```
−<process cellDesign="yes" compartment="c" id="P_TA" name="Translation apparatus">
 −<capacityConstraint>
  −<machineryComposition>
    +<listOfReactants></listOfReactants>
    +<listOfProducts></listOfProducts>
    </machineryComposition>
  −<capacity>
      <functionReference function="ribosomeEfficiencyMM"/>
      <functionReference function="fractionActiveRibosomes"/>
    </capacity>
  </capacityConstraint>
 −<operatingCosts>
    <production componentMap="translation" set="protein"/>
  </operatingCosts>
 −<targets>
  −<targetValue species="Pg_c">
      <functionReference function="protein_concentration"/>
      <functionReference function="fraction_cytosol_protein"/>
      <functionReference function="fraction_nonenzymatic_cytosol_protein"/>
    </targetValue>
  +<targetValue species="Pg_e"></targetValue>
  +<targetValue species="Pg_mp"></targetValue>
  </targets>
</process>
```

Process definition requires id and compartment, rest is optional.

(optional) A capacity constraint can be associated with the process. In this case, a machinery must be associated with the process as a list of reactants (metabolites or macromolecules) used to assemble a functional machine and a list of byproducts generated in the process. A capacity function, defined as the product of user-defined function, sets how many units a machine can process.

(optional) If the process produces, degrades or modifies a set of macromolecules. it is specified in this node. A componentMap is used to compute metabolites used and byproducts generated during the process.

(optional) Fluxes that must be produced by the process at a preset value. These can be metabolite or reaction fluxes. The flux value can be a preset value or the product of user-defined functions. It can be an absolute flux or a dilution_compensation flux. In latter case, it serves as a way to maintain the target at constant concentration, and the flux value actually scales with the growth rate.

```
−<targets>
  −<targetReaction reaction="Th">
      <functionReference function="number_flagella"/>
      <functionReference function="flagella_speed"/>
      <functionReference function="flagella_H_consumption"/>
    </targetReaction>
  </targets>
−<targets>
    <targetValue species="mrna" value="0.01"/>
    <targetValue species="trna" value="0.02625"/>
    <targetValue species="trna2" value="0.01125"/>
    <targetValue dilution_compensation="0" species="mrna" value="0.15996"/>
</targets>
```

```
<RBAProcesses>
+<listOfProcesses></listOfProcesses>
+<listOfComponentMaps></listOfComponentMaps>
</RBAProcesses>
```

Global structure: a list of processes of the cell and a list of component maps used by processes to build/degrade polymers.

```
−<listOfComponentMaps>
  −<componentMap id="translation">
    −<constantCost>
      −<listOfReactants>
          <speciesReference species="m_tfmet" stoichiometry="1"/>
          <speciesReference species="m_gtp" stoichiometry="1"/>
          <speciesReference species="m_h2o" stoichiometry="1"/>
        </listOfReactants>
      −<listOfProducts>
          <speciesReference species="m_trna" stoichiometry="1"/>
          <speciesReference species="m_fmet" stoichiometry="1"/>
          <speciesReference species="m_gdp" stoichiometry="1"/>
          <speciesReference species="m_p" stoichiometry="1"/>
          <speciesReference species="m_h" stoichiometry="1"/>
        </listOfProducts>
      </constantCost>
    −<cost component="ala" processingCost="1">
      −<listOfReactants>
          <speciesReference species="m_tala" stoichiometry="1"/>
          <speciesReference species="m_gtp" stoichiometry="2"/>
          <speciesReference species="m_h2o" stoichiometry="2"/>
        </listOfReactants>
      −<listOfProducts>
          <speciesReference species="m_trna" stoichiometry="1"/>
          <speciesReference species="m_gdp" stoichiometry="2"/>
          <speciesReference species="m_p" stoichiometry="2"/>
          <speciesReference species="m_h" stoichiometry="2"/>
        </listOfProducts>
      </cost>
    +<cost component="arg" processingCost="1"></cost>
    +<cost component="asn" processingCost="1"></cost>
```

(optional) A component map may have a constant cost part that is independent of a polymer's composition. A processing cost may be associated with this node.

For every component of the macromolecule, the component map defines the metabolites consumed/generated during its processing (production, degradation or modification). If the process has a capacity constraint, a processingCost can also be associated to each component. The number of components the machinery can process is then limited by its capacity (explicitly: the sum of processing costs cannot exceed the machine's capacity).