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Python 2.7.6 (default, Mar 22 2014, 22:59:56)
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IPython 1.2.1 -- An enhanced Interactive Python.
?         -> Introduction and overview of IPython's features.
%quickref -> Quick reference.
help      -> Python's own help system.
object?   -> Details about 'object', use 'object??' for extra details.
%guiref   -> A brief reference about the graphical user interface.

In [1]: from public.models import Metabolite
   ...:
   ...: # get first 10 metabolites
   ...: metabolites = Metabolite.objects.all()[:10]
   ...: for m in metabolites:
   ...:     # Metabolite inherits from Entry, so all fields are available
   ...:     print m.pk, m.id, m.model_type, m.wid, m.name, m.charge
   ...:

3383 3383 Metabolite A23CMP 2',3'-Cyclic AMP -1
3384 3384 Metabolite A3MP 3'-AMP -2
3385 3385 Metabolite AC acetate -1
3386 3386 Metabolite ACAL acetaldehyde 0
3387 3387 Metabolite ACCOA Acetyl-CoA -4
3388 3388 Metabolite acetamide acetamide  0
3389 3389 Metabolite acriflavine Acriflavine 1
3390 3390 Metabolite ACTP Acetyl phosphate -2
3391 3391 Metabolite AD adenine 0
3392 3392 Metabolite ADN adenosine 0

In [2]: # find all genes which have a 2 in it
   ...: from public.models import Gene
   ...: genes = Gene.objects.filter(name__contains="2")
   ...: print genes
   ...:
[<Gene: MGrrnA23S>, <Gene: MG_018>, <Gene: MG_070>, <Gene: MG_087>, <Gene: MG_108>, <Gene:
MG_142>, <Gene: MG_153>, <Gene: MG_154>, <Gene: MG_156>, <Gene: MG_159>, <Gene: MG_162>,
<Gene: MG_198>, <Gene: MG_207>, <Gene: MG_209>, <Gene: MG_218>, <Gene: MG_232>, <Gene:
MG_234>, <Gene: MG_246>, <Gene: MG_252>, <Gene: MG_316>, '...(remaining elements
truncated)...']

In [3]: from public.models import Reaction
   ...: rs = Reaction.objects.filter(name__startswith='A')
   ...: print rs
   ...: # print the stoichiometry of first reaction
   ...: print rs[0].stoichiometry.all()
[<Reaction: AspC1>, <Reaction: AtpA>, <Reaction: LplA>, <Reaction: NH3eq>, <Reaction:
TX_ACAL>]
[<ReactionStoichiometryParticipant: molecule: GLU, coefficient: -1.0, compartment: c,
evidence: []>, <ReactionStoichiometryParticipant: molecule: OA, coefficient: -1.0,
compartment: c, evidence: []>, <ReactionStoichiometryParticipant: molecule: AKG,
coefficient: 1.0, compartment: c, evidence: []>, <ReactionStoichiometryParticipant:
molecule: ASP, coefficient: 1.0, compartment: c, evidence: []>]

In [4]: from public.models import Entry
   ...: from pandas import DataFrame
   ...: import pandas as pd
   ...:
   ...: # create pandas DataFrame for all entries
   ...: entries = Entry.objects.all()
   ...: entries_df = DataFrame(columns=('id', 'model_type', 'wid', 'name'))
   ...: for k, e in enumerate(entries):
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   ...:     # Bad in place extension of DataFrame (do not do in production code)
   ...:     entries_df.loc[k] = (e.id, e.model_type, e.wid, e.name)
   ...:
   ...: entries_df = entries_df.set_index(entries_df.id)
   ...: # print the first 10
   ...: print entries_df.head(10)
        id  model_type     wid  \
id
3383  3383  Metabolite  A23CMP
3384  3384  Metabolite    A3MP
5409  5409    Reaction    Aas1
5410  5410    Reaction    Aas2
5411  5411    Reaction    Aas3
5412  5412    Reaction    Aas4
5413  5413    Reaction    Aas5
5414  5414    Reaction    Aas6
5415  5415    Reaction    Aas7
3385  3385  Metabolite      AC

                                                  name
id
3383                                  2',3'-Cyclic AMP
3384                                             3'-AMP
5409  acyl-[acyl-carrier-protein] synthetase  (n-C12:0)
5410   acyl-[acyl-carrier-protein] synthetase (n-C14:0)
5411  acyl-[acyl-carrier-protein] synthetase  (n-C14:1)
5412  acyl-[acyl-carrier-protein] synthetase  (n-C16:0)
5413  acyl-[acyl-carrier-protein] synthetase  (n-C16:1)
5414  acyl-[acyl-carrier-protein] synthetase  (n-C18:0)
5415  acyl-[acyl-carrier-protein] synthetase  (n-C18:1)
3385                                               acetate

In [5]:
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