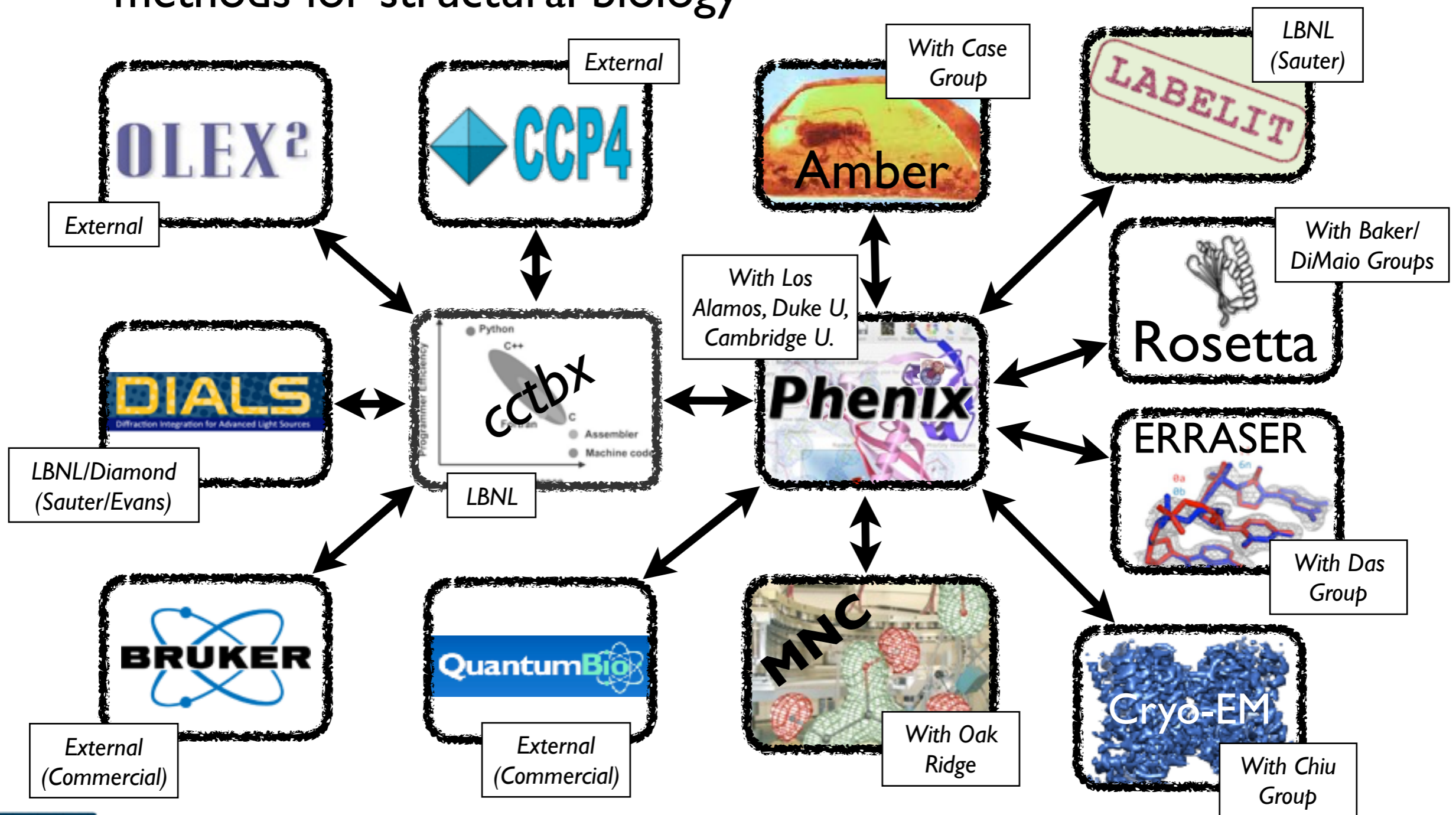
Adams PD et al., PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Cryst.* 2010, **D66**:213-221.

Phenix



Phenix - a Structural Biology Hub

- We have nucleated the development of new computational methods for structural biology



What is PHENIX?

- Package for automated structure solution
- Modern programming concepts and new algorithm development
- Designed to be used by both novices and experienced users
- Long-term development and support
- Why is it called PHENIX?
 - Python Hierarchical Environment for Integrated Xtallography

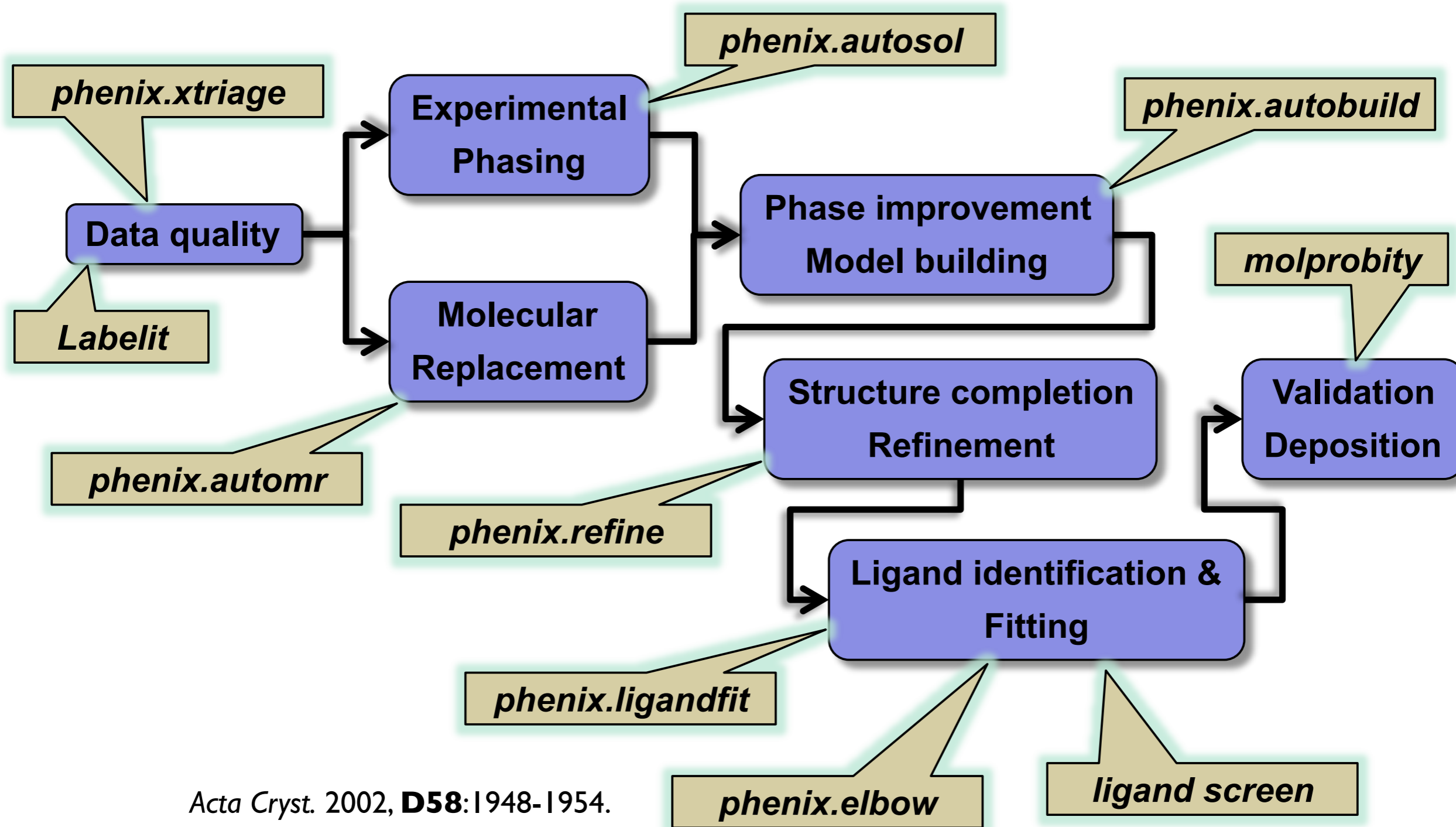


Key Features

- Python
 - Easy scripting of repetitive tasks
 - Enables rapid prototyping and development
- Advanced algorithms
 - Experimental phasing
 - Molecular replacement
 - Automated model building and rebuilding
 - Structure refinement and validation
 - Ligand coordinate and restraint generation
- Rapid development and bug fixing



Automation of Structure Solution



Acta Cryst. 2002, **D58**:1948-1954.

J. Appl. Cryst. 2002, **35**:126-136.

Acta Cryst. 2010, **D66**: 213-221

Phenix



Command Line Tools

- **Data validation**

- `phenix.xtrriage porin_fp.mtz`

- **Automated structure solution**

- `phenix.autosol data=peak.sca seq_file=nsf-d2.seq`

- **Automated model building**

- `phenix.autobuild data=scale.mtz model=mr.pdb
seq_file=correct.seq`

- **Automated ligand fitting**

- `phenix.ligandfit data=nsf-d2.mtz model=noligand.pdb
ligand=atp.pdb`

- **Structure refinement**

- `phenix.refine nsf-d2.mtz nsf.pdb`

- **Building ligand coordinates and restraints**

- `phenix.elbow --smiles="C12CC3CC(C2)CC(C1)C3"`



Phenix GUI

- Central GUI to view job control and launch new jobs

The screenshot displays the Phenix GUI interface. At the top, there is a menu bar with options: Quit, Preferences, Help, New project, Project settings, Job history, Citations, Reload last job, Coot, PyMOL, and KING. Below the menu bar is a status bar with the text: "Click or drag-and-drop files onto a program to launch it. To switch to a project, click the 'Choose this project' button."

The main interface is divided into two main sections. On the left is a table titled "Projects" with columns: ID, Last modified, # of jobs, and R-free. On the right is a sidebar with various tool categories and options.

ID	Last modified	# of jobs	R-free
✓ 1016B	Aug 17 2010 11:51 ...	19	0.3665
1BOV	Jul 05 2010 02:33 PM	2	None
2hr0	Sep 19 2009 01:16 ...	2	None
3g5u	Nov 14 2009 03:14 ...	1	None
3lna	May 18 2010 06:45 ...	5	0.3901
actin-2010	May 31 2010 06:18 ...	0	None
calmodulin	None	0	None
chennai-a2u-gl ...	Jan 19 2010 01:37 AM	6	0.2547
chennai_p9_sad	Mar 03 2010 07:18 ...	4	0.3157
qgr-2010	Mar 16 2010 03:50 ...	0	None
gui	None	0	None
haemoglobin	Mar 27 2010 09:34 ...	6	0.2977
horseHb	Oct 26 2009 08:57 ...	2	0.5026
insulin	Nov 15 2009 11:33 ...	1	0.2039
jason-kim	Jul 05 2010 05:12 PM	25	0.4706
lysozyme	Oct 24 2009 09:25 ...	3	0.3336
lysozyme-mono ...	Mar 08 2010 12:33 ...	6	0.5638
lysozyme test	Nov 15 2009 11:11 ...	1	0.2329
mmcpr-compari ...	Aug 03 2010 04:15 ...	3	None
mmcpr_dec_2009	Dec 12 2009 09:27 ...	9	0.2624
nsf-ligand	Mar 06 2010 08:56 ...	1	0.3002
p9	Nov 26 2009 11:16 ...	11	0.2612
p9-sad_pdadams	Jun 15 2010 09:58 AM	3	0.2473
porin-twin	Apr 30 2010 11:32 ...	1	None
porin-twin_inclad	Jun 09 2010 03:45 PM	3	0.1481

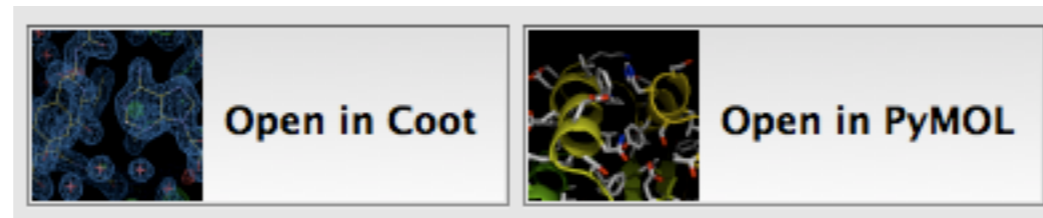
The sidebar on the right contains the following tool categories and options:

- Reflection tools**
- Model tools**
- Experimental phasing**
 - AutoSol**: Automated experimental phasing with model-building
 - Phaser-EP**: Maximum-likelihood SAD experimental phasing
 - Density modification**: Simple interface for running density modification only using AutoBuild and RESOLVE
- Molecular replacement**
- Model building**
 - AutoBuild**: Automated model-building and refinement
 - Find Helices and Strands**: Fast chain tracing
 - Fit Loops**: Fast placement of missing loops in electron density
- Refinement**
 - phenix.refine**: Automated X-ray and neutron refinement
 - ReadySet**: Utility for preparing PDB files for refinement – automatically generate restraints and add hydrogens
- Maps**

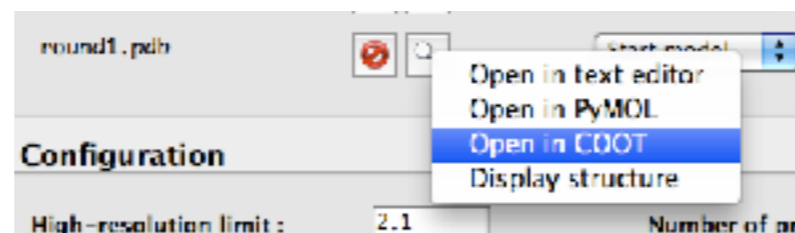
At the bottom of the interface, there is an "Output directory" field with the path `/Users/pdadams/Work/Structures/1016B` and a "Browse..." button. The status bar at the very bottom shows "PHENIX version L6.4-48b" and "Project: 1016B".

Coot/PyMOL integration

- Most results can be opened directly in graphics apps



- Any PDB file listed in GUI can also be opened



- AutoSol, AutoBuild, and phenix.refine will update Coot continuously while running
- Coot must have Python support (default on Mac)
- Specific paths to executables usually required on Linux
- *Preferences->Graphics->Full path to Coot [...PyMOL]*

Recent Developments

- Automated structure solution with weak anomalous data
- Translational NCS corrections in SAD phasing

- MR_Rosetta and morphing for rescuing poor MR solutions
- Translational NCS corrections in MR

- Automated model building for cryo-EM maps

- New Rosetta methods for RNA rebuilding (ERRASER)

- Automated ion placement in refinement
- Automated ligand pipeline

- DIALS included in Phenix distribution

- Real space refinement (for X-ray and cryo-EM)

- Low resolution refinement algorithms:
 - Rosetta refinement
 - Reference model
 - Torsion NCS
 - Structure restraints

- Feature Enhanced Maps to improve interpretability
- Polder maps for better ligand density
- Ensemble refinement to understand dynamics and structural variability

- New validation methods for cryo-EM models

- Support for mmCIF format (for structure deposition)
- Video Tutorials



Challenges

- Low resolution structure solution and refinement
- Structure completion
 - Automated identification, fitting and refinement of ligands, metals, ions, and water
 - Identification, fitting and refinement of discrete disorder (multiple conformations)
 - Representing other forms of disorder
- Automated parameterization of models in refinement
 - ADPs, TLS groups, NCS, hydrogens
- Handling different kinds of twinning and integrating it into the whole structure solution process
- Automated understanding of chemistry



PHENIX Availability

- phenix-online.org
- Supported on:
 - Linux (RedHat, Fedora)
 - Mac OSX
 - Windows
- Extensive documentation
- Nightly builds:

The screenshot shows the Phenix website with the following content:

- Phenix** Python-based Hierarchical Environment for Integrated X-ray Crystallography
- Documentation: (HTML) FAQ
- PHENIX is a software suite for the automated determination of molecular structures using X-ray crystallography and other methods.
- Download the latest official release (1.11.1) (First request download password)
- Download the latest nightly build or prerelease
- Help: Email Us Report a Bug List Archives Subscribe to Mailing List
- Using PHENIX (release 1.11.1):
 - The PHENIX Graphical User Interface
 - Assessing data quality with phenix.xtriage
 - Automated structure solution with Autosol
 - Automated molecular replacement with Phaser-MR
 - Automated model building and rebuilding with AutoBuild
 - Automated ligand fitting with LigandFit
 - Structure refinement with phenix.refine
 - Generation of ligand coordinates and restraints with eLBOW
- The PHENIX system also includes SOLVE/RESOLVE, Phaser, the CCI Applications (phenix.xtriage, phenix.refine, elbow and many more), components from MolProbity, and the Computational Crystallography Toolbox in a Python framework.
- Citing PHENIX: PHENIX: a comprehensive Python-based system for macromolecular structure solution. P. D. Adams, P. V. Afonine, G. Bunkóczi, V. B. Chen, I. W. Davis, N. Echols, J. J. Headd, L.-W. Hung, G. J. Kapral, R. W. Grosse-Kunstleve, A. J. McCoy, N. W. Moriarty, R. Oeffner, R. J. Read, D. C. Richardson, J. S. Richardson, T. C. Terwilliger and P. H. Zwart. *Acta Cryst.* **D66**, 213-221 (2010).
- Funding for PHENIX: NIH General Medical Sciences
- The PHENIX system also can be used for neutron crystallography. NIH funding supports the development of this capability through a grant to Paul Langan (Los Alamos National Laboratory) and Paul Adams. See the [Macromolecular Neutron Crystallography Consortium site](#) for more details. Citation for neutron structure refinement in Phenix: Adams PD, Mustyakimov M, Afonine PV, Langan P: Generalized X-ray and neutron crystallographic analysis: more accurate and complete structures for biological macromolecules. *Acta Cryst.* 2009, **D65**:567-573.
- The PHENIX Industrial Consortium

Version	Date	Status	Logs	Info
dev-2747	2017-04-17	successful	intel-windows-x86_64 , intel-linux-2.6-x86_64-centos5 , intel-linux-2.6-x86_64-centos5 , mac-intel-osx-x86_64 , intel-linux-2.6-centos5 , ci , intel-windows	docs ; changelog
dev-2744	2017-04-13	successful	ci , intel-linux-2.5-x86_64-centos6 , intel-linux-2.6-x86_64-centos5 , intel-linux-2.6-centos5 , mac-intel-osx-x86_64 , intel-windows , intel-windows-x86_64	docs ; changelog
dev-2733	2017-04-02	successful	intel-linux-2.6-x86_64-centos6 , ci , intel-windows , mac-intel-osx-x86_64 , intel-windows-x86_64 , intel-linux-2.5-x86_64-centos5 , intel-linux-2.6-centos5	docs ; changelog
dev-2722	2017-03-22	successful	ci , intel-linux-2.5-centos5 , intel-windows-x86_64 , mac-intel-osx-x86_64 , intel-windows , intel-linux-2.6-x86_64-centos5 , intel-linux-2.5-x86_64-centos5	docs ; changelog
dev-2621	2016-12-11	successful	intel-windows , ci , mac-intel-osx-x86_64 , intel-windows-x86_64 , intel-linux-2.5-centos5 , intel-linux-2.6-x86_64-centos6 , intel-linux-2.6-x86_64-centos5	docs ; changelog



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- Calculating polder maps with the GUI
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Dorothee Liebschner, Nigel Moriarty, Miffy Mifsud



Acknowledgments

- **Lawrence Berkeley Laboratory**

- Pavel Afonine, Youval Dar, Nat Echols, Jeff Headd, Richard Gildea, Ralf Grosse-Kunstleve, Nigel Moriarty, Nader Morshed, Billy Poon, Ian Rees, Nicholas Sauter, Oleg Sobolev, Peter Zwart

- **Los Alamos National Laboratory**

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- Randy Read, Airlie McCoy, Laurent Storoni, Gabor Bunkoczi, Robert Oeffner

- **Duke University**

- Jane Richardson & David Richardson, Ian Davis, Vincent Chen, Jeff Headd, Chris Williams, Bryan Arendall, Bradley Hintze, Laura Murray

- **EMRinger**

- Ben Barad, Yifan Cheng, Jaime Fraser (UCSF)
- Ray Wang, Frank DiMaio (UW)

- **Rosetta**

- Frank DiMaio, David Baker (U Washington)

- **Cryo-EM Structure Refinement**

- Corey Hryc, Zhao Wang, Matthew Baker, Wah Chiu (Baylor College of Medicine)
- Adam Frost (UC San Francisco), Gino Cingolani (Jefferson University, PA), Valerie Pye (Cancer Research UK), Darcie Miller (St. Jude Research Hospital), Anastasia Aksyuk (NIH), Mavis Agbandje-McKenna (University of Florida), Stuart Howes (Eva Nogales Lab), Ali Andres Malay (RIKEN, Japan)

- **Other Collaborators**

- Axel Brunger (Stanford)
- Dale Tronrud, Donnie Berholz, Andy Karplus
- Alexandre Urzhumtsev & Vladimir Lunin
- Garib Murshudov & Alexi Vagin
- Kevin Cowtan, Paul Emsley, Bernhard Lohkamp
- David Abrahams
- PHENIX Testers & Users

- **Funding:**

- NIH/NIGMS:
 - *P01GM063210, P50GM062412, P01GM064692, R01GM071939*
- PHENIX Industrial Consortium
- Lawrence Berkeley Laboratory



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