1. SBML Editor

2. Antimony Editor

SBML Model

```xml
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level2/version4" level="2" version="4">
  <model id="Boehm_JProteomeRes2014" name="Boehm_JProteomeRes2014">
    <notes>
      <body xmlns="http://www.w3.org/1999/xhtml">
        <pre>PEtab implementation of the model from Boehm et al. (2014), J. Proteome Res., 13, 12,
5685-5694</pre>
      </body>
    </notes>
    <annotation>
      <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:dc="http://purl.org/dc/
elements/1.1/" xmlns:dcterms="http://purl.org/dc/terms/" xmlns:vCard="http://www.w3.org/2001/vcard-rdf/
3.0#" xmlns:bqbiol="http://biomodels.net/biology-qualifiers/" xmlns:bqmodel="http://biomodels.net/model-
qualifiers/">
        <rdf:Description rdf:about="#arFramework3">
          <dc:creator>
            <rdf:Bag>
              <rdf:li rdf:parseType="Resource">
                <vCard:N rdf:parseType="Resource">
                  <vCard:Family>Boehm</vCard:Family>
                  <vCard:Given>Martin</vCard:Given>
                </vCard:N>
              </rdf:li>
            </rdf:Bag>
          </dc:creator>
          <dcterms:created rdf:parseType="Resource">
            <dcterms:W3CDTF>2019-11-29T09:41:48Z</dcterms:W3CDTF>
          </dcterms:created>
          <dcterms:modified rdf:parseType="Resource">
            <dcterms:W3CDTF>2019-11-29T09:41:48Z</dcterms:W3CDTF>
          </dcterms:modified>
```

Forward Changes to Antimony

Antimony Model

```
// Created by libAntimony v2.15.0
model *Boehm_JProteomeRes2014()

  // Compartments and Species:
  compartment cyt, nuc;
  species STAT5A in cyt, STAT5B in cyt, pApB in cyt, pApA in cyt, pBpB in cyt;
  species nucpApA in nuc, nucpApB in nuc, nucpBpB in nuc;

  // Assignment Rules:
  BaF3_Epo := 1.25e-7*exp(-1*Epo_degradation_BaF3*time);

  // Reactions:
  v1_v_0: 2 STAT5A => pApA; cyt*BaF3_Epo*STAT5A^2*k_phos;
  v2_v_1: STAT5A + STAT5B => pApB; cyt*BaF3_Epo*STAT5A*STAT5B*k_phos;
  v3_v_2: 2 STAT5B => pBpB; cyt*BaF3_Epo*STAT5B^2*k_phos;
  v4_v_3: pApA => nucpApA; cyt*k_imp_homo*pApA;
  v5_v_4: pApB => nucpApB; cyt*k_imp_hetero*pApB;
  v6_v_5: pBpB => nucpBpB; cyt*k_imp_homo*pBpB;
  v7_v_6: nucpApA => 2 STAT5A; nuc*k_exp_homo*nucpApA;
  v8_v_7: nucpApB => STAT5A + STAT5B; nuc*k_exp_hetero*nucpApB;
  v9_v_8: nucpBpB => 2 STAT5B; nuc*k_exp_homo*nucpBpB;

  // Species initializations:
  STAT5A = 207.6*ratio;
  STAT5B = 207.6 - 207.6*ratio;
  pApB = 0;
  pApA = 0;
  pBpB = 0;
  nucpApA = 0;
  nucpApB = 0;
  nucpBpB = 0;
```

Forward Changes to SBML

```
[2025-09-04 19:21:59]    Logger cleared.
[2025-09-04 19:22:07]    SBML model successfully overwritten.
[2025-09-04 19:22:07]    Overwrote the measurement table with new data.
[2025-09-04 19:22:07]    Overwrote the observable table with new data.
[2025-09-04 19:22:07]    Overwrote the parameter table with new data.
[2025-09-04 19:22:08]    Overwrote the condition table with new data.
[2025-09-04 19:22:08]    All files opened successfully from the YAML configuration.
[2025-09-04 19:22:08]    Model is consistent.
```