

# extract\_species\_map\_repressilator\_v1

April 9, 2024

## ☐ Anonymous



BIOMD0000000012\_url.xml  
File

extract the species from the SBML (.xml) file. the SBML file uses <http://www.sbml.org/sbml/level2/version3>. when you extract the entities from each file do not limit to the first few entries; extract all entities.

## ☐ ChatGPT

I've extracted all species entities from the SBML file. Here are the species along with their IDs and names:

- **LacI protein** with ID `PX`
- **TetR protein** with ID `PY`
- **cl protein** with ID `PZ`
- **LacI mRNA** with ID `X`
- **TetR mRNA** with ID `Y`
- **cl mRNA** with ID `Z`

These entries represent all species defined in the file. [\[>-\]](#)

## ☐ Anonymous



Repressilator\_PD\_v7\_annotations.sbgn  
File

extract the glyphs from the SBGN (.sbgn). the SBGN file uses the namespace <http://sbgn.org/libsbgn/0.2>. when you extract the entities from each file do not limit to the first few entries; extract all entities. after this provide a mapping of species and glyphs

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