1. Original model – Dan’s original code
   1. Didn’t have ADP\_x = 10
2. Change1 – made the model more like the one we want to use
   1. Set IC for ADP\_x = 9.5
   2. Set n\_A = 8/3
   3. Set pH\_x = 7.2
   4. Set IC for DPsi = 175
   5. Replaced instances where intermembrane species occur with cytosol species and set all intermembrane species DEs to 0 except Cred\_i
   6. Set AMP\_c DE to 0
   7. Changed the capacitance to the value we’re using 3.1e-6
3. Change 2 – reformatted and simplified
   1. Removed Cr\_c as a state and replaced it with Crtot – PCr\_c where Crtot = 40e-3
   2. Removed all states that we’re not modeling
4. Change 3
   1. J\_C3 no longer has Pi dependence and changed formulation to  
      x\_C3\*(Kapp\_C3\*Cox\_i^2\*QH2\_x - Cred\_i^2\*COQ\_x)
   2. J\_C4 no longer has Pi dependence and changed formulation to   
      x\_C4\*(CfO2/(CfO2+k\_O2))\*( Kapp\_C4\*Cred\_i^2\*(CfO2^0.5) - Cox\_i^2 )
5. Change 4
   1. Reconfigured code for readability
   2. Changed flux rates such that it gave the appropriate steady-state values
6. Change 5
   1. Added in adenylate kinase, which also included added AMP\_c state
   2. Added in option for proton leak