

Per Kraulis, CV

- Chemical Engineer, KTH
- Structural Biology
- Protein NMR & 3D analysis
 - Ph.D. Uppsala Univ
 - Postdoc Cambridge Univ
 - Karolinska Inst
- Bioinformatics
- Pharmacia
- Sthlm Bioinfo Center
- Biovitrum
- Tartu University
- SGC

More about me...

Linked 

- <http://se.linkedin.com/in/perkraulis>

citeulike 

- <http://www.citeulike.org/user/pekrav>
- <http://delicious.com/pekrav>
- <http://www.avatar.se/>

Systems Architect

(Scientific programmer/Systems developer)

- Software
 - MolScript
 - ANSIG (protein NMR)
- Programming
 - **Python**
 - JavaScript (Ajax)
 - C, C++, Simula, Pascal, Eiffel, Fortran...



- Relational database systems
 - **MySQL**, Oracle
- Other database systems
 - Gdbm, XML, OODBMS

Task: Software system admin

- Setup of common stuff
 - On russola & other “local” servers
 - Tools (executables)
 - Reference databases (Human genome, etc)
 - Documentation
- (Help with) sysadmin
 - Disk police
 - Queues?

Task: LIMS setup

- Geospiza LIMS for Genomics (?)
- Configuration
- Integration with analysis
- Policy for datasets
 - Persistent, coherent identifier scheme
 - Storage and backup
- ELN issue: Contur, Wiki, Google Wave,...?

Task: Analysis Pipeline

- Standard analysis for Service-for-fee
- Set up analysis modules
- Set up self-tests
- Visualization tools
 - Explore datasets
 - Identify strange problems

Task: Workflow system

- Current trend in e-Science: Taverna, Galaxy,...
-  Flownode (under development)
 - Web-integrated (fully, not just client-only)
 - Cloud-computing (Grid) enabled
 - Human interaction (via browser)
 - Programmatic interface
 - Web Services
 - REST architecture
- Implement standard analysis modules