Knowledgebase Access

mySQL setup

```
sudo apt-get install mysql-server
sudo apt-get install mysql-workbench
```

Login to database

```
mysql --user=root mysql --password=<pw>
```

Create user

```
CREATE USER 'mkoenig'@'localhost' IDENTIFIED BY 'test';
GRANT ALL PRIVILEGES ON *.* TO 'mkoenig'@'localhost' WITH GRANT OPTION;
```

Test access

```
mysql -u mkoenig -p -h localhost wholecellkb
```

Create database

```
CREATE DATABASE wholecellkb DEFAULT CHARACTER SET utf8 DEFAULT COLLATE
utf8_unicode_ci;
DROP DATABASE wholecellkb
```

Django setup

```
sudo pip install django==1.6.8
sudo pip install django-haystack xapian-haystack django-extensions
sudo pip install xhtml2pdf httplib2 nose pisa hashlib huTools BeautifulSoup docutils
epydoc odict
sudo apt-get install python-biopython
```

Code

https://github.com/dagwa/wholecell-metabolism/mkoenig/python/database

Path settings `bash.bashrc`

```
export
PYTHONPATH=${PYTHONPATH}:/home/mkoenig/wholecell-metabolism/mkoenig/python/database/
export
PYTHONPATH=${PYTHONPATH}:/home/mkoenig/wholecell-metabolism/mkoenig/python/database/wh
olecellkb
export
PYTHONPATH=${PYTHONPATH}:/home/mkoenig/wholecell-metabolism/mkoenig/python/database/pu
blic
export DJANGO_SETTINGS_MODULE=wholecellkb.settings
```

Create Django DB schema

```
python manage.py syncdb
```

Import MySQL dump
Download the SQL dump (data.sql)

https://simtk.org/frs/download.php?file_id=3426

```
mysql -u mkoenig -p test -h localhost wholecellkb < data.sql
```
Can be necessary to import the SQL manually

Edit database settings `database/settings.py`
• `DATABASES: edit host, user, password`

Overview schema

Overview of tables and relationships for navigation between table

https://github.com/dagwa/wholecell-metabolism/mkoenig/schema/index.html

Examples

```
from public.models import Metabolite, Reaction, Gene

# print some metabolites
metabolites = Metabolite.objects.all()[:10]
for m in metabolites:
    print m.pk, m.name, m.charge
# find some reactions
Reaction.objects.filter(name__startswith='A')
# find some genes
Gene.objects.filter(name__contains="2")
```