

# **Computational modeling to determine key regulators of hypoxia effects on lactate production in the glycolysis pathway**

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## MATLAB program

%This program investigates the influence of hypoxia on the production  
%of glycolysis metabolites, especially lactate (y(11)). The program  
%output is the enzymes and or metabolites concentration vs time, you can  
%modify the program to have different levels of hypoxia (h=0:0.1:1). Hence,  
%metabolites concentration can be reported vs Hif-1 or oxygen levels during  
%different time intervals of hypoxia exposure. The detailed description of  
%the model has been explained in the paper.

```
clc
close all
clear

Vmglut3=8000;           %micM/min
kmglut3=5000;          %micM
kmglut1=3000;          %micM
kcatglut1=69960;       %min-1
E0glut=0.014;          %micM
kgluth=0.0001;         %min-1
kmglut2=25000;         %micM
kcatglut2=445500;      %min-1
kdglut=0.00016;        %min-1
kmhk=40.7;             %micM
khkh=0.003;           %min-1
kdhk=0.002;           %min-1
kcathk=12000;          %min-1
E0hk=0.47;            %micM
kpgih=0.037;          %min-1
kmpgil=480;           %micM
kmpgi2=272;           %micM
kcatpgi1=125400;       %min-1
kcatpgi2=119586.8;     %min-1
kdpgi=0.00048;        %min-1
E0pgi=33.2;           %micM
kmpfk=2000;           %micM
kcatpfk=61200;         %min-1
E0pfk=42.5;           %micM
kdpfk=0.00085;        %min-1
kpfkh=0.026;          %min-1
vmaldo1=1028106;       %micM/min
kmaldo1=3;             %micM
vmaldo2=832276.3;     %micM/min
kmaldo2=1000;          %micM
kmaldo22=2000;         %micM, for metabolite 2 in reverse direction
kmgapdh1=82;          %micM
kmgapdh2=130;         %micM
kgapdhh=0.83;         %min-1
kdgapdh=0.00016;      %min-1
E0gapdh=1195;         %micM
kcatgapdh1=17400;     %min-1
kcatgapdh2=19.81;     %min-1
kcatpgk=29210;        %min-1
```

```

kmpgk=16.7; %micM
E0pgk=64.4; %micM
kdpkgk=0.0013; %min-1
kpgkh=0.3; %min-1
kmpgm1=200; %micM
kmpgm2=190; %micM
kcatpgm1=60000; %min-1
kcatpgm2=27272.7; %min-1
E0pgm=173; %micM
kdpgm=0.0197; %min-1
kpgmh=0.36; %min-1
kmeno1=16.2; %micM
kmeno2=238; %micM
kenoh=0.23; %min-1
kcateno1=11160; %min-1
kcateno2=2610.96; %min-1
E0eno=135; %micM
kdeno=0.00048; %min-1
vmpk=2819725.8; %micM/min
kmpk=1500; %micM
kmpdk=20; %micM
kpdkh=0.000017; %min-1
kdpdk=0.00048; %min-1
kcatpdk=33; %min-1
E0pdk=0.01; %micM
kmpdh=10; %micM
E0pdh=27.2; %micM
kml dh1=200; %micM
kml dh2=11000; %micM
kcattpi1=350000; %micM
kcattpi2=7700092.4; %micM
kmtpi1=870; %micM
kmtpi2=460; %micM
E0tpi=96.6; %micM
ktpih=0.3; %min-1
kdtpi=0.069; %min-1
kldhh=0.003; %min-1
kcatldh1=122000; %min-1
kcatldh2=4900; %min-1
E0ldh=1.2; %micM
kdldh=0.0013; %min-1
kcatpdh=105800; %micM
kmg6pdh=77; %micM
kmpgcm2=45; %micM
kmpgcm1=670; %micM
E0pgcm=28.2; %micM
kpgcmh=0.065; %min-1
kdpgcm=0.00016; %min-1
kcatpgcm1=73700; %min-1
kcatpgcm2=127220.9; %min-1
glucose1ph=25; %micM
Eg=10000; %micM
vmg6pdh=120120; %micM/min
E0g6pdh=4.4; %micM
kAcCoA=10000; %min-1
E0pdp=0.02; %micM
kcatpdp=300; %min-1

```

```

kmpdp=7.6;           %micM
h=0;                 %micM,0:0.1:1

%d[C]/dt=vp-vd
f=@(t,y)[kcatglut1*y(14)*Eg/(kmglut1+Eg)-kcatglut2*y(14)*y(1)/(kmglut2+y(1))-
kcatk*y(15)*y(1)/(kmhk+y(1))+Vmglut3*Eg/(kmglut3+Eg);...
%dy(1)/dt
kcatk*y(15)*y(1)/(kmhk+y(1))-
kcatpgi1*y(16)*y(2)/(kmpgi1+y(2))+kcatpgi2*y(16)*y(3)/(kmpgi2+y(3))-
vmg6pdh*y(2)/(kmg6pdh+y(2))-
kcatpgcm1*y(26)*y(2)/(kmpgcm1+y(2))+kcatpgcm2*y(26)*glucose1ph/(kmpgcm2+gluco
selph);...           %dy(2)/dt
kcatpgi1*y(16)*y(2)/(kmpgi1+y(2))-kcatpgi2*y(16)*y(3)/(kmpgi2+y(3))-
kcatpfk*y(17)*y(3)/(kmpfk+y(3));...
%dy(3)/dt
kcatpfk*y(17)*y(3)/(kmpfk+y(3))-
vmaldo1*y(4)/(kmaldo1+y(4))+vmaldo2*y(5)/(kmaldo2+y(5))+
vmaldo2*y(12)/(kmaldo22+y(12));...
%dy(4)/dt
vmaldo1*y(4)/(kmaldo1+y(4))-
vmaldo2*y(5)/(kmaldo2+y(5))+kattpi1*y(18)*y(12)/(kmtpi1+y(12))-
kattpi2*y(18)*y(5)/(kmtpi2+y(5))+kcatgapdh2*y(19)*y(13)/(kmgapdh2+y(13))-
kcatgapdh1*y(19)*y(5)/(kmgapdh1+y(5));...           %dy(5)/dt
kcatpgk*y(20)*y(13)/(kmpgk+y(13))-
kcatpgm1*y(21)*y(6)/(kmpgm1+y(6))+kcatpgm2*y(21)*y(7)/(kmpgm2+y(7));...
%dy(6)/dt
kcatpgm1*y(21)*y(6)/(kmpgm1+y(6))-kcatpgm2*y(21)*y(7)/(kmpgm2+y(7))-
kateno1*y(22)*y(7)/(kmeno1+y(7))+kateno2*y(22)*y(8)/(kmeno2+y(8));...
%dy(7)/dt
kateno1*y(22)*y(7)/(kmeno1+y(7))-vmpk*y(8)/(kmpk+y(8))-
kateno2*y(22)*y(8)/(kmeno2+y(8));...
%dy(8)/dt
kcatpdh*y(24)*y(10)/(kmpdh+y(10))-kAcCoA*y(9);...
%dy(9)/dt
vmpk*y(8)/(kmpk+y(8))-kcatpdh*y(24)*y(10)/(kmpdh+y(10))-
kcatldh1*y(23)*y(10)/(kmldh1+y(10))+kcatldh2*y(23)*y(11)/(kmldh2+y(11));...
%dy(10)/dt
kcatldh1*y(23)*y(10)/(kmldh1+y(10))-kcatldh2*y(23)*y(11)/(kmldh2+y(11));...
%dy(11)/dt
vmaldo1*y(4)/(kmaldo1+y(4))-vmaldo2*y(12)/(kmaldo22+y(12))-
kattpi1*y(18)*y(12)/(kmtpi1+y(12))+kattpi2*y(18)*y(5)/(kmtpi2+y(5));...
%dy(12)/dt
kcatgapdh1*y(19)*y(5)/(kmgapdh1+y(5))-
kcatgapdh2*y(19)*y(13)/(kmgapdh2+y(13))-kcatpgk*y(20)*y(13)/(kmpgk+y(13));...
%dy(13)/dt
%d[E]/dt=kEh[h]-kd[E-E0]
(kgluth*h)-(kdglut*(y(14)-E0glut));...
%dy(14)/dt
(khkh*h)-(kdhk*(y(15)-E0hk));...
%dy(15)/dt
(kpgih*h)-(kdpgi*(y(16)-E0pgi));...
%dy(16)/dt
(kpfxh*h)-(kdpfk*(y(17)-E0pfx));...
%dy(17)/dt
(ktpih*h)-(kdtpi*(y(18)-E0tpi));...
%dy(18)/dt

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```

(kgapdh*h)-(kdgapdh*(y(19)-E0gapdh));...
%dy(19)/dt
(kpgkh*h)-(kdpkgk*(y(20)-E0pgk));...
%dy(20)/dt
(kpgmh*h)-(kdpgm*(y(21)-E0pgm));...
%dy(21)/dt
(kenoh*h)-(kdeno*(y(22)-E0eno));...
%dy(22)/dt
(kldhh*h)-(kldlh*(y(23)-E0ldh));...
%dy(23)/dt
-kcatpdk*y(25)*(y(24))^2.3/(kmpdk+(y(24))^2.3)+kcatpdp*E0pdp*(E0pdh-
y(24))/(kmpdp+(E0pdh-y(24)));...
%dy(24)/dt
(kpdkh*h)-(kdpdk*(y(25)-E0pdk));...
%dy(25)/dt
(kpgcmh*h)-(kdpbcm*(y(26)-E0pgcm));
%dy(26)/dt
[t, y]=ode45(f, [0, 30], [2377 1033 362 46 21 44 5 8 1.3 56 4680 43 0.18
0.014 0.47 33.2 42.5 96.6 1195 64.4 173 135 1.2 27.2 0.01 28.2]);

%glucose
figure(1)
plot(t,y(:,1));
%glucose 6-phosphate
figure(2)
plot(t,y(:,2));
%fructose 6-phosphate
figure(3)
plot(t,y(:,3));
%fructose 1,6-bisphosphate
figure(4)
plot(t,y(:,4));
%glyceraldehyde 3-phosphate
figure(5)
plot(t,y(:,5));
%3-phosphoglycerate
figure(6)
plot(t,y(:,6));
%2-phosphoglycerate
figure(7)
plot(t,y(:,7));
%phosphoenolpyruvate
figure(8)
plot(t,y(:,8));
%Ac-CoA
figure(9)
plot(t,y(:,9));
%pyruvate
figure(10)
plot(t,y(:,10));
%lactate
figure(11)
plot(t,y(:,11));
%dihydroxyacetone phosphate
figure(12)
plot(t,y(:,12));
%1,3-bis phosphoglycerate

```

```
figure(13)
plot(t,y(:,13));
%glut
figure(14)
plot(t,y(:,14));
%hk
figure(15)
plot(t,y(:,15));
%pgi
figure(16)
plot(t,y(:,16));
%pfk
figure(17)
plot(t,y(:,17));
%tpi
figure(18)
plot(t,y(:,18));
%gapdh
figure(19)
plot(t,y(:,19));
%pgk
figure(20)
plot(t,y(:,20));
%pgm
figure(21)
plot(t,y(:,21));
%eno
figure(22)
plot(t,y(:,22));
%ldh
figure(23)
plot(t,y(:,23));
%pdh
figure(24)
plot(t,y(:,24));
%pdk
figure(25)
plot(t,y(:,25));
%pgcm
figure(26)
plot(t,y(:,26));
```

**Table S1.** Constants and initial conditions

Constants, initial conditions	Value ( $\mu\text{M}$ )	Ref.	Constants, initial conditions	Value ( $\mu\text{M}$ )	Ref.
[glucose1-phosphate]0	25	1	$Km_{GLUT}$	3000	2
[ $E_g$ ]	10000	3	$Km_{GLUT2}$	25000	4
[y1]0=[glucose]0	2377	5	$Km_{HK}$	40.7	6
[y2]0=[glucose 6-ph]0	1033	5	$Km_{PGI1}$	480	7
[y3]0=[fructose 6-ph]0	362	5	$Km_{PGI2}$	272	7
[y4]0=[fructose 1,6-bisphosphate]0	46	5	$Km_{PFK-1}$	2000	8
[y5]0=[glyceraldehyde 3-phosphate]0	21	5	$Km_{ALDO1}$	3	9
[y6]0=[3-phosphoglycerate]0	44	5	$Km_{ALDO2}$	1000	9
[y7]0=[2-phosphoglycerate]0	5	5	$Km_{ALDO22}$	2000	9
[y8]0=[phosphoenolpyruvate]0	8	5	$Km_{GAPDH1}$	82	10
[y9]0=[Ac-CoA]0	1.3	5	$Km_{GAPDH2}$	130	10
[y10]0=[pyruvate]0	56	5	$Km_{PGK}$	16.7	11
[y11]0=[lactate]0	4680	5	$Km_{PGM1}$	200	12
[y12]0=[dihydroxyacetone phosphate]0	43	5	$Km_{PGM2}$	190	12
[y13]0=[1,3-bis phosphoglycerate]0	0.18	13	$Km_{ENO1}$	16.2	14
[y14]0=[GLU	0.014	2,15	$Km_{ENO2}$	238	14
[y15]0=[HK]0	0.47	5	$Km_{PK}$	1500	16
[y16]0=[PGI]0	33.2	5	$Km_{PDK}$	20	17
[y17]0=[PFK-1]0	42.5	5	$Km_{PDH}$	10	18
[y18]0=[TPI]0	96.6	5	$Km_{LDH1}$	200	19
[y19]0=[GAPDH]0	1195	5	$Km_{LDH2}$	11000	19
[y20]0=[PGK]0	64.4	5	$Km_{TPI1}$	870	20
[y21]0=[PGM]0	173	5	$Km_{TPI2}$	460	20
[y22]0=[ENO]0	135	5	$Km_{G6PDH}$	77	21
[y23]0=[LDH]0	1.2	5	$Km_{PGCM1}$	670	22
[y24]0=[PDH]0	27.2	5	$Km_{PGCM2}$	45	22
[y25]0=[PDK]0	0.01	23			
[y26]0=[PGCM]0	28.2	5			
H	0:0.1:1	24			

**Table S1.** Constants and initial conditions (continue)

Constants, initial conditions	Value (min <sup>-1</sup> )	Ref.	Constants, initial conditions	Value (min <sup>-1</sup> )	Ref.
$K_{cat_{GLUT1}}$	69960	15	$K_{d_{ENO}}$	0.00048	25
$K_{cat_{GLUT2}}$	445500	Est	$K_{d_{PDK}}$	0.00048	26
$K_{cat_{HK}}$	12000	5	$K_{d_{TPI}}$	0.069	27
$K_{cat_{PGI1}}$	125400	5	$K_{d_{LDH}}$	0.0013	28
$K_{cat_{PGI2}}$	119586.8	5,22	$K_{d_{PGCM}}$	0.00016	29
$K_{cat_{PFK-1}}$	61200	5	$K_{GLUTh}$	0.0001	30
$K_{cat_{GAPDH1}}$	17400	5	$K_{HKh}$	0.003	30
$K_{cat_{GAPDH2}}$	19.81	5,31	$K_{PGIh}$	0.037	32
$K_{cat_{PGK}}$	29210	5	$K_{PFK-1h}$	0.026	32
$K_{cat_{PGM1}}$	60000	5	$K_{PAPDHh}$	0.83	33
$K_{cat_{PGM2}}$	27272.7	5,12	$K_{PGKh}$	0.3	34
$K_{cat_{ENO1}}$	11160	5	$K_{PGMh}$	0.36	35
$K_{cat_{ENO2}}$	2610.96	5,36	$K_{ENOh}$	0.23	37
$K_{cat_{PDK}}$	33	38	$K_{PDHh}$	0.000017	39
$k_{cat_{TPI1}}$	350000	5	$K_{TPIh}$	0.3	40
$K_{cat_{TPI2}}$	7700092.4	5,20	$K_{LDHh}$	0.003	41
$K_{cat_{LDH1}}$	122000	19	$K_{PGCMh}$	0.065	42
$K_{cat_{LDH2}}$	4900	43	$K_{d_{Ac-CoA}}$	10000	Est
$K_{cat_{PDH}}$	105800	5	$K_{d_{PDK}}$	0.00048	26
$K_{cat_{PGCM1}}$	73700	5	$K_{d_{TPI}}$	0.069	27
$K_{cat_{PGCM2}}$	127220.9	5,22	$K_{d_{LDH}}$	0.0013	28
$K_{d_{GLUT}}$	0.00016	44	$K_{d_{PGCM}}$	0.00016	29
$K_{d_{HK}}$	0.002	28	<b>Constants, initial conditions</b>	<b>Value</b>	<b>Ref.</b>
$K_{d_{PGI}}$	0.00048	26	$V_{m_{GLUT}}$	8000	2
$K_{d_{PFK-1}}$	0.00085	26	$V_{m_{ALDO1}}$	1028106	5
$K_{d_{GAPDH}}$	0.00016	45	$V_{m_{ALDO2}}$	832276.3	5,46
$K_{d_{PGK}}$	0.0013	28	$V_{m_{PK}}$	2819725.8	5
$K_{d_{PGM}}$	0.0197	47	$V_{m_{G6PDH}}$	120120	5

$K_{cat}$ =catalytic constant,  $K_m$ = Michaelis–Menten constant,  $V_m$ =maximum velocity,  $K_d$ =degradation constant,  $K_{Eh}$ =constant of HIF effect on enzyme production, (calculated based on experimental data reported in respective references), 1=in forward direction, 2=in reverse direction. GLUT: glucose transporter, HK: hexokinase, PGI: phosphoglucoisomerase, PFK-1: phosphofructokinase-1, ALDO: aldolase, TPI: triosephosphate isomerase, GAPDH: glyceraldehyde 3-phosphate dehydrogenase, PGK: phosphoglycerate kinase, PGM: phosphoglycerate mutase, ENO: enolase, PK: pyruvate kinase, PDH: pyruvate dehydrogenase, PDK: pyruvate dehydrogenase kinase, PDP: pyruvate dehydrogenase phosphatase, p-PDH: phosphorylated pyruvate dehydrogenase, LDH: lactate dehydrogenase, PGCM: phosphoglucomutase, G6PDH: glucose 6-phosphate dehydrogenase, Eg: extracellular glucose, h: HIF-1, Est: estimated by the proposed model.



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