S1 Table. Simulation details for Fig. 3. It contains the simulation details and the model parameters which have been used to validate the order reduction technique using COPASI software.

A: Simulation information

Simulation specification		
Simulation task	Time course	
Duration	500 s	
Interval size	5 s	
Intervals	100	
Method	Deterministic (LSODA)	
Parameter	Integrate reduced model	0
	Relative tolerance	1×10^{-6}
	Absolute tolerance	1×10^{-12}
	Max internal steps	10000

B: Model information

Original pathway (Fig. 3(a)) model specifications		
Initial Species Values		
	A	0.5 mmol/ml
	B	0.5 mmol/ml
	C	0.5 mmol/ml
	D	0.5 mmol/ml
Kinetic Parameters		
v_1 (Rate law: Noncompetitive inhibition (irr))		
	K_m	0.1 mmol/ml
	V	0.1 mmol/(ml×s)
	K_i	0.1 mmol/ml
v_2 (Rate law: Henri-Michaelis-Menten (irr))		
	K_m	0.1 mmol/ml
	V	0.1 mmol/(ml×s)
v_3 (Rate law: Henri-Michaelis-Menten (irr))		
	K_m	0.1 mmol/ml
	V	0.1 mmol/(ml×s)
Reduced pathway (Fig. 3(b)) model specifications		
Initial Species Values		
	B	0.5 mmol/ml
	D	0.5 mmol/ml
	A	0.5 mmol/ml
Kinetic Parameters		
v_1 (Rate law: Noncompetitive inhibition (irr))		
	K_m	0.1 mmol/ml
	V	0.1 mmol/(ml×s)
	K_i	0.1 mmol/ml
v_2 (Rate law: Henri-Michaelis-Menten (irr))		
	K_m	0.1 mmol/ml
	V	0.1 mmol/(ml×s)