

<pre> &lt;listOfEfficiencyFunctions&gt;   &lt;function id="medium_1" type="constant"/&gt;   &lt;function id="medium_2" type="constant"/&gt;   &lt;function id="medium_3" type="constant"/&gt;   &lt;function id="medium_4" type="constant"/&gt;   &lt;function id="medium_5" type="constant"/&gt;   &lt;function id="linearModel" type="linear"/&gt; &lt;/listOfEfficiencyFunctions&gt; </pre>	<p>Different efficiency models associated with enzymes (how efficiency evolves with growth rate).Parameters of the functions are defined protein nodes. For the simulation, the user chooses one of these models by specifying its id.</p>
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<pre> &lt;listOfComponents&gt;   &lt;component id="ala" name="ala" type="aminoAcid" weight="1"/&gt;   &lt;component id="arg" name="arg" type="aminoAcid" weight="1"/&gt;   &lt;component id="asn" name="asn" type="aminoAcid" weight="1"/&gt;   [...] </pre>	<p>Protein components. Name and type are optional. Weight is used to compute the density of the polymer.</p>
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<pre> &lt;RBAProteins&gt; +&lt;listOfEfficiencyFunctions&gt;&lt;/listOfEfficiencyFunctions&gt; +&lt;listOfComponents&gt;&lt;/listOfComponents&gt; -&lt;listOfSpecies&gt;   -&lt;protein bsu="BSU13890" compartment="mp" gene="ptsG" id="BSU13890" name="TptsG" quaternary_number="1"     sequence="MFKALFGVLQKIGRALMLPVAILPAAGILLAIGNAMQNKDMIQVLHFLSNDNVQLVAGVMESAGQIVFDNLPLLFAVC     size="699" subunit_structure="1" type="transporter" zero_cost="0"&gt;     +&lt;composition&gt;&lt;/composition&gt;     +&lt;enzymaticActivity reaction="TptsG"&gt;&lt;/enzymaticActivity&gt;   &lt;/protein&gt; </pre>	<p>Global structure of the protein file. After the required list of efficiency functions and components, the declaration of proteins follow. Most attributes of the protein node are optional, fields actually read are: compartment, id , quaternary_number and zero_cost.</p>
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<pre> &lt;composition&gt;   &lt;componentReference component="ala" stoichiometry="63"/&gt;   &lt;componentReference component="arg" stoichiometry="21"/&gt;   &lt;componentReference component="asn" stoichiometry="26"/&gt;   &lt;componentReference component="asp" stoichiometry="26"/&gt;   &lt;componentReference component="cys" stoichiometry="2"/&gt;   &lt;componentReference component="gln" stoichiometry="27"/&gt;   &lt;componentReference component="glu" stoichiometry="39"/&gt;   &lt;componentReference component="gly" stoichiometry="71"/&gt;   &lt;componentReference component="his" stoichiometry="11"/&gt;   &lt;componentReference component="ile" stoichiometry="62"/&gt;   &lt;componentReference component="leu" stoichiometry="72"/&gt;   &lt;componentReference component="lys" stoichiometry="32"/&gt;   &lt;componentReference component="met" stoichiometry="22"/&gt;   &lt;componentReference component="phe" stoichiometry="48"/&gt;   &lt;componentReference component="pro" stoichiometry="38"/&gt;   &lt;componentReference component="ser" stoichiometry="33"/&gt;   &lt;componentReference component="thr" stoichiometry="31"/&gt;   &lt;componentReference component="trp" stoichiometry="4"/&gt;   &lt;componentReference component="tyr" stoichiometry="13"/&gt;   &lt;componentReference component="val" stoichiometry="58"/&gt; &lt;/composition&gt; </pre>	<p>Composition of protein in terms of components defined in listOfComponents.</p>
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<pre> &lt;enzymaticActivity reaction="TptsG"&gt; ——— (optional) Reaction catalyzed by protein. - &lt;enzymeEfficiency function="medium_1"&gt;   - &lt;listOfParameters&gt;     &lt;parameter id="CONSTANT" value="1334026.4422"/&gt;   &lt;/listOfParameters&gt;   &lt;/enzymeEfficiency&gt; + &lt;enzymeEfficiency function="medium_2"&gt;&lt;/enzymeEfficiency&gt; + &lt;enzymeEfficiency function="medium_3"&gt;&lt;/enzymeEfficiency&gt; + &lt;enzymeEfficiency function="medium_4"&gt;&lt;/enzymeEfficiency&gt; + &lt;enzymeEfficiency function="medium_5"&gt;&lt;/enzymeEfficiency&gt; - &lt;enzymeEfficiency function="linearModel"&gt;   - &lt;listOfParameters&gt;     &lt;parameter id="X_MIN" value="0.25"/&gt;     &lt;parameter id="X_MAX" value="1.6"/&gt;     &lt;parameter id="Y_MIN" value="511.6565"/&gt;     &lt;parameter id="Y_MAX" value="2838989.867"/&gt;     &lt;parameter id="LINEAR_COEF" value="0"/&gt;     &lt;parameter id="LINEAR_CONSTANT" value="1334026.4422"/&gt;   &lt;/listOfParameters&gt;   &lt;/enzymeEfficiency&gt; - &lt;transporterEfficiency&gt;   - &lt;function type="indicator" variable="m_glc_xt"&gt;     - &lt;listOfParameters&gt;       &lt;parameter id="X_MIN" value="1e-05"/&gt;       &lt;parameter id="X_MAX" value="Inf"/&gt;     &lt;/listOfParameters&gt;     &lt;/function&gt;   - &lt;function type="michaelisMenten" variable="m_glc_xt"&gt;     - &lt;listOfParameters&gt;       &lt;parameter id="Km" value="0.8"/&gt;       &lt;parameter id="kmax" value="1"/&gt;     &lt;/listOfParameters&gt;     &lt;/function&gt;   &lt;/transporterEfficiency&gt; &lt;/enzymaticActivity&gt; </pre>	<p>If the protein is an enzyme, it MUST define parameters for every efficiency model.</p>
	<p>if the enzyme is a transporter, its IMPORT efficiency can be modulated. The import efficiency is the product of the efficiency function (above) and a set of user-defined functions reflecting substrate or cofactor availability.</p>