```
−<RBAParameters>
 −<listOfMaximalDensities>
    <maximalDensity compartment="c" value="4.8972"/>
   −<maximalDensity compartment="mp">
      <functionReference function="protein_concentration"/>
      <functionReference function="average_protein_weight"/>
      <functionReference function="fraction_membrane_protein"/>
    </maximalDensity>
  </listOfMaximalDensities>
 −<listOfFunctions>
   −<function id="protein_concentration" type="linear">
     −<listOfParameters>
        <parameter id="LINEAR_COEF" value="-0.0048302"/>
        <parameter id="LINEAR_CONSTANT" value="0.031256"/>
        <parameter id="X_MIN" value="0.25"/>
        <parameter id="X_MAX" value="1.6"/>
        <parameter id="Y_MIN" value="-Inf"/>
        <parameter id="Y_MAX" value="Inf"/>
      </listOfParameters>
    </function>
   +<function id="average_protein_weight" type="constant"></function>
   +<function id="fraction_cytosol_protein" type="constant"></function>
   +<function id="fraction_membrane_protein" type="constant"></function>
   +<function id="fraction_external_protein" type="constant"></function>
   +<function id="fraction_nonenzymatic_cytosol_protein" type="linear"></function>
   +<function id="fraction_nonenzymatic_membrane_protein" type="linear"></function>
   +<function id="fraction_nonenzymatic_external_protein" type="constant"></function>
   +<function id="number_flagella" type="linear"></function>
   +<function id="flagella_speed" type="constant"></function>
   +<function id="flagella_H_consumption" type="constant"></function>
   +<function id="ribosomeEfficiencyMM" type="michaelisMenten"></function>
   +<function id="ribosomeEfficiencyCM" type="constant"></function>
   +<function id="fractionActiveRibosomes" type="exponential"></function>
   +<function id="chaperoneEfficiencyLM" type="linear"></function>
   +<function id="chaperoneEfficiencyMedium1" type="constant"></function>
   +<function id="chaperoneEfficiencyMedium2" type="constant"></function>
   +<function id="chaperoneEfficiencyMedium3" type="constant"></function>
   +<function id="chaperoneEfficiencyMedium4" type="constant"></function>
   +<function id="chaperoneEfficiencyMedium5" type="constant"></function>
   +<function id="maintenanceATP" type="linear"></function>
  </listOfFunctions>
</RBAParameters>
```

Density constraints: up to one constraint per compartment defined in the SBML file.

User defined functions: they describe how a number of cell parameters evolve with growth rate (the variable of these functions is mu). Any number of functions can be defined, but a restricted number of type of functions is avalaible (indicator, constant, linear, exponential, michaelisMenten). For every type of function a given set of parameters must be specified.
These functions can then be used to define other parameters, such as the maximal density per compartment or target values for processes.