# Working Meeting at FermiLab

University of California Grid (UC Grid)

January 19-20, 2010

Fermi Lab, Chicago, IL

### **LBNL**

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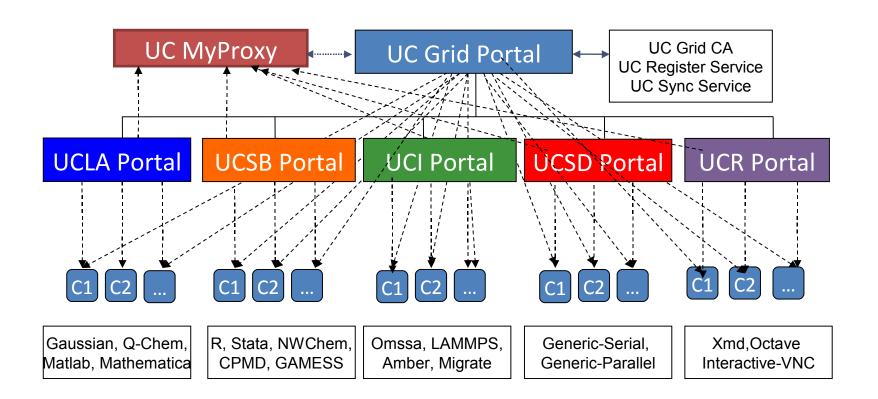
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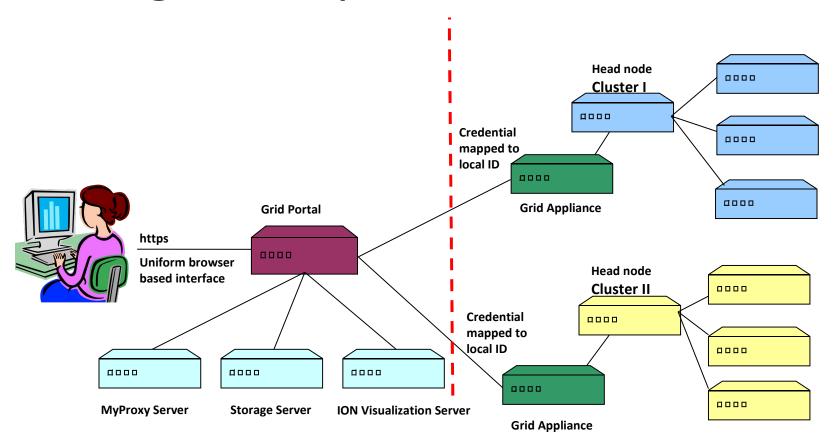




#### **UC Grid Architecture**



# Single Campus Architecture



#### The UC Grid Portal

- Provides Register Service (SOA):
  - user portal account creation and uniqueness of user name in the UC Grid, automatic CA sign, MyProxy push.
- Provides Sync Service (SOA) between campus portal and UC Grid portal:
  - Any change of an user account at a campus Grid Portal is automatically propagated to the UC Grid Portal.
  - Any change of new resources at a campus Grid Portal will also be reflected at UC Grid Portal
- From the UC Grid Portal, users can:
  - work with clusters from all the campuses those users are authorized to use.
  - transfer files across the campuses.
  - Use pooled resources across the campuses.

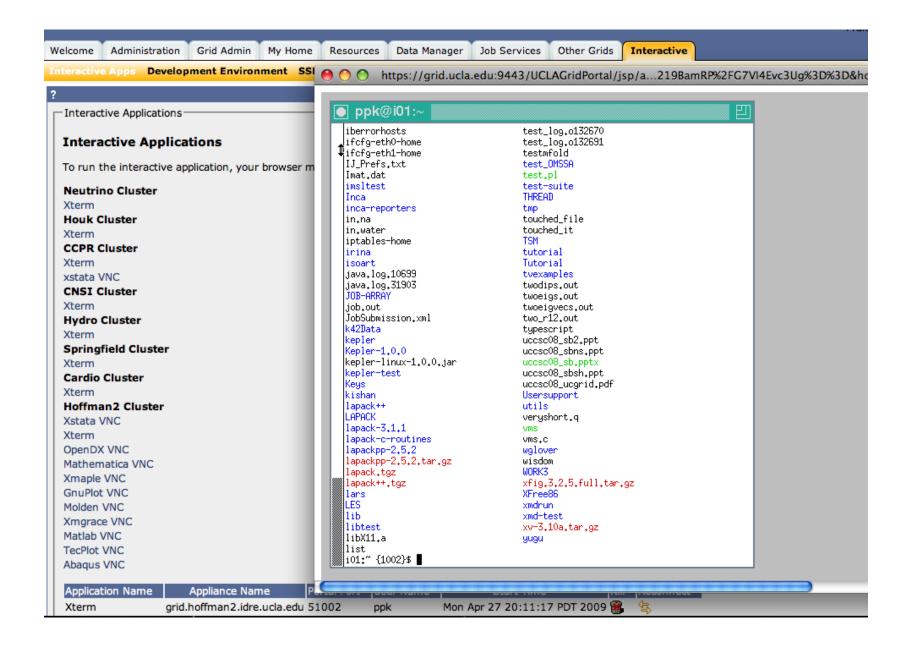
# Campus Grid Portal

- Features:
  - Resource Discovery
    - Cluster load, usage, queue information, job details
  - Data Manager
    - File management such as create, remove, rename, edit, transfer etc.
  - Job Services
    - Submit job as a cluster user
    - Submit job as a pool user
  - Interactive X window for applications
    - Matlab, Mathematica, Maple, Xstata etc.
  - Access to Teragrid

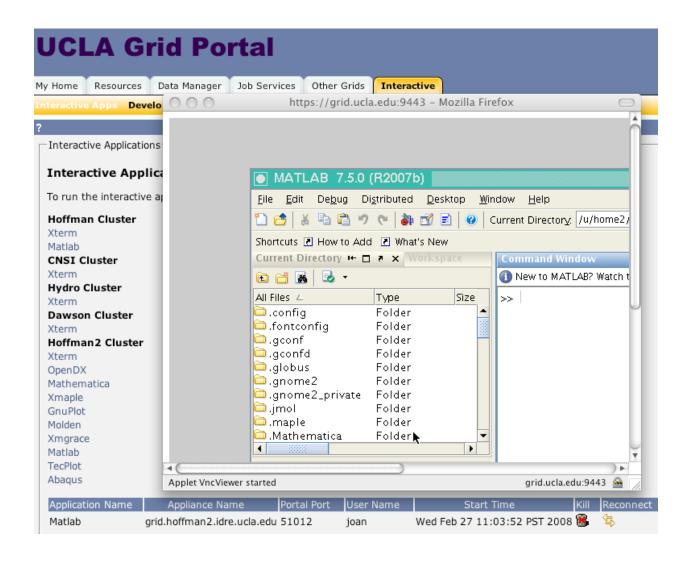
#### **Job Submission**

- General Job submission
  - Any user created executable
- Application job submission
  - Predefined executable
    - As Cluster user
    - As Pool user
- Pool user application job submission
  - UGP Chooses the target cluster for the application job.
  - Stages the input files to a guest user login id at the target cluster
  - Submits the job to run under a guest login id at the target cluster.
  - Local scheduler determines when those jobs are run.
  - UGP facilitates the transfer of the output files back to the Pool User.
  - Provide job monitoring and auditing

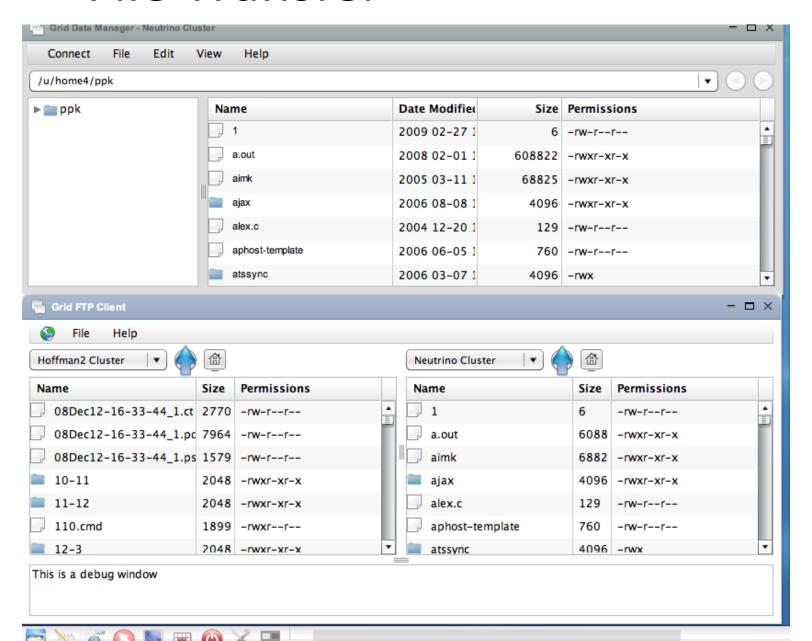
#### Interactive Xterm through VNC



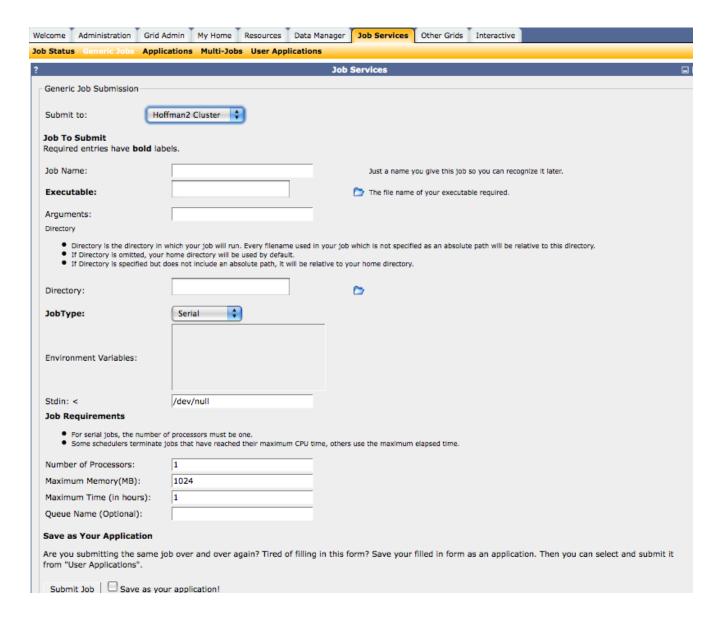
#### Interactive GUI Application through VNC



## File Transfer



#### Generic Batch Job Submission Interface

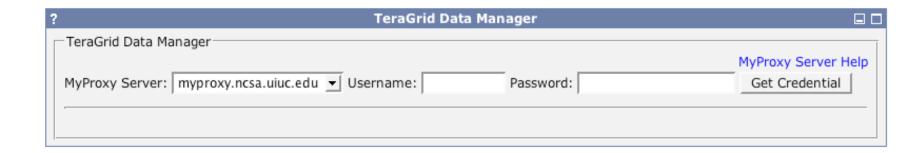


# **Predefined Application**

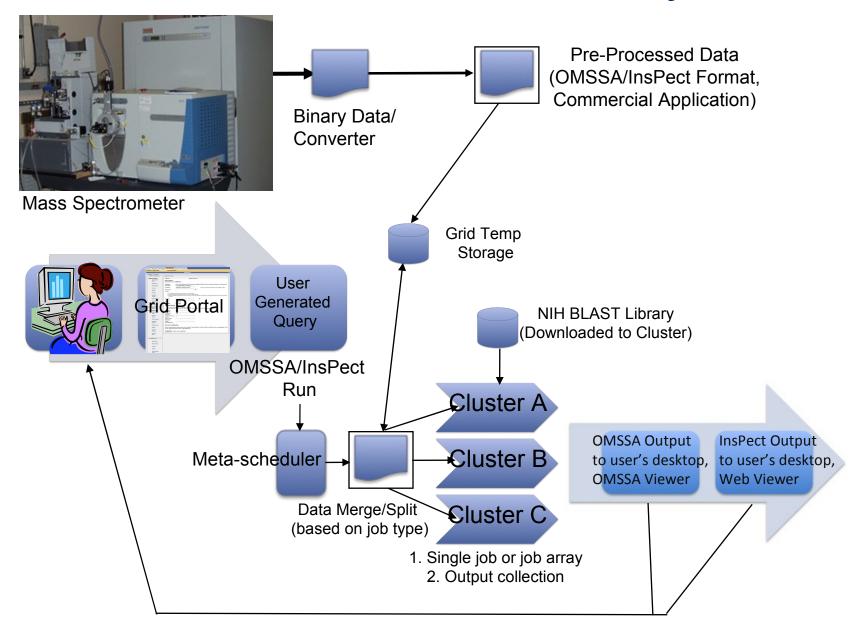
Welcome Administration Grid A	dmin My Home Resources C	Data Manager Job Services Other Grids	Interactive			
ob Status Generic Jobs Applic	ations Multi-Jobs User Applic	ations				
?		Applications	•			
Application Submission						
Predefined Applications	Amber10 parallel					
Neutrino Cluster	Submit to:	Hoffman2 Cluster				
Mathematica	Job To Submit					
Mathematica	Required entries have <b>bold</b>	labels.				
64 bit	Application Description:	A molecular dynamics software package				
Houk Cluster	Job Name:	Amber10-Hoffman2-parallel	Just a name you give this job so you can recognize it			
Gaussian03- Parallel	Arguments:		later.			
	Directory					
Gaussian03- Serial	If you specify a directory, your job will be run in that directory.					
	<ul> <li>If you don't specify a dire</li> </ul>	ctory, your job will run in your home directory.	will be relative to the directory specified or your home directory			
CCPR Cluster Stata	<ul> <li>Unless an absolute path is specified for any file used in the job, the filename will be relative to the directory specified or your home directory, if omitted.</li> </ul>					
CHCT Cluster	Click here for more inform	nation				
CNSI Cluster Gaussian03-	Directory:					
Serial	Stdin: <	/dev/null				
Q-Chem	JobType:	MPI Parallel 💠				
Hoffman2 Cluster	Job Requirements					
Gaussian	For serial jobs, the number of processors must be one.					
Amber10	Some schedulers termina	te jobs that have reached their maximum CPU time,	others use the maximum elapsed time.			
parallel	Number of Processors:	1				
Amber10	Memory Per Processor:	1024				
serial	Maximum Time (in hours):	1				
Q-Chem-	Queue Name (Optional):					
Parallel	Project Name(Optional):					
R	Save as Your Application					
Amber9		sich over and ever again? Tired of filling in	this form? Save your filled in form as an application			
parallel	parallel  Are you submitting the same job over and over again? Tired of filling in this form? Save your filled in form as an applicat Then you can select and submit it from "User Applications".					
Stata10						
Amber9 serial	Submit Job Save as	your application!				

#### Job Submission to Other Grid Resources

User interface to fill in username and password to retrieve short lived credential for submitting jobs to Teragrid



# **Proteomics Workflow Project**

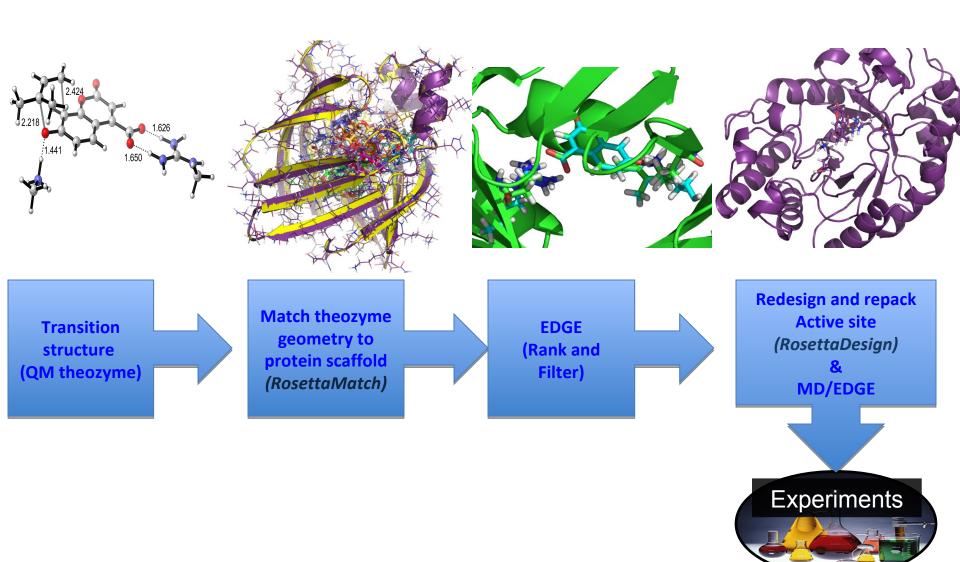


## Protein Design Processes



#### Inside-out protocol to design novel enzyme catalysts

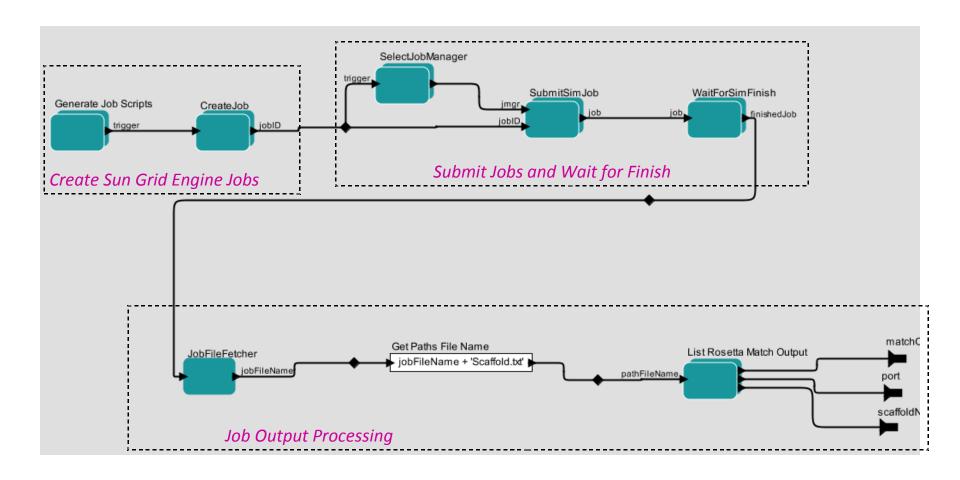
**Baker - Houk collaboration** 



## Enzyme Design Using Kepler Workflow

- RosettaMatch
  - •Goal: Finds the enzyme Scaffolds for the input theozyme
  - •Approximately 250 Jobs per submission Each creates around 2000 outputs
  - Workflow Distribute the Jobs through Scheduler/Grid
- Edge
  - •Goal: Filter out Match results that are out of user defined range
  - Least time consuming Single node job
- RosettaDesign
  - Goal: Repacks and Optimize the side chains
  - •Workflow Distribute 5 million jobs from Match run through Scheduler/Grid

# Rosetta Match SGE Composite Actor



# Command line instructions for two cluster workflow (Hoffman2 and Hydro)

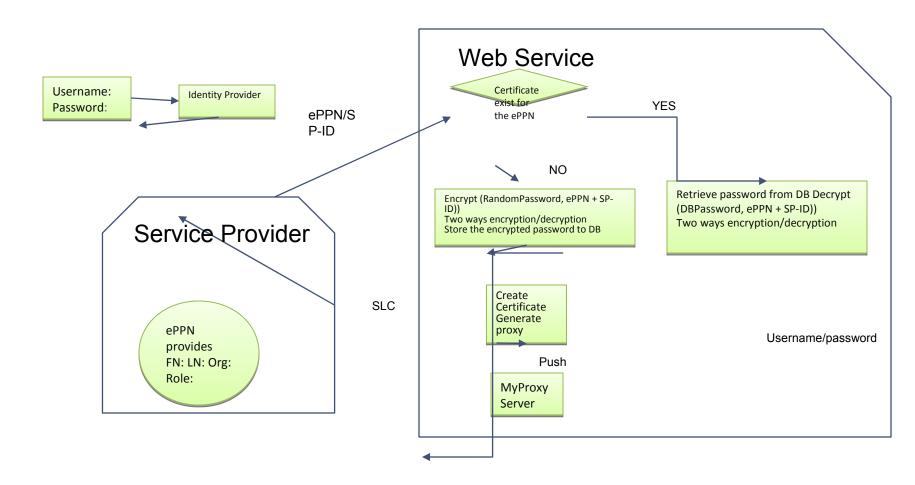
- Retrieve proxy from myproxy.ucgrid.org
- /u/local/apps/kepler/kepler.modules/build-area/kepler.sh
  - -MyProxyFilePath /tmp/x509up\_uid
  - -GlobusTaskPath4Hoffman2
  - /u/scratch/ppk/rosetta/rosetta-grid-workflow-hoffman2
  - -GlobusTaskPath4Hydro
  - /u/scratch/ppk/rosetta/rosetta-grid-workflow-hydro
  - -ScaffoldPath4Hoffman2
  - /u/home2/ppk/rosettatest/scaffold-hoffman2-one-scaffold
  - -ScaffoldPath4Hydro
  - /u/home2/ppk/rosettatest/scaffold-hydro-one-scaffold
  - /u/local/apps/kepler/rosetta-workflow/Rosetta-Match-BChain-Design-
  - Globus-TopLevel-Parallel-v1-18.xml

 TaskPaths are scratch directories for the run and ScaffoldPath is the location of input files for each cluster pre-divided by the user. Workflow directives are in the xml file

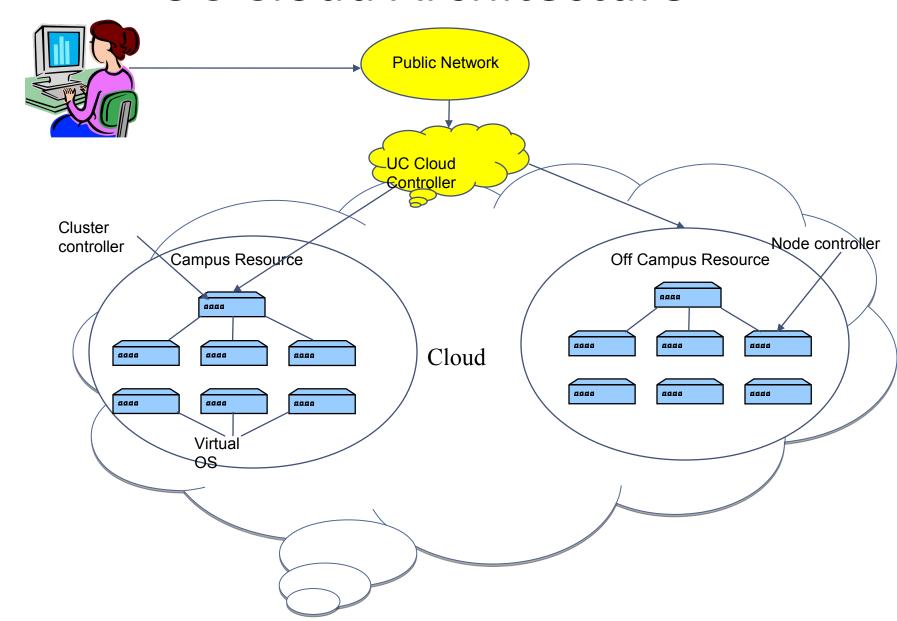
# Experimental data on Hoffman2 cluster

Workflow name	Workflow Structure	Inputs	Main configurations	Job number	Execution time
Rosetta-MatchSGE- v2-4.xml	MatchSGEJob	226 Scaffold	1) Match command number for each job: 5 Generate 108,012 pdb files.	46 Match SGE jobs.	5.36 hours
Rosetta-MatchSGE-BChain-v1-6.xml	MatchSGEJob + BChain	226 Scaffold	1) Match command number for each job: 5 Generate 216,024 pdb files.	46 Match SGE jobs.	5.19 hours
Rosetta- DesignSGE-v1- 8.xml	DesignSGEJob (each design includes cst, des and min)	10 Scaffold	1) Structure Number for Design Calculation: 10. 2) Command number for each job: 5 (cst) + 5 (des) + 50 (min) = 60. Generate 14691 pdb files.	286 Design SGE jobs	10.73 hours
Rosetta-MatchSGE-BChain- DesignSGE-v1- 9.xml	SGEMatch, BChain, SGEDesign	10 scaffold	<ol> <li>Command number for each Match job: 1.</li> <li>Structure Number for Design Calculation: 10.</li> <li>Command number for each Design job: 5 (cst) + 5 (des) + 50 (min) = 60.</li> </ol>	10 Match Jobs and 286 Design Jobs.	6.70-17.01 hours.
Rosetta- DesignSGE-v1- 8.xml	DesignSGEJob (each design includes cst, des and min)	226 Scaffold	1) Structure Number for Design Calculation: 100. 2) Command number for each job: 10 (cst) + 10 (des) + 1000 (min) = 1100.  The whole cmd number could be 50 million and the whole execution could generate 7 million files: * 14691 * 10 = 7,793,734,24. (2036 is the pdb file number for 10 Scaffold of Rosetta-MatchSGE-v2-4.xml)	Over 11,000 Design SGE jobs.	One job may last for over 18 hours.  Estimated whole execution time: (108012/2036) * 10.73 * 10 = 7.79 months.

#### Workflow to Use Shibboleth Authentication to Sign X509 Certificate



# **UC Cloud Architecture**



# UC Grid Portal Contact Information http://www.ucgrid.org

http://inca.ucgrid.org

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