

```
<?xml version="1.0" encoding="UTF-8"?>
```

```
<sbml xmlns="http://www.sbml.org/sbml/level3/version1/core " level="3" version="1"  
xmlns:layout="http://www.sbml.org/sbml/level3/version1/layout/version1" >
```

```
<listOfPackages>
```

```
<package
```

```
namespace="http://www.sbml.org/sbml/level3/version1/layout/version1"
```

```
required="false" />
```

```
</listOfPackages>
```

```
<model name="Untitled">
```

```
<listOfCompartments>
```

```
<compartment id="compartment" size="1.0" spatialDimensions="3"
```

```
constant="true"/>
```

```
</listOfCompartments>
```

```
<listOfSpecies>
```

```
<species id="P_i"
```

```
compartment="ancestor::model[1]/*/compartment[@id='compartment']"
```

```
initialAmount="0" hasOnlySubstanceUnits="false" constant="false"
```

```
boundaryCondition="false"/>
```

```
<species id="Glucose"
```

```
compartment="ancestor::model[1]/*/compartment[@id='compartment']"
```

```
initialAmount="0" hasOnlySubstanceUnits="false" constant="false"
```

```
boundaryCondition="false"/>
```

```
<species id="H2O"
```

```
compartment="ancestor::model[1]/*/compartment[@id='compartment']"
```

```
initialAmount="0" hasOnlySubstanceUnits="false" constant="false"
```

```
boundaryCondition="false"/>
```

```
<species id="G6P"
```

```
compartment="ancestor::model[1]/*/compartment[@id='compartment']"
```

```
initialAmount="0" hasOnlySubstanceUnits="false" constant="false"
```

```
boundaryCondition="false"/>
```

```
</listOfSpecies>
```

```
<listOfReactions>
```

```
<reaction id="reaction_0" reversible="false" fast="false">
```

```
<listOfReactants>
```

```
<speciesReference id="SR_H2O"
```

```
species="ancestor::model[1]/*/species[@id='H2O']" stoichiometry="1"/>
```

```
<speciesReference id="SR_G6P"
```

```
species="ancestor::model[1]/*/species[@id='G6P']" stoichiometry="1"/>
```

```
</listOfReactants>
```

```
<listOfProducts>
```

```
<speciesReference id="SR_P_i"
```

```
species="ancestor::model[1]/*/species[@id='P_i']" stoichiometry="1"/>
```

```
<speciesReference id="SR_Glucose"
```

```
species="ancestor::model[1]/*/species[@id='Glucose']" stoichiometry="1"/>
```

```
</listOfProducts>
```

```
</reaction>
```

```
</listOfReactions>
```

```
<listOfLayouts
```

```
xmlns="http://www.sbml.org/sbml/level3/version1/layout/version1">
```

```
<layout id="layout1">
```

```
<dimensions width="320" height="270"/>
```

```
<listOfCompartmentGlyphs>
```

```
<compartmentGlyph id="compGlyph"
```

```
compartment="ancestor::model[1]/*/compartment[@id='compartment']">
```

```
<boundingBox>
```

```

                <position x="10.0" y="10.0"/>
                <dimensions w="60" height="50"/>
            </boundingBox>
        </compartmentGlyph>
    </listOfCompartmentGlyphs>
    <listOfSpeciesGlyphs>
        <speciesGlyph id="P_iGlyph"
species="ancestor::model[1]/*/species[@id='P_i']">
            <boundingBox>
                <position x="63.0" y="124.0"/>
                <dimensions width="16.0" height="16.0"/>
            </boundingBox>
        </speciesGlyph>
        <speciesGlyph id="Glucose_Glyph1"
species="ancestor::model[1]/*/species[@id='Glucose']">
            <boundingBox>
                <position x="146.0" y="106.0"/>
                <dimensions width="16.0" height="16.0"/>
            </boundingBox>
        </speciesGlyph>
        <speciesGlyph id="H2O_Glyph"
species="ancestor::model[1]/*/species[@id='H2O']">
            <boundingBox>
                <position x="67.0" y="224.0"/>
                <dimensions width="16.0" height="16.0"/>
            </boundingBox>
        </speciesGlyph>
        <speciesGlyph id="G6P_Glyph"
species="ancestor::model[1]/*/species[@id='G6P']">
            <boundingBox>
                <position x="180.0" y="241.0"/>
                <dimensions width="15.0" height="16.0"/>
            </boundingBox>
        </speciesGlyph>
    </listOfSpeciesGlyphs>
    <listOfReactionGlyphs>
        <reactionGlyph id="reaction_0_Glyph"
reaction="ancestor::model[1]/*/reaction[@id='reaction_0']">
            <curve>
                <listOfCurveSegments>
                    <curveSegment type="CubicBezier">
                        <start x="120.0" y="183.0"/>
                        <end x="119.0" y="169.0"/>
                    </curveSegment>
                </listOfCurveSegments>
            </curve>
            <listOfSpeciesReferenceGlyphs>
                <speciesReferenceGlyph id="SP1_Glyph"
speciesGlyph="ancestor::model[1]/*/*/*/*speciesGlyph[@id='P_i_Glyph']"
speciesReference="ancestor::model[1]/*/*/*/*speciesReference[@id='SR_P_i']"/>
                <speciesReferenceGlyph id="SP2_Glyph"
speciesGlyph="ancestor::model[1]/*/*/*/*speciesGlyph[@id='Glucose_Glyph1']"

```

```

speciesReference="ancestor::model[1]/*/*/*/*speciesReference[@id='SR_Glucose']"
  role="substrate"/>
    <speciesReferenceGlyph id="SP3_Glyph"
speciesGlyph="ancestor::model[1]/*/*/*/*speciesGlyph[@id='H2O_Glyph']"
speciesReference="ancestor::model[1]/*/*/*/*speciesReference[@id='SR_H2O']"/>
  <speciesReferenceGlyph id="SP4_Glyph"
speciesGlyph="ancestor::model[1]/*/*/*/*speciesGlyph[@id='G6P_Glyph']"
speciesReference="ancestor::model[1]/*/*/*/*speciesReference[@id='SR_G6P']">
  <curve>
    <listOfCurveSegments>
      <curveSegment
type="CubicBezier">
        <start x="180"
y="241"/>
        <end x="120" y="183"/>
        <basePoint1 x="155"
y="230"/>
        <basePoint2 x="120"
y="200"/>
      </curveSegment>
    </listOfCurveSegments>
  </curve>
  </speciesReferenceGlyph>
</listOfSpeciesReferenceGlyphs>
</reactionGlyph>
</listOfReactionGlyphs>
<listOfTextGlyphs>
  <textGlyph id="label1" text="Reaction Layout">
    <boundingBox>
      <position x="100.0" y="85.0"/>
      <dimension width="180.0" height="25.0"/>
    </boundingBox>
  </textGlyph>
  <textGlyph id="label_h2o"
graphicalObject="ancestor::model[1]/*/*/*/*speciesGlyph[@id='H2O_Glyph']"
originOfText="H2O">
    <boundingBox>
      <position x="85.0" y="220.0"/>
      <dimensions width="50.0" height="16.0"/>
    </boundingBox>
  </textGlyph>
</listOfTextGlyphs>
</layout>
</listOfLayouts>
</model>
</sbml>

```