

Table 2. Fitting of Metabolites of *B. methanolicus*<sup>a†</sup>

metabolite	fit type	time constant <i>T</i>		no. of incorporated <sup>13</sup> C	
		a	b	a	b
tetraglutamyl-formyl-THF	PT1	45.2 ± 7.6	40.0 ± 10.9	0.88 ± 0.47	0.90 ± 0.08
hexose-1-phosphate	PT1	33.2 ± 1.3	39.7 ± 1.5	5.36 ± 0.56	5.60 ± 0.17
hexose-6-phosphate	PT1	31.6 ± 1.7	32.3 ± 2.4	5.40 ± 0.65	5.20 ± 0.12
fructose-1,6-bisphosphate	PT1	26.6 ± 3.9	27.6 ± 1.0	5.69 ± 1.14	5.50 ± 0.07
glyceraldehyde-3-phosphate	PT1	n.d.	34.1 ± 2.1	n.d.	3.03 ± 0.06
dihydroxyacetonephosphate	PT1	33.8 ± 1.2	35.4 ± 3.5	2.81 ± 0.10	3.01 ± 0.10
sedoheptulose-7-phosphate	PT1	26.4 ± 1.1	26.2 ± 1.0	6.35 ± 0.56	6.35 ± 0.08
ribose-5-phosphate	PT1	27.4 ± 10.3	29.3 ± 1.33	3.31 ± 0.61	4.22 ± 0.06
ribulose-5-phosphate	PT1	23.4 ± 1.0	23.2 ± 1.7	2.88 ± 0.29	4.50 ± 0.10
6-phosphogluconate	PT1	21.9 ± 4.4	20.0 ± 2.3	5.40 ± 0.50	5.52 ± 0.19
acetyl-CoA	PT1	56.4 ± 3.8	54.1 ± 6.6	2.09 ± 1.15	2.02 ± 0.10
phosphoenolpyruvate	PT1	42.9 ± 12.3	41.8 ± 4.6	2.88 ± 0.29	3.01 ± 0.11
2/3-phosphoglycerate	PT1	35.6 ± 2.3	43.6 ± 5.9	2.74 ± 0.17	3.02 ± 0.14
citrate	logistic	86.0 ± 21.3	64.3 ± 19.5	3.11 ± 0.63	4.26 ± 0.02
bacillithiol oxidized	logistic	312.8 ± 42.6	148.4 ± 21.3	2.86 ± 1.15	10.26 ± 9.88
UDP-glucose	logistic	119.6 ± 34.8	240.8 ± 18.4	6.07 ± 4.42	8.24 ± 0.41
AMP	logistic	257.1 ± 81.8	89.9 ± 150.5	1.28 ± 0.72	1.71 ± 0.11
ADP	logistic	No fit	70.74 ± 133.85	1.52 <sup>b</sup>	8.02 ± 8.03
ATP	logistic	129.4 ± 7.1	645.0 ± 379.0	1.21 ± 0.02	2.10 ± 0.12
GMP	logistic	No fit	226.4 ± 104.2	2.11 <sup>b</sup>	1.97 ± 0.47
GDP	logistic	No fit	No fit	1.58 <sup>b</sup>	No fit
UMP	logistic	273.0 ± 69.1	148.1 ± 35.6	3.05 ± 1.17	3.16 ± 0.05
UDP	logistic	No fit	117.3 ± 74.9	1.76 <sup>b</sup>	2.16 ± 0.06
UTP	logistic	159.9 ± 41.8	92.4 ± 128.9	4.37 ± 0.03	2.06 ± 0.05

<sup>a</sup>First order kinetic parameters of <sup>13</sup>C incorporation curves from methanol using DynaMet (a) and by targeted approach for peak extraction followed by parameter estimation using Prism (b). n.d., not detected; PT1, first order kinetics. <sup>b</sup>Maximum value obtained from automatic sample analysis.