

Table 1 - Effect of the concentration of ATP and C8D-ATP on the fit of the enzyme kinetic model of kinases

Enzyme	ATP : Kinetic model	C8D-ATP: Kinetic model	KIE _{vmax}
Shikimate kinase	Michaelis-Menton	Michaelis-Menton	1
$v_{\max}$	2339±606	3337±891	
K_m or K'	0.0065±0.003	0.0193±0.007	
RMSD ^a	0.9543	0.9911	
Hexokinase	Allosteric sigmoidal	Allosteric sigmoidal	1
$v_{\max}$	1226±189	1893±940.7	
K_m or K'	3.263±0.662	4.419±2.749	
h	1.759±0.207	1.020	
RMSD ^a	0.9959	0.9919	
Acetate kinase	Allosteric sigmoidal	Michaelis-Menton	1
$v_{\max}$	22.29±3.046	19.13±2.103	
K_m or K'	1.323±0.353	1.081±0.289	
h	1.658±0.302		
RMSD ^a	0.9880	0.9704	
Deadenylylated GS	Allosteric sigmoidal	Allosteric sigmoidal	1
$v_{\max}$	11.49±1.31	13.20±0.651	
K_m or K'	30.88±4.44	6.774±2.331	
h	3.108±0.316	4.077±0.787	
RMSD ^a	0.9972	0.9827	
PFK^b	Allosteric sigmoidal	Allosteric sigmoidal	2
$v_{\max}$	111.3±10.16	45.18±1.012	
K_m or K'	2.265±0.320	0.097±0.031	
h	1.371±0.098	1.785±0.208	
RMSD ^a	0.9982	0.9879	
Adenylylated GS	Allosteric sigmoidal	Allosteric sigmoidal	>2
$v_{\max}$	8.241±0.787	6.540±0.271	
K_m or K'	15.22±8.776	0.603±0.151	
h	3.288±	3.258±0.589	
RMSD ^a	0.9822	0.9924	

^a Root mean square deviation of the data defining the kinetic model.

^b Phosphofructokinase