

**Table III** Comparison of the estimated enzyme abundance in the rosette and the corresponding estimated time to synthesize the entire enzyme in the rosette in days ( $T_p$ )

Enzyme	Protein abundance ( $\text{mol g}^{-1}$ FW)		Days to synthesize all the protein in the rosette ( $T_p$ )		
	Enzyme activities	Quantitative proteomics	Enzyme activities	Quantitative proteomics	Average
Nitrate reductase (NR)	4.38E-11	3.60E-11	0.14	0.12	<b>0.13</b>
ATP-phosphofructokinase (PFK)	5.96E-12	NA	0.73	NA	0.73
Acid Invertase (INV)	3.58E-11	4.29E-11	0.69	0.78	<b>0.74</b>
Glucose-6-phosphate dehydrogenase (G6PDH)	2.60E-11	NA	1.57	NA	1.57
Glucokinase/hexokinase (HK)	1.40E-11	NA	1.86	NA	1.86
Alanine aminotransferase (AlaAT)	9.04E-10	1.72E-09	1.35	2.51	<b>1.93</b>
ADP-glucose pyrophosphorylase (AGPase)	1.94E-10	2.13E-10	1.82	2.12	<b>1.97</b>
Pyrophosphate-phosphofructokinase (PPF)	5.24E-11	4.67E-11	2.43	1.65	<b>2.04</b>
NADP-glyceraldehyde 3-phosphate dehydrogenase (NADP-GAPDH)	1.12E-09	2.51E-09	1.25	2.98	<b>2.11</b>
Ribulose-1,5-bisphosphate carboxylase (RuBisCO)	5.17E-08	2.56E-08	2.95	1.28	<b>2.12</b>
Glucose-6-phosphate isomerase (PGI)**	2.27E-11	1.67E-10	0.70	4.78	2.74
Phosphoenolpyruvate carboxylase (PEP carboxylase)**	1.17E-10	5.61E-10	1.14	4.36	2.75
Triose phosphate isomerase (TPI)*	3.85E-10	1.02E-09	1.65	4.42	<b>3.03</b>
Glutamine synthetase (GS)	7.65E-10	1.35E-09	2.25	3.97	<b>3.11</b>
Pyruvate kinase (PK)*	7.75E-11	3.32E-10	1.24	5.13	<b>3.18</b>
Fructose-1,6-bisphosphatase, cytosolic (cytFBPase)*	2.43E-11	1.02E-10	1.21	6.77	<b>3.99</b>
Sucrose phosphate synthase (SPS)	1.1E-10	8.80E-11	5.37	3.90	<b>4.64</b>
NAD-isocitrate dehydrogenase (NAD-IDH)	5.09E-11	7.47E-11	4.23	5.47	<b>4.85</b>
NAD-glyceraldehyde 3-phosphate dehydrogenase (NAD-GAPDH)	2.97E-09	1.83E-09	6.55	3.88	<b>5.21</b>
NADP-isocitrate dehydrogenase (NADP-IDH)	4.88E-10	6.03E-10	5.03	6.06	<b>5.54</b>
Shikimate 5-dehydrogenase (Shikimate DH)	4.51E-11	4.67E-11	6.61	5.38	<b>5.99</b>
NAD-malate dehydrogenase (NAD-MDH)*	1.06E-09	4.17E-09	2.48	9.63	<b>6.06</b>
Fructose-bisphosphate aldolase (aldolase)*	9.96E-09	3.19E-09	10.78	3.41	<b>7.10</b>
NAD-glutamate dehydrogenase (NAD-GDH)	7.39E-11	NA	7.82	NA	7.82
Phosphoglycerokinase (PGK)*	1.25E-09	4.05E-09	3.81	12.30	<b>8.06</b>
NADP-malate dehydrogenase (NADP-MDH)**	1.06E-09	1.34E-10	16.96	2.31	9.63
UDP-glucose pyrophosphorylase (UGPase)*	1.54E-10	5.15E-10	5.52	14.21	<b>9.86</b>
Fumarase (FUM)*	2.70E-10	7.40E-11	17.10	4.64	<b>10.87</b>
Fructokinase (FK)	2.94E-10	2.02E-10	14.73	7.65	<b>11.19</b>
Aconitase	9.76E-10	7.44E-10	12.89	9.99	<b>11.44</b>
Glycerate kinase (GK)**	8.59E-10	9.60E-11	25.04	3.03	14.03
Ferredoxin-dependent glutamate synthase (Fd-GOGAT)	2.61E-10	5.97E-10	8.68	19.96	<b>14.32</b>
Phosphoglucomutase (PGM)	4.57E-10	5.40E-10	18.18	17.95	<b>18.06</b>
Transketolase (TK)	2.20E-09	1.25E-09	24.20	13.67	<b>18.93</b>
Aspartate aminotransferase (AspAT)	2.17E-10	4.59E-10	16.34	30.61	<b>23.47</b>

The raw data and calculations are given in Supplementary Tables V and VII. \* and \*\* mark the enzymes that show a discrepancy bigger than 3 and 5-fold, respectively, between protein abundance calculated by the two methods. NA indicates the protein abundance column in which no peptides were quantified for the enzyme, and the  $T_p$  means could not be calculated because the translation rate was not estimated for the protein quantified and/or the protein was not quantified in the samples by proteomics analysis. Calculations were based on enzyme activities and specific activities or on quantitative proteomics. Bold type indicates values for  $T_p$  that are supported by protein quantification using both enzyme activities and emPAI values. Italics indicate enzymes for which there was a large (>4-fold) discrepancy between the protein quantification provided by these two approaches. Normal face indicates where no emPAI estimates of protein abundance were available.