

```
<RBAMetabolism>
  <listOfCompartments>
    <compartment id="Secreted"/>
    <compartment id="Cell_inner_membrane"/>
    <compartment id="Cytoplasm"/>
    <compartment id="Periplasm"/>
    <compartment id="Membrane"/>
    <compartment id="Cell_outer_membrane"/>
    <compartment id="Cell_membrane"/>
  </listOfCompartments>
  <listOfSpecies>
    <species id="M_10fthf_c" boundaryCondition="false"/>
    <species id="M_12dgr120_c" boundaryCondition="false"/>
    <species id="M_12dgr140_c" boundaryCondition="false"/>
    <species id="M_12dgr141_c" boundaryCondition="false"/>
  </listOfSpecies>
</RBAMetabolism>
```

Import / Export

```
In [2]: model = rba.RbaModel.from_xml('data/iJ01366_test/')
```

```
In [3]: model.metabolism.compartments[0]
```

```
Out[3]: <rba.xml.metabolism.Compartment at 0x7fc88c687510>
```

```
In [4]: model.metabolism.compartments[0].id
```

```
Out[4]: 'Secreted'
```

```
In [5]: model.metabolism.species[0]
```

```
Out[5]: <rba.xml.metabolism.Species at 0x7fc88c687a10>
```

```
In [6]: model.metabolism.species[0].id
```

```
Out[6]: 'M_10fthf_c'
```

```
In [7]: model.metabolism.species[0].boundary_condition
```

```
Out[7]: False
```